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(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/323,469, filed September 17, 2001; USSN 60/355,145, filed February 8, 2002; USSN 60/369,899, filed April 4, 2002; USSN 60/323,887, filed September 20, 2001; USSN 60/355,257, filed February 8, 2002; USSN 60/325,114, filed September 25, 2001; USSN 60/340,944, filed October 29, 2001; USSN 60/350,666, filed
 10 November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer; and to the use of
 15 such expression profiles and compositions in the diagnosis, prognosis, and therapy of cancer. The invention further relates to methods for identifying and using agents and/or targets that modulate cancer.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the
 20 American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is
 25 in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over 70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases.
 30 Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis and treatment of cancer patients.

Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, e.g., reproductive organs. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell. In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting

the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-68; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-68, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-68, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-68; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanoeytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et

- al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznik (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwe, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 2B-66C provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in cancer samples, particularly sequences involved in angiogenesis, prostate cancer (including androgen independent and taxol resistant prostate cancer), breast cancer, colorectal cancer, cervical cancer, bladder cancer, lung cancer, ovarian cancer, uterine cancer, glioblastoma, Ewing sarcoma, and lung fibrosis. Tables 2A-67 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%,

98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-68; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of
5 or associated with a gene of Tables 1-68, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-68 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino
10 sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a
15 "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing,
20 including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and
25 autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a
30 bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an

animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

5 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over
10 a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes
15 sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

20 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison
25 algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

 A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150, in which a sequence may be compared to a
30 reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology

algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62

scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

- 5 One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

- 10 An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

- 20 A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

- 25 The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein

encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing
5 at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally
10 occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as
15 those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g.,
20 norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter
25 symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants
30 refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the

genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a

polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkahge, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am.

- Chem. Soc. 111:2321-2322), O-methylphosphoramidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568;
- 5 Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpoy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994)
- 10 Nucleoside and Nucleotide 13:1597-xxx; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in
- 15 Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.
- 20 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly
- 25 matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.
- 30 The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also

provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals,

electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

5 As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage
10 other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with
15 isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid,
20 protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all.
25 By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant
30 for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such

nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a skin cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under

environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although
5 annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec,
10 and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This
15 occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background.
20 Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that
25 modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation;
30 growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing

metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified

by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 1-68.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed.

5 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen
10 recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself
15 is a light chain joined to V_H -CH1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate
20 that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

25 For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH
30 Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other

organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

- 5 A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a
10 portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

- In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression
15 profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue
20 from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

- The identification of sequences that are differentially expressed in cancer versus non-
25 cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the
30 known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression

profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be
5 done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

10 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred
15 embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained
20 using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips
25 comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined
30 below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and

non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensable, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See

Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1 and 3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxeavanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxeavanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the

Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)
Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et
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Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor
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Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques
Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps,
Sequences, and Genomes Chap and Hall.

10 The present invention provides a computer database comprising a computer and
software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with
data specifying the source of the target-containing sample from which each sequence specificity
record was obtained.

 In an exemplary embodiment, at least one of the sources of target-containing sample is
15 from a control tissue sample known to be free of pathological disorders. In a variation, at least
one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another
tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate
one or more of the following parameters for each target species in a sample: (1) a unique
identification code, which can include, e.g., a target molecular structure and/or characteristic
20 separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute
and/or relative quantity of the target species present in the sample.

 The invention also provides for the storage and retrieval of a collection of target data in
a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-
optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble
25 memory devices, and other data storage devices, including CPU registers and on-CPU data
storage arrays. Typically, the target data records are stored as a bit pattern in an array of
magnetic domains on a magnetizable medium or as an array of charge states or transistor gate
states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and
a charge storage area, which may be on the transistor). In one embodiment, the invention
30 provides such storage devices, and computer systems built therewith, comprising a bit pattern
encoding a protein expression fingerprint record comprising unique identifiers for at least 10
target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFasta, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer

program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

30 Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an

intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity

and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves

be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein.

- 5 In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment.
- 10 Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

- It will also be appreciated that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through
- 15 recombinant means by adding an appropriate signal sequence.

- In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to
- 20 various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands,
- 25 wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL
- 30 mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g., moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-68, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is
5 derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known
10 (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or
15 attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example,
20 photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix
25 GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative
30 amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoefler, supra; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffer, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
 5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
 10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
 15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
 20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to
 25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
 30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Apelin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases.

5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide
15 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol.
25 Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science
30 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-68 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
- 30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

- 5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.
- 10

- 15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.
- 20

- 25 In a preferred embodiment the cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

- 30 In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of
5 other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane
10 protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The
15 effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or
20 collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents
25 are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcinn, croton, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a
30 radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local

concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

15 Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

- 5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

- 10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

- 15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

- In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutin) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

- Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidial peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

- Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

- A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-Fluorescein (FITC) or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

 Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens
15 are performed to identify agents that bind and/or modulate the biological activity of the gene product.

 In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

 Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

- 5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

- 10 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

- In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes
20 are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
25 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

- Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a
30 non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeled the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumekamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

- 5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

- The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

- Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of a polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

- Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number
5 of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999)

15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer.

Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
20 the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bordetella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

- 5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

- For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

- Methods for the use of genes as DNA vaccines are well known, and include placing a cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Mixed vessels/angiogenesis: hemangiomas, lymphangiomas, wound healing, tissue remodeling, psoriasis, ischemic heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented vitellular cysts, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids

bone marrow: Ewing sarcoma, sarcoma arising from skeletal and extraskeletal connective tissues, including the peripheral nervous system
brain: glioblastoma, oligodendroglioma, astrocytoma, anaplastic astrocytoma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pinealoblastoma, pheochromocytoma
breast: ductal carcinoma in situ, tubular carcinoma in situ
cervix: cancer of the cervix, vaginal, or vulva
colon/rectum: precancerous colonic dysplasia (e.g., neoplastic polyps [adenomas], familial adenomatous polyposis; adenocarcinoma, colorectal cancer), epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet ring cell adenocarcinoma, squamous cell carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, neuroendocrine, compound), non-epithelial tumor (e.g., lipoma, sarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease [granulomatous colitis], dysplasia), rectal cancer, cancer of the anal sphincter (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
esophagus: premalignant or premalignant conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastrointestinal carcinomas (e.g., cancers of the stomach, colon, or rectum)
fibrosis: lung fibrosis [idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonia], nonspecific idiopathic pneumonitis, chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), sclerosis, scleroderma, wound healing
head and neck: tumor of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, or larynx; hypopharynx, salivary glands, paranasal sinuses, esophageal larynx; clear cell (nonglioma) carcinoma, squamous carcinoma, chondrosarcoma, chondrocytic nerve sheath tumor, hypersphincter, adenocarcinoma, apocrine sweat gland carcinoma, basaloid carcinoma, carcinoma of the renal pelvis, ureteral carcinoma, bladder, papillary adenoma, angiosarcoma, angiosarcoma, oncocytoma, leukocytoclastic lymphoblastic leukemia/lymphoma, malignant transformation of immature, precursor T (pre-B) or precursor T (pre-T) lymphocytes, or lymphoblasts, arthritis, inflammation, wound healing
liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor-like conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder, or bile ducts
lung: cancer, small cell carcinoma (not cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis [idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis], chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
ovary: ovarian carcinoma (e.g., epithelial [serous tumors, mucinous tumors, endometrioid tumors, germ cell (e.g., teratomas, choriocarcinoma, polyembryoma), embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma], stromal carcinomas (e.g., granulosa cell tumor tumors), luteal phase tumor carcinoma, peritoneal carcinoma, leiomyosarcoma)
pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, undifferentiated large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucinous hyperplasia/cystic tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinogenesis, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostatic hyperplasia, prostatic intraepithelial neoplasia
skin: basaloid, melanoma, benign (common benign localized hyperplasia of melanocytes), nevocellular nevus (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well-differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumor, sebaceous keratosis (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinoma of the skin, lung, cervix, esophagus, uvea, breast, neck, or bladder
stomach: adenocarcinoma, squamous cell carcinoma, adenocarcinoma, carcinoid, leiomyosarcoma, gastritis [chronic atrophic, H. pylori associated], hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinoma
testicles: germ cell tumors (including seminoma, embryonal carcinoma, teratomas, choriocarcinoma, yolk sac tumors), sex cord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas, adenoma and paratubular tumors (e.g., mesothelioma, tort, or tissue sarcoma), and schwann of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
uterus: epithelial tumors (e.g., adenocarcinoma, papillary endometrial, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonneoplastic sarcoma), mixed tumors (e.g., malignant mixed müllerian tumors, adenosarcoma)

60 Tables 2C-66C list genomic positioning for Pkexs lacking Unigene IDs and accession numbers in Tables 2A-66C, respectively. For each predicted exon is listed genomic sequence
 covers used for resequencing. Nucleotide locations of each predicted exon are also listed.

Pkey:	Unique Eco probe set identifier number
ExAccnt:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
RT:	Ratio of leukemia to normal body tissue

	Pkey	Ex/In	UniGeneID	UniGene Title	R1
75	100458	S74019	HS.247979	pre-B lymphocyte gene 1	46.8
	110899	T40707	HS.270862	ESTs	20.8
	103986	F06428	HS.226351	ESTs	15.4
	101447	A21305		gb:Human alpha satellite and satellite 3	13.8
	113009	T23699	HS.7245	ESTs	12.5
80	126847	Z40778	HS.191837	ESTs	11.4
	100693	BE245294	HS.187789	S164 protein	11.1
	101550	A037324	HS.1832	neurospelin	11.0
	132711	NM.005152	HS.40292	lysyl-glycyl-restricted membrane protein	10.7

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	101304	AA001021	Hs.6565	thyroid hormone receptor interactor 8	10.4
	105667	AA767626	Hs.22030	paired box gene 5 (B-cell lineage specific)	3.1
	112727	T91029	Hs.150639	ESTs	3.0
	109786	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	8.7
5	113374	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.8
	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fls, clone KA	7.7
	103524	AK219172	Hs.68649	ESTs	7.5
	112622	AW001040	Hs.203365	ESTs	6.6
	125276	AD216439	Hs.129996	enhancer of polycomb 1	6.5
10	112167	N95951	Hs.25587	ESTs, Weakly similar to T00329 hypophyl	6.4
	116355	AA769133	Hs.88650	ESTs	5.6
	123440	AD33892	Hs.112468	ESTs	5.5
	100918	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	5.4
	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (Hs	5.4
15	109260	AW976515	Hs.131915	KIAA0863 protein	5.4
	129213	AI146484	Hs.109525	ESTs, Weakly similar to FK22_HUMAN HROQU	5.4
	129819	AA344905	Hs.203365	glyEST12657 Total host II Homo sapiens	5.4
	105498	H68279	Hs.24937	transformer-2 alpha (Hs-2 alpha)	5.1
	114640	AA447591	Hs.87359	ESTs, Highly similar to REB18_HUMAN RAS-R	5.0
20	103304	BC558101	Hs.2484	T-cell leukemia/lymphoma 1A	4.9
	113663	W87415	Hs.85295	HLA-B associated transcript-1	4.8
	115844	A373062	Hs.332938	hypothetical protein MGCS370	4.8
	120712	AF193339	Hs.102505	eukaryotic translation initiation factor	4.8
	107794	AA019255	Hs.154974	gbcza5610.1 Soares retina NK2-4HR Homo	4.7
25	135101	U82275	Hs.34498	leukocyte immunoglobulin-like receptor, 4	4.6
	128988	AI527231	Hs.13258	ESTs	4.6
	113494	T91451	Hs.88538	ESTs	4.6
	115004	AA329340	Hs.4867	mannosyl (alpha-1,3)-glycoprotein beta-	4.5
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.5
30	112226	BE8622	Hs.1206	ESTs	4.4
	105169	BE245294	Hs.180769	ST64 protein	4.4
	117048	H89732	Hs.230113	EST	4.3
	123133	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667H064 (fr	4.2
35	111594	AA412227	Hs.16131	hypothetical protein FLJ12678	4.3
	108112	AL117518	Hs.3938	KIAA0978 protein	4.2
	114414	AW152166	Hs.182113	ESTs	4.2
	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	4.2
	114895	AA756265	Hs.193857	ESTs	4.2
40	123336	AA504249	Hs.187695	ESTs	4.1
	126956	AA648885	Hs.151999	ESTs	4.1
	112908	BE281000	Hs.2630	TLS-associated serine-arginine protein 2	4.1
	116840	X09864	Hs.211563	B-cell CLL/lymphoma 7A	4.0
	109232	AW975746	Hs.168852	KIAA1702 protein	4.0
45	131724	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.0
	119772	AJ250839	Hs.58241	gene for serine/threonine protein kinase	4.0
	134463	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.0
	123362	AA177086	Hs.190865	ESTs	4.0
	103226	X75042	Hs.44313	v-ret virus retroviral endonucleosic viral	3.9
	127610	AA908857	Hs.150271	ESTs, Highly similar to unnamed protein	3.9
50	119673	AI660149	Hs.44865	lymphoid enhancer-binding factor 1	3.9
	115553	AJ275986	Hs.71414	transcription factor (SMF gene)	3.9
	131944	AA15294	Hs.204342	ESTs	3.8
	123360	AA532718	Hs.176604	ESTs	3.8
	111180	AI798651	Hs.283108	hemoglobin, gamma G	3.8
55	129425	AF077953	Hs.111323	Protein inhibitor of activated STAT X	3.8
	106434	AA252111	Hs.15200	ESTs	3.8
	119073	BE245360	Hs.279477	ESTs	3.8
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	3.7
	118325	TS1136	Hs.90489	ESTs	3.7
60	115996	AA464688	Hs.336529	ribosomal protein L44	3.7
	119530	AW014622	Hs.83478	Homo sapiens cDNA FLJ12366 fls, clone MA	3.7
	104564	AA704638	Hs.193777	ESTs	3.6
	105212	AA206334	Hs.324278	Homo sapiens mRNA; cDNA DKFZp666M063 (f	3.6
	109223	AW000714	Hs.65616	ESTs	3.6
65	112605	R79374	Hs.29652	ESTs	3.5
	105733	AA767669	Hs.10242	ESTs	3.5
	120562	BE244580	Hs.302267	hypothetical protein FLJ10330	3.5
	112268	W93909	Hs.22003	solute carrier family 6 (neurotransmitter	3.5
	127634	AK920102	Hs.337651	EST	3.5
70	115147	AA247651	Hs.36399	hypothetical protein MG22454	3.5
	115165	BE299677	Hs.105461	hypothetical protein FLJ20357	3.5
	113921	AW976530	Hs.26355	hypothetical protein FLJ22402	3.5
	115635	AA521410	Hs.41371	ESTs	3.5
	125653	AW973651	Hs.293156	ESTs, Weakly similar to T8885 serine/th	3.5
75	126527	AA504563	Hs.101047	transcription factor 3 (E2A immunoglobul	3.4
	126743	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	3.4
	117031	H88363	Hs.105676	gdyre21402.1 Morfon Fetal Cochlea Homo	3.4
	123149	AJ234179	Hs.105676	ESTs	3.4
	102581	AI077228	Hs.77255	enhancer of zeste (Drosophila) homolog 2	3.4
80	103158	BE242587	Hs.118651	homotopically expressed homeobox	3.4
	107599	AW664072	Hs.60136	ESTs	3.4
	125556	ABC33064	Hs.334806	KIAA1238 protein	3.4
	103331	AB254653	Hs.147996	protein kinase, X-linked	3.4

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119387	AI655141	Hs.107720
119340	RC2284	Hs.289436
100305	NM_004941	Hs.171572
129818	T71092	Hs.172572
133445	AC005262	Hs.73937
132111	AW508557	Hs.40137
105202	AF128542	Hs.166846
116397	BE139479	Hs.161493
118922	AW208193	Hs.91065
132444	AW971789	Hs.45719
129889	AA510532	Hs.131899
123670	AI189644	Hs.112708
116291	AW410377	Hs.41502
105289	AF020638	Hs.103000
105563	AA278907	Hs.3530
104796	BE600712	Hs.33026
111657	R07384	Hs.266957
134174	AF283770	Hs.79630
126077	MF8772	Hs.210836
133723	AA020476	Hs.75786
124647	W07701	Hs.304177
126789	AA788098	Hs.189079
131308	AW516885	Hs.8438
110343	AW136703	Hs.17268
102935	BE361850	Hs.80506
111676	AD040892	Hs.109776
127311	AA492592	Hs.322404
108930	AA131743	Hs.193352
111530	BE247797	Hs.18166
104246	AF016032	Hs.201377
126965	AA011816	Hs.269677
124724	U26916	Hs.112423
114704	AF511527	Hs.101396
134599	X95226	Hs.284153
130314	NM_014674	Hs.154332
100265	D38521	Hs.112396
115905	AF606225	Hs.111339
123433	AW450922	Hs.112476
127796	AA737068	Hs.294076
117403	H84455	Hs.40039
107111	U26848	Hs.122670
100996	AW657300	Hs.291442
106358	M51933	Hs.1634
132065	AA309392	Hs.181195
130303	BE245294	Hs.180789
104596	AF607804	Hs.15423
112197	NM_003955	Hs.6537
132809	AF038144	Hs.5734
100877	X30621	Hs.27973
108147	AF72094	Hs.289221
133674	AW851121	Hs.75407
129001	AA443323	Hs.107812
131920	BE002320	Hs.287864
134709	NM_006290	Hs.211600
113877	AD30009	Hs.778657
115839	BE300269	Hs.28935
129969	NS7818	Hs.28935
129565	AW530067	Hs.103315
105711	BE391628	Hs.16244
129294	AF129440	Hs.184542
104518	H20816	Hs.112423
107796	AA058648	Hs.60797
106321	AB037742	Hs.24336
127092	AK21012	Hs.107963
131916	AA025976	Hs.34569
124971	T23800	Hs.151001
129426	AA259095	Hs.111364
118348	AW068686	Hs.10502
113219	TS96257	Hs.289326
131720	768128	Hs.3109
109593	AW196801	Hs.6665
133559	AF043722	Hs.194951
131889	AB11274	Hs.30956
117457	N29682	Hs.440071
121073	H48159	Hs.112184
125069	H81306	Hs.19446
118456	A3281911	Hs.334859
124271	AW293223	Hs.8928
112389	AW986243	Hs.4243
118886	AW062629	Hs.52081
125243	BE508452	Hs.51091
124494	NS14831	Hs.271381
104799	AA02903	Hs.271381

ESTs, Weakly similar to A54295 interor	3.4
ESTs, Moderately similar to PC4259 feni	3.4
DEAD(H) [asp-Glu-Ala-aspartic] box polypep	3.4
hypothetical protein FLJ23093	3.3
guanine nucleotide binding protein (G pr	3.3
anaplasia-promoting complex 1; melotic ch	3.3
polymersase (DNA directed), epsilon	3.3
ESTs	3.3
hypothetical protein DKFZp761B2423	3.2
KIAA0823 protein	3.2
ESTs, Weakly similar to T00370 hypothet	3.2
ESTs, Moderately similar to ZN81_HUMAN Z	3.2
hypothetical protein FLJ121276	3.2
KIAA0831 protein	3.2
TL5-associated serine-arginine protein	3.2
hypothetical protein PP2447	3.2
ESTs, Weakly similar to ALU1_HUMAN ALU	3.2
CD79A antigen (immunoglobulin-associated	3.2
ESTs	3.1
hypothetical protein	3.1
Homo sapiens clone FLB8503 PRO2286 mRNA,	3.1
ESTs	3.1
ESTs	3.1
ESTs	3.1
small nuclear ribonucleoprotein polypept	3.1
KIAA1449 protein	3.1
hypothetical protein MGCA175	3.1
ESTs	3.1
KIAA0670 protein	3.1
lysosomal aminase-like 1	3.1
ESTs	3.1
Homo sapiens mRNA; cDNA DKFZp586i1420 (f	3.1
hypothetical protein MGCI1352	3.1
Fancos anemia, complementation group A	3.1
KIAA0212 gene product	3.0
KIAA0077 protein	3.0
ESTs	3.0
ESTs	3.0
ESTs	3.0
chromodomain helicase DNA binding protei	3.0
ESTs, Weakly similar to CS50683 oligodent	3.0
cell division cycle 25A	3.0
DnaJ (Hsp40) homolog, subfamily B, membe	2.9
S164 protein	2.9
hypothetical protein HDCA004P	2.9
ESTs	2.9
meningioma expressed antigen 5 (hyaluron	2.9
KIAA0674 protein	2.9
Homo sapiens cDNA FLJ13741 ff, clone PL	2.9
Homo sapiens cDNA: FLJ22139 ff, clone H	2.9
9PC2 protein	2.9
Homo sapiens cDNA FLJ14030 ff, clone HE	2.9
tumor necrosis factor, alpha-induced pro	2.8
PRCO470 protein	2.8
transcription-like enhancer of split 1, hom	2.8
gbcyrs607.a1 Soares fetal liver spiken	2.8
trichothiodie repeat containing 1	2.8
mitotic spindle coiled-coil related prot	2.8
C2-127 protein	2.8
Homo sapiens mRNA; cDNA DKFZp586i1420 (f	2.7
ESTs	2.7
KIAA1321 protein	2.7
ESTs	2.7
ESTs	2.7
hypothetical protein FLJ14728	2.7
ESTs, Weakly similar to ubiquitously TPR m	2.7
ESTs, Moderately similar to ALU5_HUMAN A	2.7
ESTs, Moderately similar to ALU5_HUMAN A	2.7
Rho GTPase activating protein 4	2.7
thyroid hormone receptor interactor 8	2.7
RAS guanyl releasing protein 2 (calcium	2.7
transcription factor like 5 (basic helix	2.7
ESTs, Weakly similar to ALU5_HUMAN ALU	2.7
DKFZP586U0619 protein	2.7
ESTs	2.7
KIAA1814 protein	2.7
hypothetical protein FLJ20391	2.7
hypothetical protein FLJ12650	2.7
KIAA0867 protein	2.7
protein regulator of cytokinesis 1	2.7
ESTs, Weakly similar to S80222 hypothet	2.7
gltcys508.t1 Soares fetal_tesst_Nb4119W	2.7

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	120510	A796395	Hs.111377	ESTs	2.6
	129781	AA50690	Hs.124707	ESTs	2.6
	122686	AA456112	Hs.39410	ESTs	2.6
5	105995	AB023139	Hs.37892	KIAA0922 protein	2.6
	105502	BC464015	Hs.238956	ESTs	2.6
	128671	A1895045	Hs.211586	phosphoinositide-3-kinase, regulatory s	2.6
	107059	SC514410	Hs.23044	RAV51 (S. coronavirus) homolog (E coli Ra	2.6
	125602	T10077	Hs.13453	hypothetical protein FLJ14753	2.6
10	129703	BE386665	Hs.173999	Homo sapiens, clone IMAGE:3457003, mRNA	2.6
	111219	N68836	Hs.19247	ESTs, Moderately similar to ALOC_HUMAN	2.6
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.6
	125525	AC038654	Hs.180709	S104 protein	2.6
	111189	N67603	Hs.272130	ESTs, Weakly similar to S66824 reverse	2.6
15	113145	BE151985	Hs.5722	hypothetical protein FLJ23316	2.6
	125562	AI494372	Hs.39898	hypothetical protein FLJ23058	2.6
	102263	U29171	Hs.73552	casein kinase 1, delta	2.6
	118835	AA555246	Hs.50852	ESTs	2.6
	103141	X66113	Hs.75584	polymyosin-like autoantigen 2 (2.6
	109596	RA0515	Hs.21248	ESTs	2.6
20	127262	AA528125	Hs.65339	gbc871a09.s1 NCL_CGAP_Ov2 Homo sapiens	2.6
	129620	D73338	Hs.238720	CCNA-NOT transcription complex, subunit	2.6
	125905	AI679538	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.6
	123255	AA830036	Hs.105273	ESTs	2.6
25	133150	N54968	Hs.65339	hypothetical protein MGCI1051	2.6
	109638	AW577447	Hs.119120	E3 ubiquitin ligase SMURF1	2.6
	119896	AA731836	Hs.137319	ESTs	2.6
	134770	M89587	Hs.89575	CD79E antigen (NOMANO) associated	2.6
	119403	AL117554	Hs.119908	nucleolar protein (NPM)NCP58	2.6
30	125563	AF115564	Hs.71289	transcriptional regulator protein	2.6
	111719	AB559005	Hs.175822	ESTs	2.6
	103982	AA218558	Hs.7905	scoring neurin 9	2.6
	125032	T74884	Hs.25703	gbcyc28002.s1 Stratagene liver (937224)	2.5
	131426	AL122545	Hs.25703	CCNA-NOT transcription complex, subunit	2.5
35	119338	AF170805	Hs.34566	neuronal glycoprotein first binding prot	2.5
	102450	U48251	Hs.75871	protein kinase C binding protein 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	126339	AA152106	Hs.4859	cyclin I, alpha-6a	2.5
	118967	AB598570	Hs.216756	ESTs	2.5
40	123110	AA488255	Hs.193510	EST	2.5
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.5
	113247	T53856	Hs.193430	ESTs, Weakly similar to 2109250A B cell	2.5
	122624	AA441295	Hs.139433	ESTs	2.5
	106657	AB054339	Hs.33476	hypothetical protein FLJ11937	2.5
45	126127	N55426	Hs.25119	giczb60409.s1 Soares_senescent_fibroblasts	2.5
	111836	R58394	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	2.5
	121470	AA559558	Hs.324751	ESTs	2.5
	120132	W57554	Hs.425919	ESTs	2.5
	107731	AA016086	Hs.272105	ESTs, Weakly similar to I38022 hypothel	2.5
50	118122	AI186671	Hs.48008	ESTs	2.5
	106589	AK000933	Hs.28661	Homo sapiens cDNA FLJ110071.f1, clone HE	2.5
	122948	AB57162	Hs.252688	ESTs	2.5
	115652	BE093689	Hs.38179	hypothetical protein FLJ23458	2.5
	103075	NM_001004	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
55	131019	W26814	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.5
	100512	D73317	Hs.78915	G4-binding protein transcription factor,	2.5
	105393	AF161750	Hs.256583	interleukin enhancer binding factor 3, 9	2.5
	100071	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.5
	106890	AA489245	Hs.88500	mitogen-activated protein kinase B like	2.5
60	104276	AF996525	Hs.284288	hspc256 protein	2.5
	113283	T66813	Hs.12947	EST	2.5
	119078	N64521	Hs.47790	EST	2.5
	120796	A247356	Hs.96820	ESTs	2.5
	106265	AA412176	Hs.236463	Homo sapiens mRNA; cDNA DKFZp5960521.f	2.5
65	102507	U52154	Hs.153044	potassium inwardly-rectifying channel, s	2.5
	106508	AB057375	Hs.30348	ESTs	2.5
	104568	AW629981	Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.5
	103698	AA001021	Hs.5585	thyroid hormone receptor interactor 8	2.5
	113947	W94768	Hs.23413	gbrzh53003.s1 Soares_fetal_liver_spleen_	2.5
70	132112	AL021938	Hs.40154	junomeij (mouse) homolog	2.5
	129052	BC275031	Hs.158210	hypothetical protein MG2555	2.4
	117265	AA451995	Hs.43005	RAE9-like protein	2.4
	107834	AA253162	Hs.40838	ESTs	2.4
75	113113	T47910	Hs.252716	gbyb1081.1.s1 Stratagene fetal spleen (9	2.4
	133726	AB031188	Hs.187534	crystallin-binding protein-related prota	2.4
	120548	AA280366	Hs.58132	ESTs	2.4
	121545	AA412442	Hs.58132	ESTs	2.4
	131136	AB033369	Hs.23413	KIAA1273 protein	2.4
	126589	AW527809	Hs.181908	Homo sapiens cytomegalovirus partial fus	2.4
80	115475	AA933085	Hs.40193	hypothetical protein KIAA1259	2.4
	103760	AA642973	Hs.183842	ubiquitin B	2.4
	127889	AI147408	Hs.144941	ESTs	2.4
	124457	AI000600	Hs.266175	phosphoprotein associated with GEMs	2.4
	113271	AF143885	Hs.18190	EST	2.4

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	129079	AV000157	Hs.108502	hypothetical protein FLJ20150	2.4
	123630	AA608705	Hs.187772	ESTs	2.4
	123592	AA605331	Hs.112637	ESTs	2.4
	119474	RS0752	Hs.23856	hypothetical protein MGC5297	2.4
5	116728	F13687	Hs.227976	EST	2.4
	101759	M80244	Hs.184601	solute carrier family 7 (cationic amino	2.4
	131686	NM_012296	Hs.335687	GRB2-associated binding protein 2	2.4
	127841	AY136598	Hs.126246	ESTs	2.4
	102737	RS1790	Hs.239483	Human clone 23933 mRNA sequence	2.4
10	128673	D38552	Hs.1191	KIA0073 protein	2.4
	133065	BE046480	Hs.180677	zinc finger protein 162	2.4
	124540	N63332	Hs.16875	glycyl-tRNA11 Metion Fatal Cochlea Homo	2.4
	113609	TS3263	Hs.16875	ESTs, Weakly similar to Z36550 retrov	2.4
15	128826	Z40313	Hs.106330	Human sapiens clone IMAGE:23371, mRNA seq	2.4
	129055	AV068534	Hs.279583	CGI-81 protein	2.4
	134052	AA218558	Hs.7505	scoring nestin 9	2.4
	132117	BE262438	Hs.44592	beta-1.4 mannosyltransferase	2.4
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.4
20	128468	T23625	Hs.150580	putative translation initiation factor	2.4
	127407	AV089514	Hs.279681	heterogeneous nuclear ribonucleoprotein	2.4
	123242	AW162758	Hs.45202	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.4
	113518	AV067788	Hs.323554	postmitotic segregation increased 24k	2.4
	100330	AW410576	Hs.77152	minichromosome maintenance deficient (S,	2.4
25	116046	BE395293	Hs.54451	hypothetical protein FLJ20297	2.4
	123910	AA421262	Hs.179923	ESTs, Weakly similar to S66557 alpha-1C-	2.4
	101651	A_037111	Hs.75841	galactose-1-phosphate uridylyltransferase	2.4
	100114	X02308	Hs.82962	thymidylate synthetase	2.4
	125038	AA812234	Hs.270134	hypothetical protein FLJ20280	2.4
30	135151	X18686	Hs.301086	cytochrome P450, subfamily 10 (dehydro	2.4
	123258	AA489929	Hs.105274	ESTs, Weakly similar to RMR3_HUMAN REGUL	2.4
	132380	AV073665	Hs.46853	ESTs	2.4
	114046	BE018658	Hs.141003	Human sapiens cDNA: FLJ21651 fls, clone C	2.3
	133452	BE391579	Hs.75087	Flag-activated serine/threonine kinase	2.3
	134510	D53475	Hs.115907	diphosphoryl kinase, delta (150kD)	2.3
35	105734	AV52767	Hs.10888	hypothetical protein FLJ21705	2.3
	101086	AA382524	Hs.280959	histatin 1	2.3
	118345	N63786	Hs.54145	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	101194	L20071	Hs.188	phosphotransferase 1b, cAMP-specific (dn	2.3
	130398	AL009996	Hs.16411	hypothetical protein LOC57187	2.3
40	101875	BE241753	Hs.74592	special AT-rich sequence binding protein	2.3
	118751	N74210	Hs.50454	ESTs	2.3
	125174	W51835	Hs.231082	EST	2.3
	105596	AA142604	Hs.5344	adaptor-related protein complex 1, gamma	2.3
	104624	AA353125	Hs.194721	ESTs	2.3
45	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	2.3
	105014	AA121123	Hs.265267	ESTs, Weakly similar to AF161361.1 HSPC	2.3
	123423	AA198484	Hs.15068	glucosylated alpha-1,3-Galactosyl transferase	2.3
	129531	H03721	Hs.2953	ribosomal protein S15a	2.3
50	108876	AV73860	Hs.191453	ESTs	2.3
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	2.3
	132232	AV52273	Hs.42640	ESTs	2.3
	132564	AV74461	Hs.54542	ESTs	2.3
	105991	AA215701	Hs.186541	ESTs, Weakly similar to 08022 hypothel	2.3
55	100253	D38024	Hs.157425	double homeobox, 2	2.3
	105574	AA045281	Hs.266175	phosphoprotein associated with GEMs	2.3
	100780	BE561958	Hs.302033	immunoglobulin heavy constant mu	2.3
	134964	AA083516	Hs.272891	hippocatalin-like protein 4	2.3
	132786	BE083422	Hs.55851	hypothetical protein MGC2668	2.3
60	104952	AV074698	Hs.74316	desmosoplakin (DPL, DPL)	2.3
	115127	AA198035	Hs.12248	ESTs	2.3
	104857	AV029502	Hs.150568	ESTs, Moderately similar to S66557 alpha	2.3
	107592	AA684264	Hs.60049	ESTs	2.3
	113378	T80738	Hs.14757	ESTs	2.3
65	129228	U40714	Hs.235307	transyl-RNA synthetase	2.3
	106389	AA400089	Hs.308676	Human sapiens cDNA FLJ14302 fls, clone PL	2.3
	130734	AW137091	Hs.18624	KUAA1052 protein	2.3
	125728	AV954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.3
	113697	TS9183	Hs.17992	Human sapiens mRNA: cDNA DKFZp454J1726 (f	2.3
70	107194	AU076640	Hs.15243	nucleolar protein 1 (20kD)	2.3
	134267	AV17458	Hs.195209	RAE1 (RNA export 1, S.pombe) homolog	2.3
	106777	R42755	Hs.23096	ESTs	2.3
	115306	AA280288	Hs.88746	ESTs	2.3
	133363	AB86286	Hs.88746	ESTs, Weakly similar to B36296 protine-r	2.3
75	125535	AA357572	Hs.163965	chitinase (chitinase) 1	2.3
	121500	AA412163	Hs.164785	ESTs	2.3
	123808	AA620552	Hs.164785	gbr:58g11.1 Strabagene lung carcinoma	2.3
	105700	AV930830	Hs.35254	hypothetical protein FLB6421	2.3
80	120820	AA347417	Hs.36869	EST	2.3
	129721	AAW03911	Hs.266175	phosphoprotein associated with GEMs	2.3
	107711	V96141	Hs.220687	ESTs	2.3
	102564	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr	2.3
	131868	AVW40286	Hs.33352	zinc finger protein 151 (zf14-07)	2.3
	122333	AA425872	Hs.98977	ESTs, Moderately similar to 134561 hypot	2.3

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	118665	AA736405	HL54530	ESTs	2.3
	128952	AL034103	HL0735	RaP2 interacting protein 8	2.3
	133772	BE379867	HL76038	isopentenyl-diphosphate delta isomerase	2.3
5	111795	AI435437	HL24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.3
	103437	AV65698	HL184211	peptidase (mitochondrial processing) bet	2.3
	123000	AA480227	HL142559	ESTs, Weakly similar to D80022 hypophel	2.3
	125466	R08224	HL180461	ESTs	2.3
	100892	BE245294	HL180789	S164 protein	2.3
10	121613	AA416879	HL193195	ESTs, Weakly similar to 2109260A B cell	2.3
	133665	AL036883	HL75450	delta sleep inducing peptide, immunoneac	2.2
	123249	W04066	HL171637	hypothetical protein MG22626	2.2
	126103	H05652	HL40730	ESTs	2.2
	125590	R23858	HL143375	Homo sapiens, clone IMAGE:3840037, mRNA,	2.2
	104960	AA598677	HL05928	hypothetical protein FLJ20291	2.2
15	113841	AA531016	HL22399	hypothetical protein FLJ14524	2.2
	112540	R59751	HL22399	glycyl-tRNA11 Scores placenta NB2HP Homo	2.2
	105322	T87179	HL16346	ESTs, Weakly similar to SS7447 HPFB11-7	2.2
	112003	AW578731	HL301824	hypothetical protein PRO1331	2.2
20	134733	N87533	HL69421	CBF1 interacting corepressor	2.2
	114520	AA542874	HL22399	glucuronidase 1, NCI_CGAP_Lym3 Homo sapiens	2.2
	123451	AT932111	HL165372	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	130850	AB040922	HL20237	DKFZP566C134 protein	2.2
	105561	AA262881	HL328636	ESTs, Weakly similar to alternatively s	2.2
25	125597	HA1684	HL22399	glycyl-tRNA11 Scores adult brain K205H1B5	2.2
	130982	BE513030	HL279681	heterogeneous nuclear ribonucleoprotein	2.2
	122682	AA984531	HL159263	ESTs	2.2
	124250	AA300296	HL323875	EST, Weakly similar to 2109260A B cell	2.2
	131392	AA235153	HL20320	TRABD protein	2.2
	128945	AW903976	HL10540	benzimidazole-2-induced gene	2.2
30	130453	UB0735	HL173654	PAX transcription activation domain inte	2.2
	126873	W46653	HL251928	nuclear pore complex interacting protein	2.2
	103156	BE259039	HL129953	Ewing sarcoma breakpoint region 1	2.2
	103163	AB077016	HL32335	heretin 4	2.2
	105622	BE440157	HL65884	ESTs	2.2
35	131163	AA068524	HL23754	ESTs	2.2
	115292	AA279566	HL88672	ESTs	2.2
	122591	AI185219	HL95311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.2
	124977	R04915	HL190452	KIAA0366 gene product	2.2
40	103319	X53492	HL82359	tumor necrosis factor receptor superfam	2.2
	128932	HA0150	HL184884	KIAA0167 gene product	2.2
	100070	D79889	HL107708	ESTs	2.2
	128928	AA330993	HL134535	ESTs	2.2
	108451	AA079195	HL77500	glucuronidase 1, NCI_CGAP_Lym3 Homo s	2.2
45	133910	AW635281	HL77500	ubiquitin specific protease 4 (pro-onc	2.2
	106288	AD037742	HL24336	KIAA1321 protein	2.2
	134125	NM_014781	HL50421	KIAA0303 gene product	2.2
	101373	X00264	HL12177	adenosine deaminase	2.2
	112276	R53442	HL26038	ESTs, Weakly similar to D80022 hypophel	2.2
	106251	R12607	HL35101	proline-rich Glu (G-carboxyglutamic acid	2.2
50	125394	BE178502	HL173772	ESTs, Weakly similar to I78865 serine/th	2.2
	100392	X94563	HL173772	glb1Lapins diblock gene exon 1 & 2	2.2
	112653	T02843	HL173772	glb1Lapins diblock gene exon 1 & 2	2.2
	133195	AA434760	HL279949	KIAA1007 protein	2.2
	130060	AA000187	HL259842	protein kinase, AMP-activated, gamma 2 n	2.2
55	131351	AE2652	HL26280	collagen, type XVI, alpha 1	2.2
	134104	LS3253	HL79107	mitogen activated protein kinase 14	2.2
	105225	AA211777	HL145696	glbcs57002.1 Striatogene muscle 937209 H	2.2
	131320	AA505691	HL145696	splitting factor (CC1.3)	2.2
60	114419	A249013	HL105532	ESTs, Weakly similar to D86888 reverse 1	2.2
	100824	BE541733	HL180877	H3 histone, family 3B (H3.3)	2.2
	134026	AF035119	HL5700	deleted in liver cancer 1	2.2
	126524	Z54555	HL182417	heterogeneous nuclear ribonucleoprotein	2.2
	115556	AL031778	HL797	nuclear transcription factor Y, alpha	2.2
	111688	R38844	HL183475	Homo sapiens clone Z5001 mRNA sequence	2.2
65	100415	D86970	HL75822	TCFEB1-induced anti-apoptotic factor 1	2.2
	103898	AA248884	HL180403	gbk3517.seq.F Human fetal heart, Lambda	2.2
	129301	AE318111	HL180403	STRN protein	2.2
	127251	AA366428	HL26538	ESTs	2.2
70	100613	X62079	HL101047	transcription factor 3 (E2A Immunoglobul	2.2
	116332	AA491208	HL62620	chromosome 6 open reading frame 1	2.2
	128987	AW979134	HL10700	hypothetical protein	2.2
	111777	AA000100	HL41690	desmocollin 3	2.2
	128164	AW579069	HL102267	CNOT 3-like gonadotropin inducible trans	2.2
75	125935	AW288113	HL92905	SON DNA binding protein	2.2
	126984	AV656017	HL184325	CGI-76 protein	2.2
	114461	AA531167	HL126705	ESTs	2.2
	121387	AA458564	HL27774	glb-zn00001.1 Scores, testis, N/T Homo sap	2.2
	100339	AA314554	HL27774	ESTs, Highly similar to AF161346 1 HSPC0	2.2
80	128179	AW969025	HL109154	ESTs	2.2
	106711	BE390125	HL143187	hypothetical protein	2.2
	106428	HE1005	HL37802	ESTs	2.2
	123949	AA421665	HL209957	EST	2.2
	127256	AT738610	HL267967	ESTs, Moderately similar to ALUR_HUMAN	2.2

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104868	AF173867	Hs.28906	glucocorticoid modulatory element bindin	2,2
132984	BE539199	Hs.62112	zinc finger protein 207	2,2
135883	AB032977	Hs.6268	KIAA1151 protein	2,2
130557	HE1825	Hs.269911	ESTs, Weakly similar to S65824 reverse	2,2
119232	AI655226	Hs.117659	ESTs, Weakly similar to T46491 hypophel	2,2
105715	BE521800	Hs.29444	putative small membrane protein NID67	2,2
124691	R65335	Hs.110153	ESTs	2,2
113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2,2
117040	AW970600	Hs.303261	ESTs	2,2
128767	M85169	Hs.1050	pleckstrin homology, Sec7 and collectin	2,2
120602	AA080816	Hs.109302	ESTs	2,2
107162	AS111782	Hs.20013	GAP-interacting protein p29	2,2
107357	U63973	Hs.103501	rhodopsin kinase	2,2
125499	H10543		gl-y-m04c06v1 Soares infant brain INB H	2,1
126872	AW450979		gl-y-H-813-cls-a-124-Uls1 NCL_OGAP_Su	2,1
113233	TE1965	Hs.279967	CGI-59 protein	2,1
128367	AW611291	Hs.150742	ESTs	2,1
127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	2,1
114021	AW236215	Hs.16145	ESTs	2,1
104455	AL110261	Hs.157211	DKFZP6869621 protein	2,1
134066	AW402389	Hs.520	modular recognition factor 1	2,1
129765	M89933	Hs.1238	amelogenin (Y chromosome)	2,1
133461	NM_000762	Hs.334345	cytochrome P450, subfamily 1A (phenobar	2,1
109309	AA032650	Hs.6217	Homo sapiens cDNA FLJ12521 fs, clone NT	2,1
129794	AF161399	Hs.23259	hypothetical protein FLJ15433	2,1
134869	AL157618	Hs.90421	PRO2463 protein	2,1
110256	HE3947	Hs.237955	RAB7, member RAS oncogene family	2,1
128817	BE396776	Hs.198640	ankyrin, progressive (mouse) homolog	2,1
120916	NM_000734	Hs.37087	CD32 antigen, zeta polypeptide (IT3 com	2,1
134354	M03091	Hs.81217	interleukin 15 (lymphocyte chemotracta	2,1
106048	AW883367	Hs.301732	hypothetical protein MGC5306	2,1
128352	AW137413	Hs.169942	ESTs	2,1
110348	AA281682	Hs.262100	ESTs	2,1
123474	AA592029		gl-y-gp4b1.1.s.1 Jia bone marrow stroma Hom	2,1
107121	AB015427	Hs.250493	zinc finger protein 219	2,1
118609	N22617	Hs.43228	Homo sapiens cDNA FLJ11835 fs, clone HE	2,1
135051	A1271241	Hs.83484	SRY (sex determining region Y)-box 4	2,1
109442	AW236134	Hs.60999	ESTs, Weakly similar to S65657 alpha-1C-	2,1
126661	AA008935	Hs.269521	ESTs	2,1
129270	AA357185	Hs.109918	ras homolog gene family, member H	2,1
126668	AW615396	Hs.106613	ESTs	2,1
132807	AF226697	Hs.56553	CTP synthase I'	2,1
124455	AW297702	Hs.102915	ESTs	2,1
128954	AA346839	Hs.209100	DKFZP434C171 protein	2,1
132885	AL045579	Hs.62113	KIAA0717 protein	2,1
119247	BE269047	Hs.65234	hypothetical protein FLJ29595	2,1
106386	M66357	Hs.234425	Homo sapiens cDNA FLJ14782 fs, clone NT	2,1
131009	AF158802	Hs.22142	cytochrome b5 reductase b5R2	2,1
112170	BE245743	Hs.288529	hypothetical protein FLJ22635	2,1
130755	BE293620	Hs.18910	prostate cancer overexpressed gene 1	2,1
117357	N24529		glycyrrh12.s.1 Soares melanocyte 2RBHM Ho	2,1
105133	N24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2,1
127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2,1
101183	AA442324	Hs.795	H2A histone family, member O	2,1
100420	D69693	Hs.118993	Melanoma associated gene	2,1
128279	AA001696	Hs.13109	Ran binding protein 11	2,1
122311	NM_014913	Hs.131915	KIAA0683 protein	2,1
130666	R85474	Hs.16073	ESTs	2,1
113817	AB74223	Hs.293560	ESTs	2,1
115910	AA426026	Hs.187615	ESTs	2,1
108743	AG80150	Hs.71074	ESTs	2,1
129255	AG61727	Hs.109804	H1 histone family, member X	2,1
120766	AA784879	Hs.12570	tubulin-specific chaperone d	2,1
128693	AA252060	Hs.26320	TRAF4 protein	2,1
116254	AA278024	Hs.26618	ESTs, Weakly similar to S65557 alpha-1C	2,1
105955	BE279383	Hs.26557	plakophilin 3	2,1
120999	AG72375	Hs.29626	hypothetical brain protein my038	2,1
125636	H12382	Hs.25119	ESTs, Weakly similar to YE04_YEAST HYPOT	2,1
117997	N52890	Hs.47420	ESTs	2,1
104333	CG2418	Hs.29626	hypothetical brain protein my038	2,1
134315	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	2,1
135332	AK933883	Hs.89968	hypothetical protein FLJ23058	2,1
107279	S57296	Hs.323910	verteb42 ovian erythroblastic leukemia	2,1
133021	W03512	Hs.5479	hypothetical protein MGC113272	2,1
112553	AW961220	Hs.29282	mitogen-activated protein kinase kinase	2,1
121782	AA452957	Hs.334698	Homo sapiens, clone MGC15203, mRNA, com	2,1
111567	P12628	Hs.334786	hypothetical protein MGC16040	2,1
133912	H42679	Hs.77522	major histocompatibility complex, class	2,1
134076	AF086215		gl-yHone sapiens, full length insert cDNA	2,1
116665	F04405		gl-yHSC25B082 normalized infant brain cDN	2,1
133562	M69721	Hs.74870	H2.0 (Drosophila) the homeo box 1	2,1
129092	D56345	Hs.63625	poWQ-binding protein 2	2,1
106869	AW975362	Hs.292679	ESTs	2,1

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	124864	AW970168	Hs.185706	ESTs	2.0
	118485	AA530515	Hs.291049	ESTs	2.0
	116715	AL111440	Hs.170263	tumor protein p53-binding protein, 1	2.0
	130743	ALD49266	Hs.18724	Home sapiens mRNA: cDNA DKF2p664f093 (r	2.0
5	118677	AW971146	Hs.293187	ESTs	2.0
	100020				2.0
	123252	AW987716	Hs.287586	Home sapiens cDNA FLJ13648 fs, clone PL	2.0
	134877	AL049683	Hs.306121	leukocyte receptor cluster (LRC) encoded	2.0
	115334	AA702972	Hs.65300	ESTs	2.0
10	111790	AW769883	Hs.6734	ESTs, Weakly similar to S26650 DNA-bind	2.0
	129101	NM_013403	Hs.10866	zincfin	2.0
	152676	NQ2589	Hs.281038	ESTs, Weakly similar to U39022 hypophat	2.0
	111018	AI287912	Hs.3528	mitogen-activated protein kinase kinase	2.0
15	105933	AF078544	Hs.194686	solute carrier family 25 (mitochondrial	2.0
	110679	AA004798	Hs.108311	ESTs, Weakly similar to U00351 hypophat	2.0
	123961	AA320594	Hs.55952	ESTs	2.0
	134303	AW973652	Hs.283106	ESTs	2.0
	115026	AA251972	Hs.188718	ESTs	2.0
	128660	AA011597	Hs.177398	ESTs	2.0
20	134554	AI184316	Hs.85273	retinoblastoma-binding protein 6	2.0
	105992	AI198769	Hs.25370	ESTs	2.0
	123636	AA609263		gbca13cd98.1 Soares_testis_NHT Home sap	2.0
	132610	AA160511	Hs.5326	amino acid system N transporter 2; porcu	2.0
	122652	AA546441		gtcccd6005.1 Soares_NbHMPu_S1 Home sapi	2.0
25	120467	AA292562	Hs.187628	ESTs	2.0
	126046	AA804957	Hs.119840	ESTs	2.0
	128179	AA929689	Hs.127116	ESTs	2.0
	123349	AB033042	Hs.20679	cofactor required for Sp1 transcriptions	2.0
	136228	AK01674	Hs.22630	cofactor required for Sp1 transcriptions	2.0
30	128532	AA628900	Hs.117587	ESTs	2.0
	133317	AC005268	Hs.70830	U6 snRNA-associated Sm-like protein LSm7	2.0
	128896	AW978168	Hs.5912	F-box only protein 7	2.0
	127447	AA388192	Hs.193482	Home sapiens cDNA FLJ11963 fs, clone HE	2.0
	133149	AA370345	Hs.6507	A2N1 up-regulated	2.0
35	120468	AW967675	Hs.96487	ESTs, Highly similar to S95228 ribosomal	2.0
	106487	AI697340	Hs.135285	Home sapiens clone FLB8436 PRO2277 mRNA,	2.0
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.0
	126892	AA382664	Hs.143974	ESTs	2.0
	100944	L07518	Hs.150933	metin 5, gastric	2.0
40	118897	AW967413	Hs.83568	transducin-like enhancer of split 4, hom	2.0
	126304	R07785		gby1f5c06.1 Soares fetal liver spleen	2.0
	133905	BC386338	Hs.77462	heterogeneous nuclear ribonucleoprotein	2.0
	113408	NM_020908	Hs.115495	mannosidase, beta A, lysosomal	2.0
	119513	AI126951	Hs.173946	hypophthal protein FLJ10485	2.0
45	107468	AA740979	Hs.81389	ESTs	2.0
	100554	M95923		gb1human 12-ipoxygenase mRNA, partial c	2.0
	120476	NM_014802	Hs.104305	death effector filament-forming Ced-4-l	2.0
	117160	AA322302	Hs.83302	PCTAIRE protein kinase 2	2.0
50	115582	AW245047	Hs.136164	cutaneous T-cell lymphoma-associated in	2.0
	126536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU 5	2.0
	100842	U05597		gb1human axon exchanger 3 cardiac iso	2.0
	133207	AB51173	Hs.67688	ESTs	2.0
	122053	AI637498	Hs.98745	ESTs	2.0
55	121080	AA617830	Hs.28310	ESTs	2.0
	113316	T03018	Hs.265881	ESTs	2.0
	113137	AW952129	Hs.290225	ESTs, Weakly similar to FLJED-1 (H)sapie	1.9
	100416	AW050506	Hs.196914	minor histocompatibility antigen HA-1	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	103872	AB166078	Hs.21756	translation factor uaf1 homolog	1.9
60	132439	AK001942	Hs.4363	hypophthal protein DKF2p66A1524	1.9
	125082	H81188	Hs.295671	ESTs	1.9
	124677	R01073		gbye64c03.1 Soares fetal liver spleen	1.9
	123385	BE149855	Hs.17767	KIAA1554 protein	1.9
65	103738	X65965		gb1sapiens SCD-2 gene for manganese su	1.9
	104867	AA278888	Hs.225879	hypophthal protein similar to small G	1.9
	128668	AI754363	Hs.103422	Home sapiens cDNA FLJ14630 fs, clone NT	1.9
	125826	M20681	Hs.7594	solute carrier family 2 (facilitated glu	1.9
	113701	T97301	Hs.18026	ESTs	1.9
	134147	M58603	Hs.83428	nuclear factor of kappa light polypeptid	1.9
70	123895	AW467000	Hs.106685	ESTs	1.9
	112719	AI200957	Hs.19301	Home sapiens, Similar to Nedd4-like ubi	1.9
	102552	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	1.9
	131186	Z70200	Hs.246112	KIAA0785 protein	1.9
	133547	BE297558	Hs.71475	acid cluster protein 33	1.9
75	133388	AA254631	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
	112265	A052534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.9
	100336	N76101	Hs.8127	KIAA0164 gene product	1.9
	113479	AI022133	Hs.107139	ESTs	1.9
	135231	BE613615	Hs.74280	hypophthal protein FLJ22237	1.9
80	123783	AA610112		gbca1f9g05.1 Soares_testis_Nb2HFS_	1.9
	113316	NM_014007	Hs.127649	KIAA0414 protein	1.9
	132761	AB15537	Hs.323620	nuclear RNA export factor 1	1.9
	128536	AW955055	Hs.101150	Home sapiens, clone IMAGE4054156, mRNA,	1.9

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	126693	AW158478	Ha.181297	ESTs	1.9
	139373	AA305729	Ha.19272	amino acid transporter system A1	1.9
	105142	AW51428	Ha.77556	hypothetical protein FLJ22405	1.9
5	129793	AW207000	Ha.126857	Homo sapiens cDNA FLJ12936 fs, clone NT	1.9
	105888	AW970672	Ha.9247	protein kinase, cAMP-activated, alpha 1 c	1.9
	101692	AB25838	Ha.75206	protein phosphatase 3 (formerly 2B), cat	1.9
	125511	AJ271379	Ha.76194	ribosomal protein S5	1.9
	126751	AI578326	Ha.77256	enhancer of zeste (Drosophila) homolog 2	1.9
10	129111	AL080155	Ha.226372	DKFZP434J154 protein	1.9
	128750	T80270	Ha.104798	hypothetical protein LOC55565	1.9
	133551	BC279738	Ha.74578	DEADH (Pop-Gin-Ala-Asp-His) box polypep	1.9
	125704	R55804	Ha.25239	Human DNA sequences from clone RP11-438B2	1.9
	100157	D14661	Ha.119	Wnt6 (tumor 1-associating protein	1.9
15	125845	AK001440	Ha.131840	hypothetical protein FLJ100578	1.9
	134082	AW882645	Ha.89044	spouty (Drosophila) homolog 1 (antagoni	1.9
	106565	NM_014892	Ha.227602	KIAA1115 protein	1.9
	106706	AB037810	Ha.187670	KIAA1385 protein	1.9
	125761	R68351	Ha.100000	gbyh9503.1 Soares placenta Nb2HP Homo	1.9
20	116470	AI272141	Ha.83484	SRY (sex determining region Y)-box 4	1.9
	123254	AI811270	Ha.59824	BCR-1 protein	1.9
	120136	R38208	Ha.283344	similar to rat Wcaboxytyle carter II	1.9
	104996	AK001690	Ha.16390	hypothetical protein FLJ10035	1.9
	133424	AA350994	Ha.20281	KIAA1700	1.9
25	123450	AA103012	Ha.48827	hypothetical protein FLJ12655	1.9
	131803	U73737	Ha.284289	villig-associated protein VIT-1	1.9
	116548	D20433	Ha.193462	gchHUMG501407 Human promyelocyte Homo sa	1.9
	113815	AA386192	Ha.193462	Homo sapiens cDNA FLJ11903 fs, clone HE	1.9
	102045	AL039248	Ha.3094	KIAA0063 gene product	1.9
30	113877	Z70220	Ha.245112	KIAA0039 protein	1.9
	134470	X54942	Ha.53758	CDC28 protein kinase 2	1.9
	134937	AI251449	Ha.171939	ESTs	1.9
	134506	AW247364	Ha.84285	ubiquitin-conjugating enzyme E2 (homolo	1.9
	125499	BC384361	Ha.102885	ESTs, Weakly similar to JCO524 UDP-galac	1.9
35	115281	AA358223	Ha.85088	hypothetical protein MG311314	1.9
	125196	W69474	Ha.323140	ESTs	1.9
	115317	AA303799	Ha.300141	ribosomal protein L39	1.9
	112342	AW1410273	Ha.92614	longevity assurance (LAG1, S. cerevisiae	1.9
	117329	AA524065	Ha.90370	Homo sapiens cDNA FLJ22664 fs, clone H	1.9
40	116353	AB032666	Ha.131728	KIAA1140 protein	1.9
	114459	AW445217	Ha.103362	ESTs	1.9
	133903	X63692	Ha.77462	DNA (cytosine-5)-methyltransferase 1	1.9
	116383	AA455706	Ha.44581	heat shock protein hsp70-related protein	1.9
	130327	AI486351	Ha.111334	ferritin, light polypeptide	1.9
	102723	BC398165	Ha.75961	ubiquitin specific protease 14 (RNA-gua	1.9
45	120452	AL022328	Ha.104335	hypothetical protein IMAGE3510317	1.9
	116432	BE271922	Ha.71243	ESTs, Weakly similar to zinc finger prot	1.9
	115916	AB027371	Ha.91910	ESTs	1.9
	120827	AA382625	Ha.132967	Human EST clone 122857 mariner transposo	1.9
50	129602	A282193	Ha.198298	v-src avian sarcoma (Schmidt-Rappaport A-2)	1.9
	105683	BE250951	Ha.181368	U5 snRNP-specific protein (220 kD), orth	1.9
	132316	U34351	Ha.26570	gch/human nonmuscle myosin heavy chain II	1.9
	131422	AW857721	Ha.26570	Human PUC clone RP3-515N1 from Z2q11.2-q	1.9
	128434	AI190914	Ha.143880	ESTs	1.9
55	117086	AA581602	Ha.41840	ESTs	1.9
	120206	AA104967	Ha.172207	non-POU-domain-containing, octamer-bindi	1.9
	121335	AA404418	Ha.19440	gch-zv0402.1 Soares testis_fetus_N63H9_	1.9
	105906	AA401533	Ha.19440	ESTs	1.9
	125165	W45350	Ha.100000	gch-zv0402.1 Pancreatic islet Homo sapi	1.9
60	109875	H03260	Ha.30365	ESTs	1.9
	109152	AW390723	Ha.73451	ESTs, Weakly similar to S65004 rebafrin,	1.9
	126203	AK001035	Ha.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.9
	122530	AW956741	Ha.40368	adaptor-related protein complex 1, sigma	1.9
	134555	BE273688	Ha.182447	heterogeneous nuclear ribonucleoprotein	1.9
65	125525	AA351050	Ha.222149	Human clone 137330 mRNA, partial cds	1.9
	127248	AL036939	Ha.3463	ribosomal protein S22	1.9
	106465	AA971576	Ha.225951	liposomenase-related function protein 4	1.9
	106970	AA521398	Ha.24252	ESTs	1.9
	134276	AW87810	Ha.3698	olefin proteinase-associated overexp	1.9
	125255	AA102220	Ha.19440	gch-zv0402.1 Stratagene colon (S37204)	1.9
	132443	AW245148	Ha.268371	hypothetical protein FLJ20274	1.8
	104531	AA002054	Ha.18920	ESTs	1.8
	111468	H52547	Ha.205481	ESTs	1.8
	114317	AA524639	Ha.489	succinate dehydrogenase complex, subunit	1.8
75	128158	N55989	Ha.16390	hypothetical protein FLJ10035	1.8
	113762	AK001567	Ha.311002	Homo sapiens cDNA FLJ10705 fs, clone NT	1.8
	119229	T03229	Ha.9880	gch/FBSC2 Fetal brain, Stratagene Homo sa	1.8
	105930	AF016371	Ha.9880	peptidyl prolyl isomerase II (cyclophilin	1.8
	127245	AA323568	Ha.3463	gch/EST1610 Corneal epithelium II Homo sapiens c	1.8
80	100967	BE012145	Ha.251094	high-mobility group (nonhistone chromoso	1.8
	105149	BE089288	Ha.8958	Homo sapiens cDNA FLJ12024 fs, clone HE	1.8
	104642	R29657	Ha.117930	22 weak old human fetal live	1.8
	124235	AF038026	Ha.3463	gch/Homo sapiens full length insert cDNA	1.8
	127155	AA284593	Ha.100000	gch-zv0402.1 Soares ovary tumor NBH0T H	1.8

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5	126554	AJ275866	Hs.71414	transcription factor (SMF gene)	1.8
	107021	AK031342	Hs.14570	hypothetical protein FLJ22530	1.3
	110023	AW294701	Hs.31040	ESTs	1.3
	114899	AK003342	Hs.77545	Homo sapiens mRNA; cDNA DKFZp761M0223 (f)	1.8
	127315	AF116622		ghbHomo sapiens clone FLB4217 mRNA seque	1.8
	110394	HG2682	Hs.268798	ESTs	1.3
	132593	BE244200	Hs.55075	KIAA0410 gene product	1.3
	127684	AA696331	Hs.32555	KIAA0379 protein	1.8
10	127297	AW629435	Hs.140720	GSK-3 binding protein FRAT2	1.3
	104249	AF040421	Hs.22435	leukocyte immunoglobulin-like receptor,	1.8
	112652	BE266999	Hs.235782	solute carrier family 21 (organic anion,	1.8
	110312	BE265936	Hs.11896	hypothetical protein FLJ12069	1.3
	100417	NM_014003	Hs.78054	pre-mRNA splicing factor similar to S. c	1.3
15	120532	AA262354	Hs.186548	ESTs, Weakly similar to I38022 hypothet	1.8
	127629	AA233279	Hs.28173	hypothetical protein FLJ28515	1.3
	107059	H5287	Hs.2093	CDC-like kinase 1	1.3
	110636	H2868	Hs.18110	ESTs	1.8
	132957	BE244044	Hs.61469	hypothetical protein	1.3
20	115657	AJ361354	Hs.48820	TATA box binding protein (TBP)-associat	1.8
	132161	AF11634	Hs.193799	hypothetical protein FLJ22561	1.3
	129510	AW998504	Hs.123073	CDC2-related protein kinase 7	1.3
	126805	F32658	Hs.101359	chromosome 6 open reading frame 32	1.8
	128295	U33127	Hs.110121	SEC7 homolog	1.3
	127323	AW922993	Hs.73939	transcription elongation factor A (SII),	1.3
25	104590	AW373062	Hs.53623	nuclear receptor subfamily 1, group 1, m	1.8
	111959	RA0978	Hs.271458	ESTs, Moderately similar to ALU1_HUMAN A	1.3
	109303	AA199857	Hs.265291	ESTs	1.3
	112631	AA572447	Hs.293833	Homo sapiens mRNA; cDNA DKFZp454W087 (f)	1.8
30	127303	AA369551		ghbEST177953 Pancreas tumor LI Homo sap	1.3
	115892	Y92113		ghbzh48e01.1 Soares fetal liver spleen,	1.8
	123331	AA487013		ghbnc32g22a.1 Gossler Wilms tumor Homo s	1.3
	111998	RH1505	Hs.268912	ESTs	1.3
	121545	AA400897	Hs.193707	ESTs	1.3
35	105012	AF099158	Hs.9329	chromosome 20 open reading frame 1	1.8
	118761	AW799109	Hs.226755	ESTs	1.3
	128765	AF073310	Hs.143643	neurin receptor substrate 2	1.3
	118103	AA401733	Hs.154134	ESTs	1.3
	134595	NM_020401	Hs.26622	mitogen-activated protein kinase kinase	1.8
40	134212	AA654363	Hs.17719	EBF50-PDZ Interactor of 64 kD	1.8
	128033	AI248705	Hs.149321	ESTs	1.3
	126972	NM_016255	Hs.95289	Autosomal Highly Conserved Protein	1.3
	111122	N57675	Hs.16492	DNF ZP5643022 protein	1.8
	114798	AA159181	Hs.54900	serologically defined colon cancer anti	1.3
45	106349	AW954310	Hs.127270	KIAA1545 protein	1.3
	135303	BE622827	Hs.99486	hypothetical protein FLJ13044	1.8
	115223	AF045458	Hs.47061	meo-S1 (C, elegans)-like kinase 1	1.3
	116554	Z26324	Hs.75004	ESTs, Weakly similar to I38022 hypotheti	1.3
	124554	N69961		ghbza27503.1 Soares fetal liver spleen	1.8
50	120259	AW014786	Hs.192742	hypothetical protein FLJ12735	1.3
	123044	AK001035	Hs.130381	B-cell CLL/lymphoma 11A (zinc finger pro	1.3
	125051	Y92051	Hs.110134	ESTs, Highly similar to CRE5-binding pro	1.8
	136026	N92165	Hs.93231	ESTs	1.3
55	129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE3873720, mRNA	1.8
	126758	AF57486	Hs.119122	ribosomal protein L13a	1.3
	114122	RA6128	Hs.12751	ESTs	1.3
	133047	AA310600	Hs.63657	peptide-N-glycanase similar to yeast PNG	1.3
	133639	L37368	Hs.75104	RNA-binding protein S1, serine-rich dome	1.8
60	130672	U61084	Hs.226307	phorbol (similar to) apolipoprotein B m	1.3
	133498	BE296927	Hs.85301	calcium binding protein P22	1.8
	131144	AA305255	Hs.23828	HSPCR38 protein	1.3
	104261	AW248364	Hs.5408	RNA polymerase I subunit	1.8
	115507	AI083658	Hs.50601	hypothetical protein MGC10985	1.3
	130073	T05003	Hs.10056	hypothetical protein FLJ14521	1.3
65	115303	AI214019	Hs.152759	activator of G-protein kinase	1.3
	112657	AW944878	Hs.10769	hypothetical protein MGC41174	1.3
	102960	AJ904730	Hs.76053	DEADH (Asp-Glu-Ala-Asp/His) box polytyp	1.3
	125549	R20215		ghbgy18b09.1 Soares infant brain IN18 H	1.8
70	133797	AL133921	Hs.76272	reticulokinesin-binding protein 2	1.3
	125048	AW440065	Hs.58425	hypothetical protein FLJ23203	1.3
	103403	X55406		ghH.sapiens cyclin E gene,	1.8
	123546	AA638817	Hs.112597	EST	1.3
	124694	T05109		ghbpe9406.1 Soares fetal liver spleen	1.8
	102406	U63177		(KINE)	1.3
75	130895	T97205	Hs.17993	ESTs, Weakly similar to 2109260A B cell	1.3
	123951	AB012932	Hs.170043	metastasis-associated 1-like 1	1.8
	118533	N71861	Hs.49413	ESTs	1.3
	123107	AA492250		ghbza58f12.1 NCI_C6AP, GCE1 Homo sapiens	1.8
80	125956	AW519428	Hs.73887	neutral sphingomyelinase (H-SMase) activ	1.3
	100154	H50720	Hs.81892	KIAA0101 gene product	1.3
	108765	N52921	Hs.269472	ESTs, Moderately similar to ALU7_HUMAN A	1.8
	128839	AL121086	Hs.291608	KIAA0285 gene product	1.3
	109539	AL137728	Hs.12258	Homo sapiens mRNA; cDNA DKFZp434B0920 (f	1.8
	102495	NM_006762	Hs.79356	Lysosomal-associated multispinning motor	1.8

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	100221	D28383	gltHuman mRNA for ATP synthase B chain,	1.8
	101741	NM_003199	transcription factor 4	1.8
	101701	NM_002436	membrane protein, palmitoylated 1 (F5K0)	1.8
5	107119	A075499	ESTs	1.8
	134362	U47742	zinc finger protein 220	1.8
	127964	F06298	gltHSC 13F081 normalized infant brain cDN	1.8
	101437	M20681	solute carrier family 2 (facilitated glu	1.8
	105204	AA185734	ubiquitin 1	1.8
10	112716	AW590680	von Willebrand factor	1.8
	109779	AB023996	beta-1,3-glucuronidyltransferase 1 (glucur	1.8
	111369	AA353740	tumor protein p53-binding protein, 1	1.8
	155204	AF067516	cell division cycle 2-like 1 (P1T5LUP pr	1.8
	105788	AD009398	solute carrier family 22 (organic anion	1.8
15	110997	AW862823	KIAA0421 protein	1.8
	111620	R14853	EST, Weakly similar to 138058 hypophel	1.8
	115815	H11695	disrupter of silencing 10	1.8
	115904	AF167560	ESTs	1.8
	107510	BE613332	ESTs, Weakly similar to GNMSLL retrovir	1.8
	116435	AA186761	hypothetical protein DKFZp586K0717	1.8
20	112399	R83620	KIAA1719 protein	1.8
	127426	AA458476	ESTs	1.8
	125175	WS2395	EST	1.8
	132972	AA034365	Homo sapiens cDNA FLJ11392 fls, clone HE	1.8
25	125982	R98091	gltcyG0e1 Lr1 Soares fetal liver spleen	1.8
	115620	AA359597	CUG triplet repeat, RNA-binding protein	1.8
	128115	A435690	ESTs	1.8
	106880	A493206	ESTs	1.7
	101199	L22075	guanine nucleotide binding protein (G pr	1.7
30	104159	BC369593	hypothetical protein FLJ20595	1.7
	101368	H13059	proline-rich protein Haellit subfamily 2	1.7
	103648	AW248439	junction plakoglobin	1.7
	130717	AA334274	DKFZp564B0769 protein	1.7
	124991	N25485	maternal G10 t(unc)l	1.7
	124770	AA694414	ESTs	1.7
35	126926	AA179472	ESTs, Highly similar to AA1029 integrin	1.7
	101636	BE392781	ADP-ribosylation factor 6	1.7
	132553	AA494291	ESTs	1.7
	127172	AA492208	KIAA1201 protein	1.7
40	130621	AW913087	LUCY7 (S. cerevisiae)-like	1.7
	118525	H73110	ESTs, Moderately similar to AA7582 B-c	1.7
	108845	AK362501	ESTs, Weakly similar to phosphatidylseri	1.7
	128052	AA904617	ESTs	1.7
	128193	AJ224442	putative methyltransferase	1.7
45	113965	AJ268666	ESTs, Weakly similar to 138022 hypophel	1.7
	106620	D52962	KIAA1789 protein	1.7
	125226	W28363	nuclear receptor subfamily 2, group F, m	1.7
	114564	BE083271	ring finger protein 3	1.7
	101800	NM_006433	granuprin	1.7
50	130094	NM_001471	gamma-aminobutyric acid (GABA) B recepto	1.7
	120112	AA180240	Homo sapiens cDNA: FLJ21028 fls, clone C	1.7
	109978	H53396	ESTs	1.7
	121252	AA393607	ESTs	1.7
	127768	AW085002	ESTs	1.7
	125445	AA527222	VW domain binding protein 1	1.7
55	100352			1.7
	118653	AA081218	Homo sapiens cDNA FLJ114206 fls, clone HT	1.7
	134333	AW888411	leukemia-associated phosphoprotein p18 (1.7
	123541	AW976511	ESTs	1.7
60	134191	W26552	KIAA0736 gene product	1.7
	103305	WS2279	gltH sapiens Fas, Apo-1 gene (promoter a	1.7
	112411	R43090	ESTs, Moderately similar to ALU1_HUMAN A	1.7
	100598	AL121734	cell division cycle 42 (GTP-binding prol	1.7
	113610	T93279	gltcy250I.1.1 Sitagliptin lung (S37210) H	1.7
65	103593	AA275341	aldehyde oxidase 1	1.7
	126317	Z80446	ESTs, Weakly similar to 138022 hypophel	1.7
	126956	AK000214	hypothetical protein FLJ20207	1.7
	105105	R61532	hypothetical protein FLJ29336	1.7
	132791	AD205551	RING1 and YY1 binding protein	1.7
	116996	H53935	ESTs	1.7
70	133335	BE251012	nuclear distribution gene C (Anid3ans)	1.7
	120959	BE247692	putative nuclear protein	1.7
	106621	AL040056	uncharacterized hypophthalmus protein HT0	1.7
	106181	AB036551	ESTs	1.7
	125461	AA461930	ESTs	1.7
75	127585	AA604144	ESTs	1.7
	112035	AB55289	ribosomal protein L36	1.7
	102870	M64437	breakpoint cluster region	1.7
	108039	AA280319	PRO1575 protein	1.7
	125698	AK001823	Homo sapiens mRNA: cDNA DKFZp564C2478 (l	1.7
80	114740	N70103	gltcy250I.1.1 Soares fetal liver spleen	1.7
	120304	AA192489	ESTs	1.7
	103433	X88001	Rab geranylgeranyltransferase, beta subu	1.7
	116189	AA463902	ESTs, Weakly similar to 138022 hypophel	1.7

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	105269	AF174499	Hs.6764	histone deacetylase 6	1.7
	125431	AW651639	Hs.75984	polymorphitic/epidermal autoantigen 2 (1.7
	133579	X75346	Hs.75074	mitogen-activated protein kinase-activated	1.7
	105355	AB031447	Hs.26958	Homo sapiens, clone IMAGE:4033044, mRNA,	1.7
5	129601	AB032964	Hs.115726	KIAA1138 protein	1.7
	113739	AA366599	Hs.179304	ESTs	1.7
	100840	U04916	Hs.153418	cell division cycle 2-4hs 1 (PITSURE pr	1.7
	122870	AA847744	Hs.35540	ESTs	1.7
10	119495	BE144608	Hs.55533	ESTs	1.7
	126669	R81308	Hs.333256	ESTs, Weakly similar to ALUS_HUMAN ALU	1.7
	109891	H04757	Hs.323176	ESTs	1.7
	126804	U04936	Hs.765256	KIAA1895 protein	1.7
	132977	AA953322	Hs.301404	RNA binding motif protein 3	1.7
15	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	1.7
	104730	AW139789	Hs.16370	Homo sapiens cDNA FLJ11652 fs, clone HE	1.7
	102205	BE342291	Hs.197540	hypoxia-inducible factor 1, alpha subunit	1.7
	112545	AW139458	Hs.22077	Homo sapiens cDNA: FLJ21635 fs, clone C	1.7
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.7
20	101757	AW553745	Hs.286035	hypothetical protein FLJ22586	1.7
	133279	AL137480	Hs.9834	KIAA1014 protein	1.7
	125912	AF126595	Hs.107213	hypothetical protein FLJ20555	1.7
	119811	AW137640	Hs.221444	Homo sapiens, Similar to hypothetical pr	1.7
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	1.7
25	133134	AF196620	Hs.65948	RNA binding motif protein 6A	1.7
	115278	AX002163	Hs.301724	hypothetical protein FLJ11301	1.7
	133817	AW578716	Hs.7644	H1 histone family, member 2	1.7
	130753	AA206223	Hs.188	phosphodiesterase 4C, cAMP-specific (dun	1.7
	107463	AW562022	Hs.315154	hypothetical protein similar to actin re	1.7
30	121008	NM_016153	Hs.2730	heterogeneous nuclear ribonucleoprotein	1.7
	125546	H05950	Hs.19610	ghyml1d12.1 Sources infant brain 1MB H	1.7
	129991	R20396	Hs.179925	ESTs, Weakly similar to ALUS_HUMAN ALU	1.7
	119015	N85490	Hs.28700	hypothetical protein FLJ20094	1.7
	100698				1.7
35	116456	AF271732	Hs.68090	bridging integrator-3	1.7
	119860	R53325	Hs.66680	ESTs	1.7
	105021	H07960	Hs.306044	CGI-05 protein	1.7
	102098	N25485	Hs.330310	maternal G10 transcript	1.7
	126730	AA442429		gkcy70g92.1 Sources fetal_tetus_Nb2HF8_	1.7
40	113427	T85105	Hs.15471	ESTs	1.7
	122317	T85263	Hs.290874	ESTs, Weakly similar to ALUS_HUMAN ALU S	1.7
	130503	BE208481	Hs.295112	KIAA0616 gene product	1.7
	117348	N24157		gkcy90b12.51 Sources melanocyte 2NbrM Ho	1.7
45	127033	AF163301	Hs.9058	sulfate transporter 1	1.7
	128554	AW572147	Hs.101395	hypothetical protein MGC11352	1.7
	124733	R20547	Hs.100830	ESTs	1.7
	106310	R58185	Hs.17240	ESTs	1.7
	122538	AL137476	Hs.128609	Homo sapiens mRNA: cDNA DKFZp3340623 (f	1.7
50	101075	U03552	Hs.78024	heterogeneous nuclear ribonucleoprotein	1.7
	126659	T16245		gb:NIB100SR Normalized infant brain, Ben	1.7
	127717	F12209	Hs.173380	CK2 interacting protein 1; H00024c prote	1.7
	105441	N26522	Hs.8035	quindrate phosphoribosyltransferase (n	1.7
	104188	AA478423	Hs.300570	Homo sapiens mRNA: cDNA DKFZp54747072 (f	1.7
	134750	L29073	Hs.1139	cold shock domain protein A	1.7
55	106026	BE253927	Hs.24983	hypothetical protein from EURONAGE 2021	1.7
	113211	T89576	Hs.189740	ESTs	1.7
	111070	NM_006201	Hs.171634	PCTAIRE protein kinase 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone GT98758-A	1.7
	129710	AJ277841	Hs.120963	ELG protein	1.7
60	132833	U78525	Hs.57783	eukaryotic translation initiation factor	1.7
	125775	AW514586	Hs.29205	alpha integrin binding protein 63	1.7
	113675	T81034	Hs.14841	ESTs	1.7
	100487	AA076540	Hs.15243	nucleolar protein 1 (20kD)	1.7
65	119302	T25725		gb:EST1D152 CD34+DIRECTIONAL Homo sapie	1.7
	128245	AA393101	Hs.170408	ESTs	1.7
	130322	NM_016427	Hs.154545	POT domain containing guanine nucleotide	1.7
	135363	AW589501	Hs.119	Wilms' tumor 1-associating protein	1.7
	125181	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1.7
	132347	BE270116	Hs.169580	ESTs, Weakly similar to T21554 hypothel	1.7
	127206	AW815683	Hs.337558	ESTs	1.7
70	121880	AW546155	Hs.7759	hypothetical protein AL133206	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	114601	AA075566		gltrzm800c.s1 Stratagene ovarian cancer	1.7
	126278	AA417302	Hs.63042	DKFZp55A157 protein	1.7
	129964	AA388036	Hs.142390	ESTs	1.7
75	133634	AL035071	Hs.234279	microtubule-associated protein, PP1EB fa	1.7
	107028	AA825223	Hs.21255	ESTs, Weakly similar to 138022 hypothel	1.7
	104638	AA493453	Hs.247817	H2B histone family, member A	1.7
	133398	N18023	Hs.287270	ret proto-oncogene (multiple endocrine	1.7
	115794	AA424900	Hs.112227	membrane-associated nucleic acid binding	1.7
80	102083	T35931	Hs.75117	interleukin enhancer binding factor 2, 4	1.7
	100198	AW247090	Hs.57101	minichromosome maintenance deficient (S	1.7
	130858	AB037855	Hs.171917	hypothetical protein FLJ11085	1.7
	110493	A247707	Hs.36915	ESTs	1.7

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5	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00255 hypot	1.7
	128764	AW024282	Hs.104938	hypothetical protein MGC15806	1.7
	134065	X78992	Hs.78959	tyrosine response factor 2 (EGRF-response	1.7
	101002	BF516731	Hs.91945	interferon regulatory factor 1	1.7
	130945	U20582	Hs.2149	actin like protein	1.7
	106974	A1817130	Hs.9195	Homo sapiens cDNA FLJ13698 fls, clone PL	1.7
	126752	A1073373	Hs.326923	EST, Weakly similar to I38022 hypothetical	1.7
	133327	AL290127	Hs.7104	Kraspel-like factor 15	1.7
	127005	T81309	Hs.251064	insulin-like growth factor 2 (somatomedi	1.7
10	105615	AA281959	Hs.5210	gfia maturation factor, gamma	1.7
	116295	AA742696	Hs.91216	ESTs, Weakly similar to 2004399A chromos	1.7
	111587	A1723857	Hs.20734	ESTs	1.7
	104570	JW871870	Hs.131628	ESTs	1.7
15	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase	1.7
	130430	W27893	Hs.150590	putative translation initiation factor	1.7
	119244	AW407584	Hs.275805	ribosomal protein S18	1.7
	131152	HM_004380	Hs.25599	CRBP binding protein (Rubikstein-Taybi s	1.7
	133419	BE242676	Hs.73172	growth factor independent 1	1.7
20	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.7
	116482	AW207000	Hs.126857	Homo sapiens cDNA FLJ12036 fls, clone NT	1.7
	132555	AW501131	Hs.171753	CD22 antigen	1.7
	125840	AB020986	Hs.12067	ubiquitin specific protease 22	1.7
	115416	AA283893	Hs.337079	ESTs	1.7
25	120041	AA830882	Hs.59368	ESTs	1.7
	128295	AG261459	Hs.270114	ESTs	1.7
	122520	AA448804	Hs.292154	stromal cell protein	1.7

Table 2B:

Prxy: Unique Eos probe-set identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

30	Prxy	CAT number	Accession
	108451	13785_27	AA079195 AA084955 AA126308 AA044958
35	124236	4691_1	AF080008 BB407242 HS6212 H66282
	115992	173_2	WS92113 AW702794 BE00413E WB1984 AA679375 T94184 AA679335 BE503126 AW502118 BE467357 AA584550 AW1339964 RS3353
			AW088477 AB87846 AW502624 WB1697 WS1696 AA447817 AA47667 F13631 AW256271 AA055366 AW509027 AA677404 AA831616
			AT124782 AA688402 AA765864 AA765530 AA035698 AA594019 AB267368 AA458946 RS3354 AF264824 AA568816 AA601493
40	118665	1394292_1	FD4455 BE171330
	125165	1952047_1	WA5350 WA5406
	126324	1602163_1	R07785 T85948 T85972
	126053	1601238_1	H64450 H64454
	125499	1562851_1	H10543 R11878
45	126127	1205802_1	N95428 W24040 AW751365 H81987
	125546	356478_1	HO9650 R18413 AA570553 AW973425
	125549	1702179_1	R20215 R18767
	126761	1744008_1	RE6351 R66394
	127155	200358_1	AA204892 AA478122 AA477923
50	125957	1583542_1	H41894 WA5213
	126882	1766316_1	R38091 WS2888
	127245	226662_1	AA323958 AA370288
	127246	227560_1	AA364195 AA323029 AW962050
	127282	211725_1	AA828125 AA634883 AA330555
55	126659	1541208_1	T16245 R19694 F13545 H10299 T56048 T55279 H18006
	127303	258778_1	AA366951 AA470399 AA489425
	127315	379338_1	AF116622 AT114567 AA540834 AA377999
	126730	297853_1	AA442458 T1947
	103898	1872133_3	AA243684
60	126872	142696_1	AW450579 AA136653 AA138655 AW419381 AA64356 AA450703 BE168945 AA805054 AW238033 BE011212 BE011359 BE011367
			BE011358 BE011362 BE011215 BE011365 BE011363
			RS9751 R70467 H83771 H80879 H80879
	112540	1605283_1	AA03322 AA003324
	127705	966283_2	AA404418 AT127248
	121335	279548_1	AA299946 AA299949
65	120734	208882_1	AA642974 AA084223
	114620	320522_8	AA454641
	122652	25401_30	AA605263
	123636	genbank_AA605263	U05987
	100842	ligr_H74398	U05987
70	116548	genbank_D04433	D20433
	122183	genbank_AA610112	AA610112
	128032	genbank_T74884	T74884
	123808	genbank_AA620552	AA620552
	102316	entrez_U34301	U34301
75	102408	entrez_U343177	U343177
	134076	40321_1	AF086215 W02702 AA284268 V25655
	104542		R29657
	113119	genbank_T47910	T47910
	104799	genbank_AA028703	AA028703
80	127964	135151_1	F06286 R18057
	120809	genbank_AA345495	AA345495
	113610	genbank_T93279	T93279
	113947	genbank_W84768	
	101045	entrez_J06614	

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120669	genbank_N57818	
117031	genbank_H68353	
101447	enrez_XJ21005	
124540	genbank_NE3232	
124554	genbank_NE5961	
117348	genbank_K24157	
117357	genbank_K24629	
124677	genbank_R01073	
124694	genbank_R06108	
103138	enrez_XG5065	
103305	enrez_XG2279	
103392	enrez_XG4563	
103403	enrez_XG5406	
119229	genbank_T03229	
119302	genbank_T25726	
129225	Q3A5G_1	AA100230 AA100274
105225	genbank_AA211777	
121262	genbank_AA401807	
112853	genbank_T02843	T02843
121387	genbank_AA403654	
114601	genbank_AA075566	
100221	enrez_D26383	D26383
123167	genbank_AA482250	AA482250
114740	378676_1	N70103 N70020 AW383189 AI207465 W00935 W00906 AA551569 AI343537 AA1335155
123331	genbank_AA407013	
107764	fig_H72241	M05923
100654	genbank_AA599484	
123423	genbank_AA599209	
123474	genbank_AA599209	
120661	genbank_AA160895	

TABLE 3A: About 1346 Genes Up-regulated in Acute Lymphocytic Leukemia (ALL) Compared to Normal Adult Hematopoietic Tissues

Table 3A lists about 1346 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult hematopoietic tissues. These were selected from 35403 probesets on the Affymetrix/Gen Hu1.0 GeneChip array such that the ratio of "average" leukemia to "average" normal adult hematopoietic tissues was greater than or equal to 3.0. The "average" leukemia level was set to the 85th percentile amongst various ALL samples. The "average" normal adult hematopoietic tissue level was set to the 75th percentile amongst various non-malignant hematopoietic tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Key:
Unique Eco probe/Identifier number
ExAccr: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of leukemia to hematopoietic tissues

Key	ExAccr	UnigeneID	Unigene Title	R1
129408	AA449780	Hs.75511	connective tissue growth factor	57.88
100458	ST4019	Hs.247979	pre-B lymphocyte gene 1	49.45
133774	XS4070	Hs.75057	hist coat 27D protein 1	46.42
102564	US6423	Hs.73967	MAD (mothers against decapentaplegic, D)	41.49
130650	AB040951	Hs.284208	DKFZP434N161 protein	35.88
132922	AF746745	Hs.6066	Rho guanine nucleotide exchange factor	35.74
112284	AA823297	Hs.26329	ras-related protein	33.26
106706	AB037810	Hs.18760	KIAA1308 protein	32.30
101050	AU077324	Hs.1832	neuropeptide Y	30.68
102455	U48705	Hs.75562	discolin domain receptor family, member	26.81
101638	BE240846	Hs.75511	connective tissue growth factor	25.46
113374	T70925	Hs.286165	ESTs, Weakly similar to ALUT_HUMAN ALU S	24.66
134125	NM_014781	Hs.50421	KIAA0203 gene product	24.63
106943	AF188222	Hs.5973	lensin	23.14
130019	AF54513	Hs.146428	collagen, type V, alpha 1	23.08
116073	BE245360	Hs.279477	ESTs	22.53
130444	M12125	Hs.300772	Isoprenylated (beta)	21.95
100420	D06963	Hs.118893	Melanoma associated gene	21.05
114324	AF036481	Hs.23077	Wolfram syndrome 1 (wdr39)	18.95
101400	M11699	Hs.194148	v-src-1 Yersinghella enterocoli oncogene	18.45
102750	NM_005100	Hs.768	A kinase (PRKA) anchor protein (gcrwr)	17.88
100803	BE245294	Hs.100786	S164 protein	16.75
131686	AB012124	Hs.31696	transcription factor-like 5 (basic helix	16.60
106410	AB031787	Hs.70229	neurofilin 2	16.51
101304	AA001021	Hs.6585	thyroid hormone receptor-like receptor 8	15.60
131524	AB040927	Hs.310404	KIAA1434 protein	15.01
107794	AA010256	Hs.100786	gcrwr5610a1 Scores rail NZBHR Homo	14.78
126213	A1145494	Hs.103625	ESTs, Weakly similar to RXD2_HUMAN RXD2	14.75
118958	AK220641	Hs.194329	hypothetical protein FLJ1174	14.24
134116	XG8264	Hs.211579	melanoma cell adhesion molecule	14.06
134545	A1902899	Hs.85155	bulky response factor 1 (EGF-response	14.03
114009	A248544	Hs.103000	KIAA0931 protein	13.03
115110	AB001671	Hs.11307	KIAA1453 protein	13.75
130107	AF112977	Hs.172887	phosphoryl-CoA hydroxylase (Rafum-diseas	13.60
133558	XG6945	Hs.748	fibroblast growth factor receptor 1 (fms	13.50
100871	T85231	Hs.170591	tubulin, beta 5	13.50
101462	AL035608	Hs.73853	bone morphogenetic protein 2	13.46
120609	AK346485		gH-EST52657 Fetal heart H1 Homo sapiens	13.33

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	12340	AA504264	Hs.182937
	103460	A021593	Hs.14331
	102460	U08019	Hs.211552
5	100168	H73444	Hs.394
	115844	A1373062	Hs.332936
	130103	Y13492	Hs.149498
	102407	AW602154	Hs.22143
	113632	T94907	Hs.168572
	118951	NM_000448	Hs.73956
10	100305	NM_004941	Hs.171872
	109737	AA055415	Hs.13233
	122777	AA626437	Hs.334437
	116147	AA747571	Hs.36339
15	132303	BE177330	Hs.325093
	103176	AL021154	Hs.76884
	103558	M01955	Hs.1634
	104584	AA704538	Hs.153777
	106777	AF037261	Hs.33787
20	121054	AW975653	Hs.97387
	119400	T92767	Hs.7041
	128610	AB911363	Hs.191391
	134555	U34879	Hs.85729
	131555	T47364	Hs.278613
25	132879	NM_012446	Hs.168333
	113783	AL356598	Hs.7041
	123503	AW975051	Hs.263156
	117031	AB83753	Hs.251864
	100762	T81309	Hs.161071
30	102816	AL137572	Hs.270682
	113089	T43070	Hs.39122
	132089	W22007	Hs.2178
	101663	NM_003208	Hs.25220
	104876	AI933128	Hs.10678
35	106370	AF038843	Hs.111138
	129406	AB015255	Hs.334827
	115354	AA281836	Hs.105649
	123077	AA485229	Hs.253373
	131273	AW206008	Hs.128760
40	126177	AW752702	Hs.75517
	133699	B6501689	Hs.28169
	110655	AB007928	Hs.191837
	111626	R36975	Hs.92127
	129047	Z40773	Hs.106557
45	116674	A1769015	Hs.166895
	129087	A1340027	Hs.332170
	114837	BE244930	Hs.265585
	122039	A1050491	Hs.172108
	112483	AW969785	Hs.271277
50	103487	AA743603	Hs.109
	105676	AL390303	Hs.103291
	128158	NM_064413	Hs.738
	114384	T34462	Hs.231852
	133331	Y114487	Hs.194718
55	114787	AA158509	Hs.706455
	125502	AW977191	Hs.124347
	132325	AB706565	Hs.306478
	127968	AA830201	Hs.326443
	114695	AL151423	Hs.132526
60	114875	AA236059	Hs.263520
	129898	AW67231	Hs.125630
	106283	W21498	Hs.31178
	117130	AA748860	Hs.125630
	105553	AA296756	Hs.31178
65	103657	Z73677	Hs.247302
	105631	AA295448	Hs.289072
	106375	AW872878	Hs.106459
	114518	AW163857	Hs.112476
	123433	AW458922	Hs.85269
70	134558	NM_001773	Hs.48419
	115893	AI652127	Hs.102558
	128621	AA032197	Hs.146696
	122798	AW366286	Hs.29196
	112554	RT1408	Hs.29196
	122969	N57611	Hs.28726
75	131559	AA453208	Hs.226117
	134027	Z87360	Hs.7935
	134138	AB023169	Hs.545694
	120030	AW70525	Hs.85146
80	101005	NM_005239	Hs.85146
	115423	AI499516	Hs.89303
	104046	AW22407	Hs.73848
	131965	W79263	Hs.35962
	126426	AA125984	Hs.35962

peptidylprolyl isomerase A (cyclophilin	13.25
S100 calcium-binding protein A13	13.25
myosin, light polypeptide like	13.14
adenomedullin	13.09
hypothetical protein MGC5370	13.00
anconhalin	12.92
CTF-like factor 2 (ets domain transcript	12.23
ESTs	11.85
recombination activating gene 1	11.73
DEADH (Asp-Glu-Ala-Asp/Glc) box polypep	11.63
ESTs, Moderately similar to A47592 B-cell	11.55
hypothetical protein MGC2048	11.49
hypothetical protein MGC2454	11.40
Homo sapiens cDNA FLJ21210 fls, clone C	11.37
inhibitor of D binding 3, dominant neg	11.17
cell division cycle 25A	11.15
ESTs	11.12
vimentin beta (SH3-containing adaptor mol	11.08
ESTs	10.30
glycylZn05.s1 Stratagene lung (537210) H	10.83
ESTs	10.33
hydroxysteroid (17-beta) dehydrogenase 1	10.80
interferon, alpha-inducible protein 27	10.79
single-stranded-D-binding protein	10.70
hypothetical protein DKFZ76785226	10.65
ESTs, Weakly similar to T78855 serpin/th	10.60
glycylZn02.s1 Morden Fetal Cochlea Homo	10.45
Insulin-like growth factor 2 (somatomedi	10.44
extracellular matrix protein 1	10.36
ESTs	10.33
hypothetical protein MGC15737	10.29
H2B histone family, member Q	10.23
like-glycylZn05.s1	10.23
apocyrin (Drosophila) homolog 2	10.18
KIAA2112 gene product	10.18
ESTs	10.13
ESTs	10.05
Homo sapiens cDNA FLJ21778 fls, clone H	9.95
hypothetical protein FLJ10546	9.87
collagen, type IV, alpha 2	9.80
KIAA0459 protein	9.65
glycylZn007.s1 Soares placenta Nc2HP Homo	9.58
ESTs	9.50
ESTs	9.48
hypothetical protein PP1057	9.46
ESTs	9.46
ESTs, Moderately similar to S65957 alpha	9.45
Homo sapiens cDNA FLJ11321 fls, clone PL	9.40
nucleoporin 98BD	9.30
hypothetical protein from EUROMAGE 3636	9.28
dipeptidase 1 (m)	9.23
neuritin	9.17
ribosomal protein L14	9.11
ESTs, Weakly similar to S65557 alpha-1C-	9.10
zinc finger protein 255	9.03
hypothetical protein FLJ12116	9.01
ESTs	9.00
Homo sapiens mRNA cDNA DKFZ76100511 f	8.93
Homo sapiens mRNA cDNA DKFZ564N1063 f	8.93
ESTs	8.99
hypothetical protein FLJ14005	8.99
bladder cancer overexpressed protein	8.88
ESTs	8.85
GCH1 sapiens gene encoding piskophilin 1	8.83
histidyl geranyltransferase	8.82
hypothetical protein FLJ22175	8.80
suppressor of var1 (S.cerevisiae) 3-like	8.75
ESTs	8.67
Q134 antigen	8.67
ESTs	8.67
Homo sapiens, clone MGC:5352, rF, comp	8.60
splicing factor (OCT.3)	8.58
EST	8.53
glycylZn007.s1 Soares fetal liver spleen	8.45
RAB3, member RAS oncogene family	8.45
H1 histone family, member 0	8.45
KIAA0952 protein	8.43
ESTs	8.43
w-e1s avian erythroblastosis virus E26 o	8.33
ESTs	8.33
carcinoembryonic antigen-related cell ad	8.30
ESTs	8.30
glycylZn007.s1 Stratagene neuroepithelium	8.28

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108866	AW248434	Hs.91571	hypothetical protein
107885	T40059	Hs.71969	Homo sapiens mRc-cd DNFZy664F033 (tr
114239	AL137667	Hs.267445	Homo sapiens mRc-cd DNFZy645231 (tr
124281	A0333756	Hs.111301	arsenite resistance protein ARS2
117069	Hs.3698		gdyr16a11.51 Soares fetal liver spleen
119432	AL120247	Hs.40109	KIA0672 protein
115967	A1745379	Hs.42911	ESTs
132355	D67542	Hs.46326	iccap3/transferase 2 (secretor status in
108339	AW151340	Hs.51615	ESTs, Weakly similar to ALU1_HUMAN ALU S
131894	NM_000246	Hs.3076	MHC class II transactivator
104867	N33553	Hs.10336	ESTs
120266	A1807164	Hs.205442	ESTs, Weakly similar to T34006 hypothetical
130404	A0672727	Hs.76753	endoglin (Cider-Rendu-Weber syndrome 1)
115725	AA417612	Hs.38775	ESTs
127216	A1790103	Hs.143702	ESTs, Weakly similar to S70029 probable
131693	AW663778	Hs.110796	SART protein
113107	A1821027	Hs.8429	ESTs
122282	8E246031	Hs.98401	Homo sapiens mRc full length insert cDN
111040	A1435052	Hs.14931	ESTs
127967	A1022103	Hs.124511	ESTs
125317	Z99346	Hs.112461	ESTs, Weakly similar to L39022 hypothetical
105242	A1654657	Hs.27668	ESTs, Weakly similar to serine/threonine
100421	D66865	Hs.79276	KIA0232 gene product
114359	NM_016929	Hs.263021	chloride intracellular channel 5
119772	A1260439	Hs.55241	gene for serine/threonine protein kinase
124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11
134361	8E519343	Hs.62206	acyl-Coenzyme A dehydrogenase, very long
105476	AL117562	Hs.123628	Human D sequence from clone RP6-576B10
113265	T65601	Hs.169446	ESTs
122707	NM_002039	Hs.239706	GRB2-associated binding protein 1
130055	A1666248	Hs.145355	v-abl Abelson murine leukemia viral onco
109766	A1F145713	Hs.61490	schwannomin-interacting protein 1
107957	Z85842	Hs.57346	ESTs
123116	AW190412	Hs.163738	FERM1, RhoGEF (NRNGEF) and pleckstrin dom
123190	AA468212	Hs.105226	EST
129674	AA020815	Hs.11463	UMP-CMPase
115274	CD1566	Hs.86671	ESTs
102671	U80116	Hs.239999	for and a half LIM domains 1
115645	AA464930		ghn4405.s1 NCL-GAP, Aiv1 Homo sapiens
134651	A0111124	Hs.90232	KIA0652 gene product
107160	ME2852	Hs.154365	ETV-like factor 1 (ets domain transcript
125042	T78902	Hs.255432	ESTs, Moderately similar to ALU1_HUMAN A
116472	AL157345	Hs.42179	brachydomain and PWD finger containing 3
106700	AA121616	Hs.193540	ESTs, Moderately similar to 2109200A B c
109411	R96661	Hs.109555	sex comb on midleg (Drosophila)-like 1
127652	A1021512	Hs.157983	ESTs
126511	AL133072	Hs.199009	protein containing CXC domain 2
107727	AA149707	Hs.173091	ubiquitin-like 3
118069	A1762507	Hs.47676	ESTs
106025	AV653765	Hs.173334	ELL-RELATED R POLYMERASE II, ELONGATIO
122111	AW592206	Hs.36765	Kap3 protein
119674	W60379	Hs.57773	ESTs
126607	W67425	Hs.114568	ESTs
121545	AA412442	Hs.36132	ESTs
113267	T66647	Hs.194040	ESTs, Weakly similar to L39022 hypothetical
126712	AA265592	Hs.200631	ESTs, Weakly similar to alternatively sp
132087	H14486	Hs.3903	Odc4 effector protein 4; binder of Rho
118697	N22706	Hs.43234	ESTs
102285	MM4782	Hs.172609	interleukin 3 receptor, alpha (low affin
101168	L29320	Hs.154259	cyclin-dependent kinase 7 homologue of Xe
121481	AA411631		gdm20p05.s1 Soares, Jettie, NHT Homo sap
130003	AW292315	Hs.7215	ESTs
101851	DE26904	Hs.62045	midkine (neural growth-promoting factor
113528	A1190741	Hs.177415	Finkel-Biskali-Roskelly murine sarcoma viru
132657	AA159331	Hs.273359	genomic nucleosome binding protein (G pr
113560	T91015	Hs.258626	ESTs
123440	A1733692	Hs.112488	ESTs
103050	AA405770	Hs.162362	ESTs
133899	L406592	Hs.211552	myosin, light polypeptide like
113573	R89379	Hs.150900	ESTs
112453	R63899	Hs.28455	ESTs
125221	AA236115	Hs.120785	ESTs
134961	AL034349	Hs.79005	protein tyrosine phosphatase, receptor 1
127610	AA500697	Hs.150771	ESTs, Highly similar to unspliced protein
105486	AW449258	Hs.6187	ESTs
107796	AA058848	Hs.60797	retaryotic translation elongation factor
127254	A1752244	Hs.73369	PCV1 (yeast homolog)-like
105906	AF200419	Hs.110347	HTD18 protein
110637	H03109	Hs.106520	ESTs
117698	N62293	Hs.45107	ESTs
126994	AF205498	Hs.107740	Kruppel-like factor 2 (lung)
129131	A1026106	Hs.177534	dist-specificity phosphatase 10
108528	AA650598	Hs.232022	ESTs, Highly similar to GBA5_HUMAN GUAN

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131009	AF198802	Hs.22142
129389	NM_012445	Hs.288125
125778	AF176149	Hs.129995
124567	W24320	Hs.102941
105640	AA001021	Hs.6505
106474	BE383668	Hs.42484
105908	AI133151	Hs.265131
120087	AF185780	Hs.79219
100514	AIU07687	Hs.28491
108378	A338460	Hs.74615
133350	AA49220	Hs.71573
115673	AA400341	Hs.28998
133410	Y07847	Hs.73088
131281	AA251716	Hs.25227
105510	Z02047	Hs.283978
128755	AW193432	Hs.295450
114530	AA501038	Hs.191757
120120	BE547257	Hs.59791
120593	AA748356	Hs.103522
125632	AA528600	Hs.117507
129537	NM_004609	Hs.1179
115302	AL108719	Hs.47578
126137	AA312594	Hs.59115
114465	BE821055	Hs.137131
125552	A484372	Hs.58068
127380	AF070554	Hs.15535
106955	RO5428	Hs.226351
102952	AAW80358	Hs.33958
109415	BE265385	Hs.35945
111115	AK002039	Hs.26243
127282	AA347158	Hs.185780
113074	AK001335	Hs.31137
101654	AA436989	Hs.127017
103317	BC3441	Hs.165501
133894	AW021235	Hs.180453
109260	AW978515	Hs.131915
112772	AI952283	Hs.35437
130500	AL257515	Hs.38022
113009	T23899	Hs.7245
118835	AA535246	Hs.50852
125625	A03884	Hs.180789
117086	AA581602	Hs.41840
101980	ALD32807	Hs.154682
104488	NS5191	Hs.109511
127955	AA714731	Hs.281457
127894	AL121053	Hs.5534
113305	T92655	Hs.280240
120784	AW752101	Hs.15580
115004	AA329340	Hs.4087
125740	BE158595	Hs.83523
117463	N72185	Hs.44189
108155	BE240294	Hs.180789
122040	AA847758	Hs.111030
109638	AW977747	Hs.119120
112727	T91029	Hs.15089
120723	AA176888	Hs.299284
122127	AW207175	Hs.105771
128046	AA604957	Hs.119840
119774	AB032977	Hs.5298
106255	AA412176	Hs.235453
111987	NM_015310	Hs.6753
123619	AA602954	Hs.105933
128122	AL287491	Hs.100293
128473	T82277	Hs.81381
102283	AW151552	Hs.137687
124668	AA448172	Hs.1215
101801	M86407	Hs.23044
107059	BE614410	Hs.10846
109098	AA138658	Hs.324751
121740	AA558958	Hs.34956
131938	AF176085	Hs.27519
109913	HA7415	Hs.26949
105384	AA219172	Hs.45119
118559	N68456	Hs.385
102010	U02687	Hs.169119
105921	AA421973	Hs.132067
124298	H91679	Hs.147995
120827	AA382525	Hs.53675
103331	AA825463	Hs.293314
130502	AL136653	Hs.50421
115219	AA522776	Hs.9658
121899	ES5241	Hs.111790
135217	AA453880	

6.61	cytochrome b5 reductase bGR2
6.50	spondin 2, extracellular matrix protein
6.58	enhancer of polycomb 1
6.59	Homo sapiens cD FLJ21531 fls, clone C
6.58	thyroid hormone receptor/interactor 8
6.58	hypothetical protein FLJ10618
6.53	CC3-101 protein
6.52	Rai/GS-like gene; KIAA0569 protein
6.50	spemidinspermene N1-acetyltransferase
6.50	platelet-derived growth factor receptor,
6.50	hypothetical protein FLJ10074
6.48	Homo sapiens cD FLJ11591 fls, clone HE
6.40	RMS-related on chromosome 22
6.45	ESTs
6.45	Homo sapiens PFO2751 mR, complete cds
6.45	ornithoformyl development protein 1
6.43	ESTs, Weakly similar to S65657 alpha-1C-
6.40	hypothetical protein MG31383
6.40	ESTs
6.38	ESTs
6.38	TATA box binding protein (TBP)-associate
6.33	ESTs
6.30	hypothetical protein FLJ20089
6.29	hypothetical protein FLJ11099
6.29	hypothetical protein FLJ20568
6.25	Homo sapiens clone 24582 mR sequence
6.25	ESTs
6.25	hypothetical protein FLJ10120
6.23	ESTs, Weakly similar to A46510 X-linked
6.23	Homo sapiens cD FLJ11177 fls, clone PL
6.23	ESTs
6.21	protein tyrosine phosphatase, receptor I
6.20	H2A histone family, member A
6.19	ligase IV, D, ATP-dependent
6.19	rTS beta protein
6.18	KIAA0853 protein
6.18	ESTs, Moderately similar to U9026 MLN 6
6.17	ESTs
6.17	ESTs
6.16	ESTs
6.15	S164 protein
6.14	ESTs
6.13	calpain 3, acidic
6.13	procollagen 17
6.13	ESTs, Weakly similar to heterogenous ri
6.13	Homo sapiens cD FLJ12961 fls, clone NT
6.10	ESTs, Moderately similar to ALU2_HUMAN A
6.10	hypothetical protein FLJ111025
6.08	mannosyl (alpha-1,3)-glycoprotein beta-
6.05	nuclear receptor subfamily 1, group I, m
6.04	ESTs
6.03	S164 protein
6.03	ESTs
6.02	E3 ubiquitin ligase SMURF1
6.01	ESTs
6.00	ESTs
5.99	ESTs
5.98	KIAA1151 protein
5.98	Homo sapiens mR; cD DMF2p5950521 (f
5.98	KIAA0542 protein
5.96	glcnzotc02a1 NCLCGAP_Px2 Homo sapiens
5.95	ESTs
5.95	O-linked N-acetylglucosamine (Glc) tr
5.95	guanine nucleotide binding protein 11
5.94	ESTs, Highly similar to KGB1_HUMAN RIBOS
5.93	actinin, alpha 3
5.92	RANF51 (S. cerevisiae) homolog (E coli fls
5.90	KIAA1077 gene product
5.90	ESTs
5.88	neural polyphosphatase tract binding prot
5.89	ESTs
5.88	ESTs
5.88	ESTs
5.88	limb-related tyrosine kinase 3
5.85	ESTs, Weakly similar to T25731 hypotheli
5.85	glypA40/z11 Scoville fetal liver spleen
5.84	Human EST clone 122987 mariner transposo
5.82	protein kinase, X-linked
5.80	decidual protein induced by progesterone
5.78	Homo sapiens cD FLJ11423 fls, clone MA
5.78	KIAA0283 gene product
5.77	hypothetical protein FLJ111790

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	123973	C14805	
	126055	R07374	Ha.29652
	110151	H18935	Ha.31608
5	125889	AA810532	Ha.131899
	102638	U57319	Ha.9216
	121851	AA470587	Ha.93472
	124521	R53932	Ha.335335
	109890	A1150548	Ha.23155
10	120584	AW136478	Ha.5094
	126433	AA329505	
	100455	AW088914	Ha.75789
	106555	NM_014852	Ha.227602
	120912	AA376650	Ha.187650
	127209	AA305023	Ha.61864
	107856	AF207589	Ha.330425
15	105887	A1001277	Ha.302634
	102126	AW505870	Ha.78951
	100054	AA102785	Ha.22414
20	108758	NM_005057	Ha.1827
	102211	BE314524	Ha.78776
	107427	W28975	Ha.45735
	135175	M91463	Ha.93558
	111754	AA203268	Ha.29029
25	119405	TG3855	Ha.91095
	126454	A1990045	Ha.54790
	133855	A8011155	Ha.107290
	123250	AA830335	Ha.102673
	122861	AA337224	Ha.110494
30	112045	AA383343	Ha.22116
	132806	BE513337	Ha.234895
	109001	A1056548	Ha.72116
	118155	BE042515	Ha.207689
	128401	R01965	Ha.265895
35	129286	A1051967	Ha.110122
	120314	T10013	Ha.221040
	132815	A1515169	Ha.57475
	113983	W87415	Ha.55096
40	105002	AA224244	Ha.182704
	132025	AA011117	Ha.3745
	110732	AW070638	Ha.174174
	122891	T03822	Ha.293147
	125758	A1059444	Ha.293960
	128426	AF077953	Ha.111323
45	103217	NM_001841	Ha.73037
	132251	U00743	Ha.306194
	105386	AA855118	Ha.191538
	109454	AA322255	Ha.285232
50	113053	W15073	Ha.5027
	134392	AA218558	Ha.7935
	119316	A1144530	Ha.209334
	108019	A1077773	Ha.249159
	109421	AW604652	Ha.332422
55	111529	AF027088	Ha.112360
	119718	W09216	Ha.92049
	106154	BE540255	Ha.6994
	106644	W39433	Ha.23971
	119580	AL075310	Ha.92250
60	125777	AL137491	Ha.145211
	112944	H18053	Ha.13254
	103149	NM_006201	Ha.171834
	130437	AA152105	Ha.4859
	103890	AW015877	Ha.38057
	104855	T03940	Ha.223575
	129914	NM_012421	Ha.13321
	130308	AF057804	Ha.15423
	116312	BE379794	Ha.53403
	124191	T03539	Ha.240549
70	125583	AA195957	Ha.95022
	130591	N59645	Ha.189745
	116355	AA788133	Ha.98550
	115553	AA729386	Ha.714144
	127822	A1087003	Ha.285509
75	128495	NM_005904	Ha.100602
	117657	U93905	Ha.44708
	127890	AA294934	Ha.293902
	134843	AA426280	Ha.900561
	120595	AA528283	Ha.292737
80	102075	BE290197	Ha.179555
	100034	J03019	Ha.99913
	112597	BE535515	Ha.154243
	115034	AW216258	Ha.98493
	131868	AW468286	Ha.335332

glt-C14805 Clontech human axon podyA+- mR	5.77
ESTs	5.76
hypothetical protein FLJ20041	5.75
ESTs, Weakly similar to T03070 hypothetical	5.75
casepase 7, apoptosis-related cysteine pr	5.73
ESTs	5.73
ESTs	5.70
ESTs	5.70
ring finger protein 10	5.70
glt-EST28707 Cerebellum II Homo sapiens c	5.70
W-myc downstream regulated	5.69
KWA1116 protein	5.68
ESTs	5.68
SEC24 (S. cerevisiae) related gene famil	5.68
Homo sapiens. Similar to G protein-coupl	5.67
terized (Drosophila) homolog 5	5.65
protein phosphatase 1, regulatory (inhib	5.65
APFX control - TrpG-3	5.63
ESTs	5.63
none growth factor receptor (TNFR super	5.61
positive transmembrane protein	5.60
hypothetical protein FLJ23476	5.60
solute carrier family 2 (facilitated glu	5.60
ESTs, Weakly similar to I35022 hypothetical	5.59
ESTs	5.58
transcription termination factor, R po	5.58
dictes, large (Drosophila) homolog 5	5.58
ESTs	5.57
ESTs	5.55
QDC14 (cell division cycle 14, S. cerevi	5.55
geminin	5.55
hypothetical protein FLJ25992 similar to	5.55
Homo sapiens cD FLJ13675 fls, clone PL	5.55
ESTs	5.53
ESTs	5.53
HE51 (S. cerevisiae)-like	5.51
none comb on midleg homolog 1	5.50
H.A-B associated transactin-1	5.49
ESTs, Moderately similar to alternative	5.49
mkt fct globule-ECF factor 5 protein	5.49
KWA4501 protein	5.48
ESTs, Moderately similar to A46010 X-in	5.48
ESTs	5.48
Protein inhibitor of activated STAT X	5.47
canonoid receptor 2 (macrophage)	5.46
immunocyte repeat containing 12	5.45
ESTs	5.43
ESTs, Moderately similar to A46010 X-in	5.43
ESTs, Weakly similar to A47582 B-cell gr	5.43
sorting nexin 5	5.41
Homo sapiens cD-FLJ21874 fls, clone H	5.38
adrenergic, alpha-2A-, receptor	5.38
ESTs	5.38
protein (mouse)-like 1	5.38
ESTs	5.38
Homo sapiens cD: FLJ22044 fls, clone H	5.35
hypothetical protein DKF2p547N043	5.35
high-mobility group protein 2-like 1	5.35
Homo sapiens mR: cD DKF2p434K1111 (f	5.35
ESTs	5.34
PCTAIRE protein kiso 1	5.34
cyclin L anti-6c	5.33
ESTs	5.33
B-cell CLL/lymphoma 6, member B (tinc II	5.33
rearranged L-myc fusion sequence	5.33
hypothetical protein HDCC024P	5.31
hypothetical protein	5.30
ESTs, Moderately similar to S95557 alpha	5.28
ESTs	5.28
cumbrs (Drosophila) homolog 1	5.28
ESTs	5.26
transcription factor (SMF gene)	5.26
G-protein-coupled receptor 49	5.25
MMD (mothers against decapentaplegic, Or	5.24
Sae-Thr protein kiso related to the my	5.23
ESTs, Weakly similar to IGHUS5 protein d	5.22
proteoglycan-binding protein	5.21
ESTs	5.20
cyclin dependent kiso inhibitor 1A (p2	5.20
adrenergic, beta-1-, receptor	5.20
hypothetical protein HDCC024P	5.20
X-ray repair complementing defective rep	5.20
zinc finger protein 151 (PHZ-67)	5.20

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	105914	A1W245880	Hs.9701	growth arrest and D-damage-inducible,	5.18
	102758	NM_001546	Hs.34563	inhibitor of D binding 4, dominant neg	5.18
	103050	AA167101	Hs.213194	hypothetical protein M5C10085	5.18
5	112518	T33909	Hs.75355	glycyl-710L1 Scaevola fetal liver spleen	5.18
	133640	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	5.18
	135180	C00070	Hs.96	phorbol-12-myristate-13-acetate-induced	5.18
	135339	A0564123	Hs.42590	ADP-ribosylation factor-1-like 5	5.18
	134001	ST8525	Hs.89695	insulin receptor	5.17
	133362	AK001519	Hs.7194	CG-74 protein	5.17
10	135206	AD024703	Hs.96334	ring finger protein 11	5.15
	111480	R04543	Hs.19706	ESTs	5.15
	118488	N67411	Hs.168835	glycyl-336B.1 Morton Fetal Cochlea Homo	5.14
	125757	A0274906	Hs.168835	ESTs, Highly similar to 1814460A p53-oss	5.15
	127140	A0273507	Hs.303966	ESTs	5.15
15	109223	AW000714	Hs.65818	ESTs	5.14
	103538	Z73497	Hs.247802	Human D sequence from clone U240C2 on	5.12
	133388	AW245631	Hs.152447	heterogeneous nuclear ribonucleoprotein	5.12
	100511	M76576	Hs.116840	ESTs	5.10
	109441	ST7583	Hs.20072	gbltHERVK101HUMTV reverse transcriptase	5.10
20	109337	A084666	Hs.19715	myosin regulatory light chain interactin	5.10
	122906	A182216	Hs.19715	ESTs, Weakly similar to ZN01_HUMAN ZINC	5.10
	128242	A092626	Hs.285755	ESTs, Moderately similar to A1US_HUMAN A	5.10
	112374	NM_016323	Hs.28563	cyclin-E binding protein 1	5.10
25	124205	BC27388	Hs.162447	heterogeneous nuclear ribonucleoprotein	5.10
	104216	AC022313	Hs.3089	plexin B2	5.09
	135051	A1272141	Hs.83484	SRX (sex determining region Y)-box 4	5.08
	131628	Z4C784	Hs.238809	ESTs	5.08
	111722	R23924	Hs.23595	EST	5.07
	107334	AF257770	Hs.25390	poly(C)-binding protein 4	5.05
30	110243	H06893	Hs.333513	gly-yl14p3.1 Scaevola breast 2NH18at Homo	5.05
	125837	AW968123	Hs.154151	small inducible cytokine subfamily E, me	5.05
	103987	AL120051	Hs.144700	protein tyrosine phosphatase, receptor t	5.04
	112578	A118468	Hs.33605	ephrin-B1	5.03
35	124953	F05650	Hs.101375	Homo sapiens mR: cDN DKFZp434t205 (fr	5.03
	131379	AK001123	Hs.28175	hypothetical protein FLJ10211	5.03
	109451	N32264	Hs.44330	ESTs	5.02
	101395	BC257931	Hs.76995	proliferating cell nuclear antigen	5.02
40	131038	W07778	Hs.169388	hypothetical protein DKFZp761H2024	5.01
	101208	L25081	Hs.179335	ras homolog gene family, member C	5.01
	104873	NM_015310	Hs.6763	KIA00942 protein	4.99
	103141	X06113	Hs.75584	polymyositis/scleroderma autoantigen 2 (4.98
	111280	A0923395	Hs.51885	KIAA1209 protein	4.98
45	128142	T67162	Hs.135127	ESTs, Weakly similar to unnamed protein	4.98
	113857	AW243158	Hs.5297	DKFZP564A2416 protein	4.96
	105202	AF128542	Hs.168946	polymerase (D directed), epsilon	4.96
	114341	AF270491	Hs.28249	hepatocellular carcinoma-associated anti	4.95
	100815	W020474	Hs.501746	RAP2A, member of RAS oncogene family	4.95
50	103208	AW411340	Hs.31314	retinoblastoma-binding protein 7	4.95
	121121	AA389371	Hs.189095	similar to SALL1 (sal (Drosophila))-like	4.95
	123321	T86652	Hs.178294	ESTs	4.95
	101145	L13210	Hs.79339	cell, galactoside-binding, soluble, 3	4.95
	100551	M73880	Hs.129053	Homo sapiens NOTCH1 (NT) mR, complete	4.93
55	126182	AA271331	Hs.283771	ESTs	4.93
	127525	AA055151	Hs.3528	mitogen-activated protein kinase 5a	4.92
	133959	AA589112	Hs.78	GA-binding protein transcription factor,	4.92
	120873	AA358015	Hs.99423	gbltEST56864 Fetal lung III Homo sapiens	4.92
	125219	AB04331	Hs.99423	ATP-dependent R helicase	4.91
	102790	BE245277	Hs.154195	E4F transcription factor 1	4.90
60	123496	NM_005754	Hs.220689	G12-binding protein transcription factor,	4.90
	130381	L47345	Hs.155202	transcription elongation factor B (SII)	4.89
	132389	AA310383	Hs.190044	ESTs	4.88
	100260	D38491	Hs.322478	KIAA0117 protein	4.88
65	105685	N08630	Hs.22752	ESTs	4.88
	111603	R11529	Hs.29634	EST	4.88
	120514	AA250335	Hs.154332	gbltZ591602.1 Scaevola_NthHUMp_S1 Homo sapi	4.88
	130314	NM_014674	Hs.203948	KIAA0212 gene product	4.86
	108958	AF174282	Hs.203948	TEA domain family member 3	4.86
	126503	W08610	Hs.156736	ESTs	4.85
	100406	A092600	Hs.118397	AE-binding protein 1	4.85
	116238	AV660717	Hs.47144	DKFZP569N0519 protein	4.84
	105288	N99573	Hs.3585	ESTs, Weakly similar to AF126743 1 DU	4.83
	119753	AA346206	Hs.28471	ESTs, Weakly similar to T14267 Xln prote	4.82
75	113070	A0522977	Hs.6295	KIAA1151 protein	4.81
	107908	AF087999	Hs.42826	ESTs	4.80
	119678	A058666	Hs.6106	R binding motif protein 4	4.80
	100415	D06570	Hs.58222	TGF-beta-induced anti-apoptotic factor 1	4.79
	123300	T12374	Hs.296323	gblt1G5265101 normalized infant brain cDN	4.78
80	133101	AA000299	Hs.180952	cyclin 4 (p22)	4.78
	103507	AJ000512	Hs.796323	serum/glucocorticoid regulated kinase	4.78
	107866	AA010611	Hs.50418	EST	4.78
	166330	A373523	Hs.52011	ESTs	4.78
	131479	D06161	Hs.273	glucosylceramidase (Krabbe disease)	4.78

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133140	AF180881	Hs.5582
134854	AK001741	Hs.3739
102890	AB037742	Hs.24336
101524	NM_000448	Hs.73958
113095	AA828380	Hs.129733
114924	AJ38063	Hs.87329
127543	AK000787	Hs.157392
115986	AW682629	Hs.52081
101382	AU076772	Hs.1279
128509	R47400	Hs.23850
127930	AA069872	Hs.123304
127824	AB1151616	Hs.127811
110049	H12449	Hs.31159
127115	H77859	Hs.65450
104727	NB1203	Hs.20047
127552	AJ303428	
127304	AI014577	Hs.99962
105409	AW502076	Hs.301855
114969	AW162998	Hs.24094
115125	AA193508	Hs.85988
118349	AW605585	Hs.91052
123130	AA487200	
130881	AA088875	Hs.25933
132074	AA47486	Hs.3852
130897	AF128023	Hs.167496
131121	AA120995	Hs.23136
116046	BC36293	Hs.84671
112868	AW398359	Hs.10667
116877	AA708953	Hs.168732
131241	BE591914	Hs.24564
132027	AF151020	Hs.161444
133323	BC338654	Hs.70937
114269	AA178769	Hs.23450
122713	AJ084453	Hs.99438
133671	BE515037	Hs.177556
134453	AJ272141	Hs.83484
115510	BE299330	Hs.72249
115322	LJ6866	Hs.76556
129315	NM_014658	Hs.174038
104674	AB059862	Hs.26289
106276	AA625947	Hs.25750
105216	AA524743	Hs.44693
120376	AA327469	
121743	AA367636	
128011	AJ347067	Hs.124636
124454	AJ898510	Hs.112496
103409	NM_004454	Hs.43697
120484	AA253170	Hs.96473
127046	AA321948	Hs.293966
133184	AA010121	Hs.6685
123184	BE247767	Hs.15186
106827	AK000706	Hs.16125
115475	AB033065	Hs.40193
119468	AB11535	Hs.6657
133862	BE409533	Hs.29629
13941	AB031016	Hs.22399
131980	R46277	Hs.250538
128795	AA531287	Hs.105005
116480	C14008	Hs.189476
111713	C15253	Hs.220500
113721	AF143955	Hs.18190
111657	R07384	Hs.268667
102009	BE245149	Hs.82643
135242	AB583167	Hs.9700
127590	BE548749	Hs.148016
109785	AB011131	Hs.12376
109700	FC0909	
124882	AB98962	Hs.101539
131765	AB381270	Hs.134110
115654	NM_008577	Hs.294284
102034	AJ903474	Hs.230
109176	R43685	Hs.12257
111650	R16722	Hs.124246
132993	AB023154	Hs.62254
128017	AA115333	Hs.107969
132802	AJ984442	Hs.59838
116814	AB068222	Hs.162536
120530	AA348913	
101434	AW50066	Hs.1430
102018	U03398	Hs.1504
104619	AA001635	Hs.287414
106718	AB31198	Hs.238928
128076	H73863	Hs.114243

Rho guanine exchange factor (GEF) 12	4.78
hypothetical protein FLJ10879	4.78
KIAA1321 protein	4.76
recombination activating gene 1	4.75
ESTs	4.75
HSPC072 protein	4.75
homo sapiens cD FLJ20780 fls, clone CO	4.75
KIAA067 protein	4.75
complement component 1, r subcomponent	4.74
ESTs	4.74
ESTs	4.73
ESTs	4.73
EST, Weakly similar to ALU5_HUMAN III A	4.73
reticulin 4	4.73
zinc finger protein, subfamily 2A (FYVE	4.72
protein) p493 Selected chromosome 21 cD	4.71
proteoglycan 2, bone marrow (aral hi	4.70
DiGeorge syndrome critical region gene B	4.70
KIAA1376 protein	4.70
ESTs	4.70
ESTs, Moderately similar to ALU5_HUMAN A	4.70
glucal3902.s1 Stratagene lung (397210) H	4.70
ESTs	4.70
KIAA1368 protein	4.70
PAN binding protein 6	4.69
ESTs	4.69
hypothetical protein FLJ120297	4.68
ESTs	4.68
ESTs	4.68
Homo sapiens cD FLJ11640 fls, clone HE	4.68
hypothetical protein	4.68
H3 histone family, member A	4.68
mitochondrial ribosomal protein S25	4.67
ESTs	4.67
melanoma antigen, family D, 1	4.66
SRX (sex determining region Y)-box 4	4.66
three-POZ containing protein similar to	4.66
MADS box transcription enhancer factor 2	4.66
spondyloepiphyseal dysplasia, late	4.65
ESTs	4.65
ESTs	4.65
gbc279d09.1 Soares, Jettis_NHT Homo sap	4.65
gbc279d09.1 Soares, Jettis_NHT Homo sap	4.65
ESTs	4.65
ets variant gene 5 (ets-related molecule	4.64
ESTs	4.64
EST	4.63
ESTs	4.63
thyroid hormone receptor interactor 8	4.63
KIAA0670 protein	4.62
hypothetical protein FLJ20699	4.61
hypothetical protein KIAA1259	4.61
hypothetical protein bc10-0869.5	4.61
peroxisomal long-chain acyl-coA thioeste	4.60
hypothetical protein FLJ14654	4.58
Homo sapiens mRNA full length insert cDN	4.58
ESTs	4.58
glyceraldehyde-3-phosphate dehydrogese	4.58
ESTs	4.58
EST	4.57
ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
protein tyrosine kase 9	4.55
cydin E1	4.55
ESTs	4.55
picozo (presynaptic cytomatrix protein)	4.53
glc3C3H052 normalized infant brain cDN	4.53
ESTs	4.53
hypothetical protein PR02730	4.52
ESTs, Highly similar to beta-1,3-N-acety	4.52
filamin	4.52
ESTs	4.50
ESTs	4.50
KIAA0937 protein	4.49
ESTs	4.49
KIAA1086 protein	4.48
KIAA0284 protein	4.48
gh:EST55442 Infant adrenal gland II Homo	4.48
coagulation factor XI (plasma thrombocle	4.48
tumor necrosis factor (ligand) superfamily	4.48
transcription intermediary factor 1a	4.48
HT002 protein; hyperkalemia-initiated cati	4.48
ESTs	4.48

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5	11899	A057404	Hs.58698	ESTs	4.47
	115582	AW245047	Hs.136194	cutaneous T-cell lymphoma-associated tum	4.46
	12565	N22522	Hs.30942	ephrin-B2	4.45
	105719	BEE21800	Hs.29444	putative small membrane protein ND067	4.45
	117169	R87866	Hs.95120	ESTs, Weakly similar to H2H10 homolog	4.45
	102757	AW985454	Hs.30942	ephrin-B2	4.45
	120637	A4811804		gbc3b3a05.s1 NC_CGAP, GCB1 Homo sapiens	4.45
	131579	NS2922	Hs.29089	ESTs	4.45
10	135287	U2870	Hs.9786	zinc finger protein 275	4.45
	112540	R69751		gby40A0.s1 Soares placenta Nb2IP Homo	4.45
	125724	AL360190	Hs.29978	Homo sapiens mRNA full length insert cDNA	4.44
	115498	A4241970		gbc3b3a05.s1 NC_CGAP, GCB1 Homo sapiens	4.43
	102263	U29171	Hs.75852	coixin like 1, delta	4.43
	124312	H94647	Hs.102329	ESTs	4.43
15	112366	AF035318	Hs.12533	Homo sapiens clone 23705 mRNA sequence	4.43
	115955	AF263013	Hs.44198	intracellular membrane-associated calcic	4.43
	103562	NW_002702	Hs.2315	POU domain, class 5, transcription factor	4.42
	100169	AL037228	Hs.82043	D123 gene product	4.40
20	109828	AA143802	Hs.71781	ESTs	4.40
	125908	AF263555	Hs.239646	baculoviral MP repeat-containing 6	4.40
	125996	BE161095	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	4.40
	129512	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.40
	134570	U86615	Hs.172280	SWI/SNF related, matrix associated, acti	4.40
	132073	U52566	Hs.94030	Homo sapiens mRNA cDNA DNFZp59BCE1024 (f	4.40
25	102311	BE915004	Hs.16244	mitotic cyclin coded-coil related prot	4.40
	128793	AB011125	Hs.105749	KIAA0553 protein	4.40
	107292	BE156479	Hs.4789	Homo sapiens serologically defined fra	4.38
	126144	H84455	Hs.40639	ESTs	4.38
30	130783	X07282	Hs.171495	nitric acid receptor, beta	4.38
	135102	U82993	Hs.321709	purinergic receptor P2X, ligand-gated io	4.38
	100284	D43767	Hs.66742	small inducible cytokine subfamily A (Cy	4.37
	117269	N21621	Hs.91142	KH-type splicing regulatory protein (FUS	4.36
	104261	AW248364	Hs.5409	R polymerase 1 subunit	4.35
35	108699	BE409867	Hs.69499	hypothetical protein	4.35
	123519	D51089		gbcHUM1840EG Human fetal brain (TF)w	4.35
	127445	AA068286	Hs.193942	ESTs	4.35
	130772	BE270640	Hs.19192	cyclin-dependent kinase 2	4.35
	134525	AA977658	Hs.104309	ESTs	4.35
40	133897	L14922	Hs.166563	replication factor C (activator 1) 1 (14	4.35
	128070	AA069944	Hs.303808	ESTs	4.35
	135045	AA494054	Hs.93589	hypothetical protein DNFZp564B1102	4.33
	101881	NM_004957	Hs.754	polyphosphatase synthase	4.33
	129538	AB007066	Hs.185140	KIAA0403 protein	4.33
45	130574	NM_003528	Hs.2178	H2B histone family, member Q	4.33
	107763	AA018220	Hs.106730	chromosome 22 open reading frame 3	4.32
	126818	T71092	Hs.172572	hypothetical protein FLJ20903	4.31
	129407	AL137597	Hs.11114	hypothetical protein cDNA1191N3.1	4.30
	110846	BE272343	Hs.287075	endoplasmic reticulum chaperone SIL1, ho	4.30
50	111433	R01452	Hs.40193	hypothetical protein KIAA1259	4.30
	114860	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	4.30
	118553	AW975861	Hs.191548	ESTs	4.30
	115155	A1184751	Hs.75874	pregnancy-associated plasma protein A	4.30
	126911	AA428049	Hs.1501	syndecan 2 (heparan sulfate proteoglycan	4.30
55	131230	NM_005865	Hs.274407	protease, serine, 16 (2-yrms)	4.30
	103349	D64110	Hs.77311	BTG family, member 3	4.29
	100175	BE238769	Hs.325500	acetyl-Coenzyme A acetyltransferase 2 (mit	4.29
	105335	AW201165	Hs.25447	ESTs	4.28
	122507	BE557820	Hs.99210	ESTs	4.28
60	105937	AA814807	Hs.7395	hypothetical protein FLJ23182	4.28
	133874	AW651121	Hs.75487	Homo sapiens cDNA FLJ22139.1a, clone H	4.28
	102826	NM_007274	Hs.6579	cytosolic acyl coenzyme A thioester hyd	4.28
	103272	NM_006690	Hs.2838	nucleic enzyme 3, DPr(-)-dependent, mito	4.28
	111887	R38835	Hs.12328	KIAA1005 protein	4.28
65	123536	N85785	Hs.181165	eukaryotic translation elongation factor	4.28
	133736	D40689	Hs.75319	glycoprotein M6A	4.27
	130356	AF127577	Hs.155017	nuclear receptor interacting protein 1	4.27
	119830	AW056222	Hs.53478	Homo sapiens cDNA FLJ12366.1a, clone MA	4.27
	106758	AB014564	Hs.22616	KIAA0554 protein	4.25
70	103709	F09749	Hs.157405	ESTs	4.25
	110463	H52931	Hs.166067	ESTs	4.25
	124472	NS2517	Hs.102670	EST	4.25
	103970	R40322	Hs.248420	ESTs, Moderately similar to A47582 B cel	4.24
	131487	F13036	Hs.27373	Homo sapiens mRNA cDNA DNFZp564O1763 (f	4.23
	107216	D61069	Hs.211579	metastasis cell adhesion molecule	4.23
75	123562	AA177088	Hs.190065	ESTs	4.23
	125995	W02410	Hs.209555	ESTs	4.23
	126221	N20514	Hs.172965	ESTs	4.23
	127092	T26985		gbcHBT069H919 Infant brain, LUNL array	4.23
80	132349	AW979554	Hs.181286	serine protease inhibitor, Kunitz type 1	4.23
	118946	N28834		gbc2b733.s1 Soares_fetal_lung_NbH1.19W	4.22
	101531	A1199711	Hs.576	fucosidase, alpha-L-1, tissue	4.21
	105322	T87179	Hs.16346	ESTs, Weakly similar to S57447 HP08B-7	4.21
	104219	AB002323	Hs.7720	dynamin, cytoplasmic, heavy polypeptide 1	4.20

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	102825	BE262396	Hs.7137	clones 23667 and 23775 zinc finger prote	4.20
	103571	A0575749	Hs.211608	nucleoprotein 153kD	4.20
	103942	A-995931	Hs.31314	reticulohelium-binding protein 7	4.20
5	112685	R67650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.20
	123107	AA225048	Hs.104207	ESTs	4.20
	132659	Z75190	Hs.54481	low density lipoprotein receptor-related	4.20
	130084	A0292372	Hs.173724	cosine like, brain	4.19
10	145553	BE219600	Hs.22505	hypothetical protein FLJ10119	4.18
	129628	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.18
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	4.18
	110637	AD241470	Hs.259982	ESTs	4.18
	127520	T51239	Hs.154545	glyoxal12.2.1 Stratopone fetal spleen (S	4.17
	130522	NM_014247	Hs.154545	PDZ domain containing guanine nucleotide	4.17
15	104768	D82319	Hs.11055	RALBP1 protein	4.17
	123360	AA532718	Hs.178604	ESTs	4.17
	133110	AA304777	Hs.65228	ESTs	4.16
	130923	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphatase	4.16
	109878	BE620775	Hs.4866	Homo sapiens cD FLJ14367 lts, clone HE	4.16
20	119255	BE539705	Hs.285363	ESTs	4.16
	124214	H58608	Hs.161523	ESTs	4.15
	106193	AA057478	Hs.23212	ESTs	4.15
	105169	BE245294	Hs.180789	S164 protein	4.15
	132304	AA810202	Hs.44296	hypothetical protein FLJ23234	4.15
25	131600	NM_004377	Hs.25331	carbamate phosphotransferase 1, muscle	4.14
	131308	M53415	Hs.26714	activin A receptor, type II	4.14
	121993	AW927880	Hs.98661	ESTs	4.14
	110779	A391472	Hs.12551	ESTs, Highly similar to C212_HUMAN 28.3	4.13
	126283	A0328977	Hs.6298	KAA1151 protein	4.13
	104446	AF384568	Hs.7351	cyclic AMP phosphoprotein, 19 kD	4.13
30	131475	AA952841	Hs.27283	KAA1468 protein	4.13
	128933	NM_002060	Hs.334595	GATA-binding protein 2	4.12
	131341	AI493276	Hs.9187	ESTs	4.11
	134633	L20565	Hs.83901	phosphodiesterase 4A, cAMP-specific (den	4.11
35	104461	AI637039	Hs.11481	Homo sapiens clone 24061 cDNA: mR seque	4.11
	128056	AI99131	Hs.276973	potassium large conductance calcium-acti	4.10
	114757	AI970579	Hs.291031	ESTs	4.10
	134653	AF765883	Hs.87385	ESTs	4.09
	105472	D03004	Hs.1063	pyruvate dehydrogenase (liponamide) alpha	4.08
	103102	X51177	Hs.69815	interleukin 5 receptor, alpha	4.08
	106779	BE276013	Hs.172364	Homo sapiens mR for FLJ00036 protein,	4.08
	133615	M52843	Hs.75235	ELAV (embryonic lethal, abnormal vision,	4.08
	130178	U20682	Hs.1516	iodine-like growth factor-binding protein	4.07
	124659	AW68730	Hs.289688	Homo sapiens cD FLJ11916 lts, clone HE	4.07
45	127861	AW295020	Hs.198529	ESTs	4.07
	112129	AB037715	Hs.183639	hypothetical protein FLJ10210	4.07
	100918	AK001336	Hs.31137	protein tyrosine phosphatase, receptor I	4.06
	124977	RI0173	Hs.10793	gdybA03.s1 Soares fetal liver spleen	4.05
	102722	F13271	Hs.79981	Human clone 23360 mR sequence	4.05
50	111117	AB037721	Hs.173871	KAA1300 protein	4.05
	122805	AA449120	Hs.95209	ESTs	4.05
	126392	A139254	Hs.3280	caspase 6, apoptosis-related cysteine pr	4.05
	130780	AW379130	Hs.18583	phosphodiesterase 5A	4.05
	104220	AB002324	Hs.301094	KAA0326 protein	4.05
55	112774	R65770	Hs.35455	ESTs	4.04
	111128	AW65384	Hs.15874	LATS (large tumor suppressor, Drosophila	4.04
	113146	BE151986	Hs.5722	hypothetical protein FLJ23316	4.04
	124340	AF058646	Hs.103804	heterogeneous nuclear ribonucleoprotein	4.03
	105498	H82279	Hs.24937	transformer-2 alpha (htra-2 alpha)	4.03
60	112631	R82040	Hs.48555	gdyb0606.s1 Soares placenta Nb2HP Homo	4.03
	118244	N62816	Hs.10793	ESTs	4.03
	118720	N73515	Hs.10793	gdyb04007.s1 Soares fetal liver spleen	4.03
	129232	R98881	Hs.107655	sex comb on midleg (Drosophila)-like 1	4.03
	134192	H01345	Hs.24139	Homo sapiens cD FLJ23137 lts, clone L	4.03
65	131993	BE336886	Hs.3416	adipose differentiation-related protein	4.02
	110933	T77781	Hs.3416	gdyb0401.s1 Soares fetal liver spleen	4.02
	125674	AI036166	Hs.323378	coated vesicle membrane protein	4.01
	116640	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.01
	105057	AA134233	Hs.336942	Homo sapiens cD FLJ21488 lts, clone C	4.00
70	105158	AF076367	Hs.234545	hypothetical protein NFJF29	4.00
	116245	AB033107	Hs.42796	KAA1281 protein	4.00
	119946	AA932283	Hs.58925	ESTs	4.00
	121975	AA740679	Hs.96631	ESTs	4.00
	132637	A-352702	Hs.322541	Homo sapiens, Similar to R16N cD 2780	4.00
	133659	NM_006525	Hs.166975	salting factor, arginine/serine-rich 5	4.00
75	109468	NM_015310	Hs.6763	KAA0042 protein	3.99
	106829	AW95993	Hs.27099	hypothetical protein FLJ23293 similar to	3.99
	134062	AF082645	Hs.88744	spirotry (Drosophila)-related 1 (antagoni	3.98
	105946	AA142946	Hs.5204	adaptor-related protein complex 1, gamma	3.98
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type nce	3.98
80	102589	AJ076728	Hs.8867	cysteine-rich, angiogenic inducer, 51	3.98
	104146	AF080614	Hs.146381	R binding motif protein, X chromosome	3.98
	111465	A058269	Hs.15470	putative zinc finger protein NY-REN	3.98
	126459	AK001779	Hs.110445	CGI-57 protein	3.98

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5	134388	A1W465434	Hs.87576	small nuclear ribonucleoprotein polypept	3.98
	105664	BE116364	Hs.238042	hypothetical protein FLJ14295	3.97
	115206	AW183665	Hs.186572	ESTs	3.96
	103853	AF272390	Hs.111782	myosin 5C	3.96
	110542	H53373	Hs.332938	hypothetical protein MGC9370	3.96
10	106757	AF168801	Hs.165443	Homo sapiens cD FLJ13696 fs, clone PL	3.96
	130589	AL110226	Hs.16441	DNFZP34MR24 protein	3.95
	122788	A182836	Hs.95614	hypothetical protein FLJ20574	3.95
	104518	U02816	Hs.112423	Homo sapiens mR cD DKFZp586I420 (f	3.95
	130640	NL_004753	Hs.17144	short-chain dehydrogenase/dehydroge	3.95
15	110847	N01016	Hs.709807	ESTs, Weakly similar to 2004393A chrom	3.95
	116156	AA461045	Hs.50701	ESTs	3.95
	122096	AA431162	Hs.98690	ESTs	3.95
	122160	AF765281	Hs.97439	ESTs	3.95
	123630	AA740678	Hs.112392	ESTs	3.95
20	126280	Z19417	Hs.84072	gH-HSR268122 STRATAGENE Human skelet	3.95
	126547	U47732	Hs.21576	transmembrane 4 superfamily member 3	3.95
	134757	AA913267	Hs.42206	IL2-inducible T-cell kinase	3.95
	117256	AL133427	Hs.303951	Homo sapiens mR full length insert cDN	3.95
	112251	AL050297	Hs.22003	ESTs, Highly similar to T02701 hypotheti	3.95
25	112268	W09609	Hs.324342	solute carrier family 6 (neurotransmitt	3.94
	131844	AA182924	Hs.1244	ESTs	3.94
	101607	X50111	Hs.151515	CD5 antigen (p24)	3.94
	121613	AA418879	Hs.180642	ESTs, Weakly similar to Z105293A B cell	3.93
	115815	AW905328	Hs.159649	ribosomal protein L13	3.93
30	126584	AW589427	Hs.209100	Homo sapiens cD FLJ21683 fs, clone C	3.93
	126753	AA083531	Hs.209100	gH-zn9d10.1 Stratagene hNT neuron (S37	3.93
	123201	H18359	Hs.209100	ESTs	3.93
	128954	AA346839	Hs.209100	DNFZP34C171 protein	3.92
	122839	AA477141	Hs.210850	gH-zu37p06.1 Scores ovary tumor NBH0T	3.92
35	130348	AB032957	Hs.246304	KIA1131 protein	3.91
	125847	AW161065	Hs.104335	ESTs	3.91
	120452	AL022339	Hs.230815	hypothetical protein IMAGE3510317	3.91
	123143	AA487595	Hs.21103	gH-zu55p02.1 Stratagene fetal reti 63	3.91
	105729	H46612	Hs.132354	Homo sapiens HSPC285 mR, partial cds	3.91
40	108605	AW772268	Hs.1735	Homo sapiens mR cD DNFZp564C076 (fr	3.90
	126714	AF114451	Hs.96487	egf-like module containing, match-like	3.90
	121611	M31669	Hs.80642	whitin, beta 5 (actinin A5 beta polypep	3.90
	120468	AW957675	Hs.271593	ESTs, Highly similar to S00228 ribosomal	3.89
	101356	AW878229	Hs.84045	sig1 transducer and activator of trans	3.89
45	133680	L77564	Hs.194331	mitogen-activated protein kinase 6	3.88
	105114	BE022787	Hs.295446	hypothetical protein FLJ20268	3.88
	115134	AW98073	Hs.21107	ESTs, Highly similar to A55713 inositol	3.88
	107850	AA022910	Hs.242636	ESTs, Moderately similar to s10024C cyto	3.88
	130507	AA322886	Hs.278439	neurotigin	3.88
50	101975	AA176374	Hs.263099	nuclear actinogenic sperm protein (his	3.88
	104257	AF043244	Hs.263099	nucleolar protein 3 (agaplosis represor	3.88
	122232	BE253927	Hs.263099	hypothetical protein from EUROMAGE.2021	3.88
	113248	TC3057	Hs.11556	gH-c16d01.s1 Stratagene lung (S37210) H	3.88
	114044	BE324742	Hs.2324	ESTs	3.88
55	115414	AA662240	Hs.2324	AF1514 protein	3.88
	129598	N30436	Hs.17240	Homo sapiens cD FLJ11566 fs, clone NT	3.88
	102134	AL039667	Hs.530404	proteinase 2	3.87
	106310	RS5185	Hs.21475	ESTs	3.87
	116470	A127214	Hs.28535	SRV (sex determining region Y)-box 4	3.86
60	110947	AW298410	Hs.28535	ESTs	3.85
	115839	BE300266	Hs.5247	transducin-like enhancer of split 1, hom	3.85
	103534	AW970672	Hs.227143	protein kinase, AMP-activated, alpha 1 c	3.85
	105209	AD023149	Hs.71052	KIAA6990 protein	3.85
	108746	AA127017	Hs.4983	ESTs	3.85
65	110665	A1884870	Hs.323401	ESTs	3.85
	110759	AD089560	Hs.41351	dog-30-like protein	3.85
	117068	H51257	Hs.215	EST	3.85
	130556	NM_001135	Hs.75981	agucanin 1 (chondroitin sulfate proteog	3.85
	102273	BE381815	Hs.6770	ubiquitin specific protease 14 (U9-gua	3.84
70	112960	AL110209	Hs.192113	LCAT-like lysocosphalipase	3.84
	114114	AA025436	Hs.27027	ESTs	3.84
	106208	AK001674	Hs.22530	hypothetical protein DKFZp762M1311	3.84
	122311	NM_014913	Hs.131915	cellular required for Sp1 transcription	3.84
	124271	AW253223	Hs.22978	KIAA0853 protein	3.83
75	106560	AL049561	Hs.8920	hypothetical protein FLJ20291	3.83
	112167	N59591	Hs.22570	Homo sapiens mR cD DKFZp564C0122 (f	3.83
	122354	AL157575	Hs.153610	ESTs, Weakly similar to T00325 hypotheti	3.83
	114462	R02926	Hs.126993	KIAA0751 gene product	3.83
	128198	AW265421	Hs.173540	gH-y81d06.s1 Scores fetal liver spleen	3.81
80	127003	AW816515	Hs.272137	ESTs	3.81
	109210	AA695722	Hs.5101	ATPase, Class V, type 10D	3.81
	132843	BE568452	Hs.11408	ESTs	3.80
	106827	AA461486	Hs.338477	protein regulator of cytokinesis	3.80
	124232	H53391	Hs.181102	hypothetical protein FLJ20435	3.80

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5	132005	AA149707	Ha.173091
	131392	AA235153	Ha.293328
	131775	AB014546	Ha.31921
	126257	N99638	
10	121950	AA429515	Ha.293637
	116067	AA454827	Ha.27798
	104658	AA302654	Ha.79050
	104493	AW90427	Ha.124
15	100163	W44671	Ha.47061
	116223	AF045458	Ha.104938
	123696	AL117718	Ha.188526
	128764	AW024282	Ha.296039
20	111574	AW024145	Ha.98402
	117396	W20128	Ha.271004
	119052	R10889	Ha.188602
	121806	AA404313	Ha.189479
25	122410	AA446554	Ha.156529
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	127379	AA789386	Ha.295605
	121095	AA320134	Ha.173737
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	106613	AZ135465	Ha.193737
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	118737	AA199686	Ha.101533
	124169	BE079334	Ha.101947
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	124879	R73588	Ha.7655
	128527	AA304393	Ha.118983
45	103644	M13355	Ha.44931
	106344	N90344	Ha.7970
	127867	C18530	Ha.211573
	133828	T28472	Ha.154434
50	107387	D66563	Ha.90073
	104180	AA455705	Ha.306117
	106098	BE278344	Ha.8107
	133691	M85299	Ha.293736
55	120717	AA934681	Ha.44054
	119263	T15677	Ha.153328
	102305	AL043202	Ha.5269
	106556	BE298210	Ha.293560
60	110708	N33878	Ha.173311
	114357	RA1677	Ha.7446
	115265	AW972872	Ha.47224
	123034	AL359571	Ha.15423
65	126396	T06298	Ha.75074
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	103523	AJ59444	Ha.270368
	102644	T59816	Ha.129653
70	133513	AF138407	Ha.5831
	116450	AJ544550	Ha.260707
	104596	AF067803	Ha.97019
	133579	K73536	Ha.251928
75	124656	N29317	Ha.2340
	102534	A635113	Ha.230963
	103136	BE295339	Ha.97128
	134992	AA644441	Ha.275651
80	106730	BE467313	Ha.315111
	102880	AA360240	Ha.105640
	123731	AA639338	Ha.51259
	126973	W46652	Ha.183078
85	103646	AW249439	Ha.267182
	116333	AF155627	Ha.3636
	120922	AA481003	Ha.3821
	127437	AW309554	Ha.180138
90	106378	AA638781	Ha.3330
	123000	AA584156	Ha.296356
	101464	AA852431	Ha.95667
	101397	M26380	Ha.223241
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	106112	AL117518	Ha.114191
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	127742	AW293496	
100	112938	BE281000	
	131802	AL371498	
	135162	AF187925	
	124984	BE313210	
105	118844	AL035264	
	125429	AL022654	
	125596	R25698	

ubiquitin-like 3	3.79
TBRAD1 protein	3.79
KIAA0648 protein	3.79
gbcz33g11.1 Soares fetal liver spleen	3.79
gbcz33g05.1 Soares_testis_JNT Homo sap	3.79
ESTs	3.78
Homo sapiens cD: FLJ121933 fls, clone H	3.77
transforming growth factor, beta receptor	3.77
gene predicted from cD with a complete	3.77
unc-51 (C. elegans)-like like 1	3.77
nuclear transcription factor Y, alpha	3.76
hypothetical protein MGC15936	3.75
ESTs	3.75
ESTs	3.75
gbcz33g02.1 Soares fetal liver spleen	3.75
ESTs	3.75
ESTs, Weakly similar to 130022 hypothetical	3.75
ESTs	3.75
ESTs	3.75
Homo sapiens mRNA for KIAA1667 protein,	3.75
translocase of inner mitochondrial member	3.74
mannosidase, alpha, class 2A, member 2	3.74
ras-related G3 botulinum toxin substrate	3.73
M-phase phosphoprotein 9	3.73
ESTs	3.73
ESTs	3.73
gbcz33g09.1 Siratogene hNT neuron (937	3.73
ESTs	3.73
ESTs	3.73
RAP1A, member of RAS oncogene family	3.73
ESTs	3.72
transcription factor 3 (E2A immunoglobulin	3.72
opsin 1 (cone pigment), long-wave-sensit	3.72
kinasin family member 5B	3.71
gh.C18530 Human placenta cD (Tfujizawa	3.71
U2 small nuclear ribonucleoprotein axul	3.71
Melanoma associated gene	3.71
heat shock protein hsp70-related protein	3.71
DKFZP434B027 protein	3.70
heparan sulfate proteoglycan 2 (perlecan	3.70
ESTs, Weakly similar to unknown [H.sapi	3.70
gbcz33g22.1 infant brain, Swine Soares Hom	3.70
chromosome segregation 1 (yeast homolog)	3.70
gbcz33g11.18016F1 NIH_MGC_17 Homo sapiens c	3.70
KIAA0306 protein	3.70
Homo sapiens cD FLJ14835 fls, clone OV	3.70
ESTs	3.70
ninein (GSK3B interacting protein)	3.70
EST	3.70
aldehyde dehydrogenase 5 family, member	3.70
ESTs	3.70
C10E11 homolog (44.9.D)	3.70
chromosome 6 open reading frame 5	3.70
Homo sapiens mRNA cD DKFZp561B176 (P	3.69
hypothetical protein HDAC24P	3.69
mitogen-activated protein kinase-activat	3.68
Homo sapiens mRNA cD DKFZp561B0521 (f	3.68
ESTs, Weakly similar to 170855 serine/th	3.68
Ewing sarcoma breakpoint region 1	3.68
kinase inhibitor of metalloproteinase 1	3.68
ESTs	3.68
EST	3.68
gbcz33g201.1 Siratogene lung carcinoma	3.68
nuclear pore complex transacting protein	3.67
junction plakoglobin	3.67
hypothetical protein FLJ10039	3.67
ESTs	3.67
heterogeneous nuclear ribonucleoprotein	3.67
nuclear receptor co-repressor/HDAC3 comp	3.67
Homo sapiens, clone IMACEA139775, mR	3.67
DH dehydrogenase (ubiquinone) flavopro	3.67
lipoprotein lipase	3.67
TDCK-like protein	3.66
KIAA0878 protein	3.66
neurobeachin	3.66
ESTs	3.66
TUS-associated serine-arginine-protein 2	3.66
Homo sapiens mRNA cD DKFZp434M162 (P	3.65
F-box protein 30	3.65
exukaryotic translation elongation factor	3.65
hypothetical protein	3.65
ESTs	3.65
gbcz33g44.1.2 Soares infant brain INIB H	3.65

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125792	AA496205	Hs.193703
125955	AA70232	Hs.130336
130776	AF167706	Hs.19280
131949	AK000010	Hs.258798
131912	CI4504	Hs.45184
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134203	AA161219	Hs.759
133605	AL038165	Hs.75187
109235	AB381800	Hs.306354
125447	AB322222	Hs.128303
122642	AD27765	Hs.111982
122748	AA58822	Hs.193815
103840	AW575851	Hs.47367
103533	AA234531	Hs.246112
108807	AB52236	Hs.49376
114699	AA127365	
125040	Z8444	Hs.24119
131028	AB79165	Hs.2227
131110	NM_015358	Hs.32022
100164	AW372032	Hs.173714
120637	BE149556	Hs.306621
131089	Z6245	Hs.22870
125628	AA417435	Hs.301685
122148	AW301216	Hs.103545
102337	AB14853	Hs.170133
104520	AI702384	Hs.76925
112954	AA52893	Hs.6555
125197	AF385270	Hs.278554
128124	AI125748	Hs.130194
129553	AW015763	Hs.113065
123598	AA203429	Hs.79474
126835	AK301731	Hs.103502
129225	BE222494	Hs.160919
136131	AI592743	Hs.94953
128555	AA775076	Hs.185807
102025	Z26539	Hs.167185
101572	AA437199	Hs.656
102277	U31099	Hs.158326
103867	Z80788	Hs.247616
112373	AW563557	Hs.7947
119584	AL041224	Hs.65379
125422	AA503220	Hs.153717
126381	M7955	Hs.275215
129168	AI132988	Hs.109052
129153	AA487264	Hs.154574
128789	AW538576	Hs.153551
104172	AA478418	
134263	AW573443	Hs.8096
101759	M82044	Hs.184501
104942	NM_015348	Hs.10235
123443	BE244537	Hs.157382
110707	AI239832	Hs.15617
106781	AI492261	Hs.32450
112940	AK301757	Hs.281348
115301	T11832	Hs.127297
125978	BE6843	Hs.35608
128002	AI385957	Hs.125293
119847	H51135	Hs.334604
134956	NM_020401	Hs.23202
121309	AA293834	Hs.97312
122679	AA811286	Hs.152837
105061	AA585355	Hs.13250
127207	AA371165	Hs.44833
129563	AF119664	Hs.27299
105951	R48700	Hs.20733
115543	AA404275	Hs.123253
130473	U11693	Hs.1572
104246	AF010632	Hs.201377
120562	BE244580	Hs.302257
101211	AA355357	Hs.283429
100774	J05581	Hs.89603
108407	AA371619	
113538	AI554547	Hs.15167
113876	A1799751	Hs.5635
110731	NM_014899	Hs.188006
125545	AI301480	Hs.131840
112945	AW135458	Hs.20071
131686	NM_012295	Hs.30687
125413	AB67951	Hs.74566
129360	AI000534	Hs.110708
128419	IR39007	Hs.77578
101973	U41514	Hs.80120
103616	NM_002647	Hs.32971

Homo sapiens mR: cD DKFZp58802324 (3.65
ATP-binding cassette, sub-family C (CFTR	3.65
cysteine-rich motor neuron 1	3.65
hypothetical protein FLJ22003	3.65
Homo sapiens cD FLJ12284 fs, clone MA	3.65
EST	3.64
diphtheria toxin receptor (epa-toxin-bind	3.64
translocase of outer mitochondrial membr	3.64
calcitonin gene-related peptide receptor	3.63
ESTs	3.63
KIAA0590 gene product	3.63
ESTs	3.63
KIAA1785 protein	3.63
KIAA0788 protein	3.63
hypothetical protein FLJ22644	3.63
glucosyl059.1 Stk2ap gene lung carcinoma	3.63
Homo sapiens mR: cD DKFZp58852222 (f	3.63
CCAAATenhancer binding protein (CEBP),	3.63
paranilin 1	3.63
MORF-related gene X	3.62
Homo sapiens cD FLJ11963 fs, clone HE	3.62
Homo sapiens mR full length Insert cDN	3.62
ESTs	3.62
KIAA0515 protein	3.61
forkhead box O1A (rhabdomyosarcoma)	3.61
hypothetical protein FLJ14991	3.60
Homo sapiens EST from clone 208495, full	3.60
hepatocellular-like protein	3.60
ESTs	3.60
ESTs	3.60
tyrosine 3-monooxygenase/hypophan 5-mo	3.60
Homo sapiens mR: cD DKFZp58810524 (f	3.59
inhibitor of D binding 2, downl seq	3.59
Homo sapiens, Similar to complement comp	3.59
Homo sapiens, Similar to PRO0478 protein	3.58
glutamate receptor, metabotropic 5	3.58
cell division cycle 25C	3.58
prostaglandin D2 receptor (DP)	3.58
H4 histone family, member L	3.58
ESTs	3.58
ESTs	3.58
ESTs	3.58
hydroxysteroid (11-beta) dehydrogenase 1	3.58
chromosome 14 open reading frame 2	3.58
Homo sapiens mR: cD DKFZp667N054 (t	3.57
carvein 2	3.57
glucosyl02s1.2 Soares_Jolal_Jelus_Nb2HF8_	3.57
R (guanine-7-) methyltransferase	3.57
solute carrier family 7 (calcionic amino	3.57
chromosome 5 open reading frame 4	3.56
incretin peptide receptor Agouti-related	3.55
ESTs, Weakly similar to ALU4_HUMAN ALU 5	3.55
ESTs	3.55
hypothetical protein FLJ10895	3.55
Homo sapiens cD FLJ11381 fs, clone HE	3.55
ESTs	3.55
ESTs	3.55
Homo sapiens mR for KIAA1870 protein,	3.55
mitogen-activated protein kinase	3.55
ESTs	3.54
ESTs, Weakly similar to ALU5_HUMAN ALU 5	3.54
ESTs	3.54
ESTs	3.54
transcriptional regulator protein	3.54
Homo sapiens cD: FLJ22556 fs, clone H	3.53
hypothetical protein FLJ22009	3.53
radiogenital dysplasia (Aarskog-Scott sy	3.53
lysosomal	3.53
hypothetical protein FLJ10330	3.53
SMC (mouse) homolog, X chromosome	3.53
mucin 1, transmembrane	3.53
glucosyl769s1 Stk2ap gene ovarian cancer	3.53
ESTs, Weakly similar to S37482 finger pr	3.53
ESTs	3.53
KIAA0878 protein	3.52
hypothetical protein FLJ10578	3.51
Homo sapiens cD: FLJ21836 fs, clone C	3.51
GRB2-associated binding protein 2	3.51
dihydropyrimidine-ase 3	3.51
sarcophytin, epsilon	3.50
ubiquitin specific protease 9, X chromos	3.50
UDP-N-acetyl-alpha-D-galactoseamine:polyp	3.50
phosphoinositide-3-kinase, class 3	3.50

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105535	AA459519	Hs.297681
116767	AI038593	Hs.50030
126634	AW061109	Hs.43627
130851	R66282	Hs.20247
134353	AI138201	Hs.81210
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102696	BE540274	Hs.239
113037	R17268	Hs.259673
111028	H59346	Hs.30151
111680	AI935413	Hs.30692
115613	AW136661	Hs.173546
116975	H51076	Hs.263001
100210	D26561	Hs.3104
110147	H16700	Hs.268739
115600	AA081395	Hs.42173
119068	R30261	Hs.50070
120347	AA211068	Hs.120247
122702	A1220089	Hs.99439
125552	H06701	Hs.276396
126461	A031460	Hs.267096
128572	AA533022	Hs.256593
118397	BE135479	Hs.161452
127599	AW578827	Hs.63951
123066	A1929302	Hs.181195
105693	BE259951	Hs.181368
128874	H06245	Hs.106301
119994	AA230228	Hs.59197
104000	A1145527	Hs.80475
101488	BE547216	Hs.181128
101045	J05614	
120149	AA227606	Hs.94834
107025	AA625523	Hs.21755
101716	AF050668	Hs.2563
102999	A1B15569	Hs.75730
123075	AW293173	Hs.101340
124865	AA594979	Hs.238307
127669	N25969	Hs.22851
129793	AW207000	Hs.126597
120095	AA693774	Hs.59601
110915	BE092285	Hs.29724
130542	U64675	Hs.175925
100489	BE73749	Hs.750
115027	AA743331	Hs.272572
119298	NM_001241	Hs.155473
126486	A1065133	Hs.152316
130021	M24470	Hs.1435
127166	AW954605	Hs.263395
114989	AA251089	
133817	AW578716	Hs.7644
133562	M60721	Hs.74570
105810	AA209072	Hs.59972
129007	AK001521	Hs.107882
100662	A1369680	Hs.816
120159	BE07031	Hs.92927
134866	AW020280	Hs.320
100369	D79989	Hs.115779
104260	AF008192	Hs.194283
100134	AA305748	Hs.49
116015	AA338448	Hs.50334
119251	T15753	Hs.65250
127176	BE387162	Hs.290658
123422	AA59484	Hs.146349
123654	AA761073	Hs.103400
105209	AB020038	Hs.103000
111219	N68836	Hs.13247
127963	AI299013	Hs.87779
109412	BE343313	Hs.209473
118794	AW031051	Hs.115210
112040	R43256	
111180	A1793851	Hs.283108
117329	AA524065	Hs.39570
104711	A1263696	Hs.194061
109265	AA195025	Hs.35992
109557	AW524045	Hs.5427
120753	AA312551	Hs.230157
120870	AA365118	Hs.97379
127094	F13215	Hs.287649
127746	AI229495	Hs.120189
123553	AA494291	Hs.111977
130652	M31699	Hs.1735
135101	U82715	Hs.94498
127199	AI865740	Hs.124027
112278	Z41968	Hs.26039

serine (or cysteine) protease inhibitor	3.50
ESTs	3.50
SRF (sex determining region Y)-box 22	3.50
ESTs, Weakly similar to S65657 alpha 1C-	3.50
nuclear receptor subfamily 4, group A, member 1	3.50
hypothetical protein FLJ12376	3.50
forkhead box M1	3.49
and transport of synaptic vesicles	3.49
ESTs, Weakly similar to U38022 hypothetical	3.49
p21 (CDKN1A)-activated kinase 2	3.49
hypothetical protein FLJ10486	3.48
ESTs	3.48
KIAA0042 gene product	3.48
ESTs	3.48
Homo sapiens cD FLJ103066 fs, clone NT	3.48
Homo sapiens cD FLJ22030 fs, clone K	3.48
nuclear fragile X mental retardation protein	3.48
ESTs	3.48
ESTs, Weakly similar to U38022 hypothetical	3.48
ESTs	3.48
interleukin enhancer binding factor 3, 9	3.48
ESTs	3.47
nucleolar protein family A, member 1 (H	3.47
DJ (Hsp51) homolog, subfamily B, member	3.47
US-mRNP-specific protein (220 kD), orth	3.47
ESTs, Weakly similar to PC4259 keratin	3.46
ESTs	3.46
polymerase (R) II (D directed) polyp	3.46
EUK1, member of ETS oncogene family	3.46
gH:Human proliferating cell nuclear anti	3.46
ESTs	3.46
ESTs, Weakly similar to U38022 hypothetical	3.45
tyrosin, precursor 1 (substance K, au	3.45
sig1 recognition particle receptor (I	3.45
ESTs, Weakly similar to A42442 integrin	3.45
lysosyl-IR synthetase	3.45
solute carrier family 7 (calcium amino	3.45
Homo sapiens cD FLJ10293 fs, clone NT	3.44
ESTs	3.44
hypothetical protein FLJ13187	3.43
RAN binding protein 2-like 1	3.43
FLJ596-binding protein 1A (T240)	3.43
hemoglobin, alpha 2	3.43
cyclin T2	3.43
hypothetical protein PRO0971	3.43
guanosine monophosphate reductase	3.43
alpha domain, transmembrane domain (TM),	3.42
gblz04005.s1 NCL_CQAP_GCB1 Homo sapiens	3.42
H1 histone family, member 2	3.41
H20 (Drosophila)-like homeo box 1	3.41
testal Alzheimer antigen	3.41
hypothetical protein FLJ10659	3.41
SRF (sex determining region Y)-box 2	3.41
putative 47 kDa protein	3.41
acidulase recognition factor 1	3.41
KIAA0166 gene product	3.41
putative GR6 protein	3.40
macrophage scavenger receptor 1	3.40
testes development-related NYD-SP22	3.40
EST	3.40
ESTs, Highly similar to A39561 D excis	3.40
gblz03040.s1 Gessler Wilms tumor Home s	3.39
TRAF family member-associated NFkB activ	3.39
KIAA0051 protein	3.39
ESTs, Moderately similar to ALUC_HUMAN1	3.38
Homo sapiens cD FLJ23087 fs, clone L	3.38
hypothetical protein FLJ10520	3.38
ESTs	3.38
g-hyplTe11.s1 Scores infant brain IN1B H	3.38
hemoglobin, gamma G	3.38
Homo sapiens cD FLJ22664 fs, clone H	3.38
ESTs, Weakly similar to U38022 hypothetical	3.38
ESTs	3.38
ESTs	3.38
ESTs, Weakly similar to A46010 X-linked	3.38
ESTs, Weakly similar to T27074 hypothetical	3.38
ESTs	3.38
inhibin, beta B (activin AB beta polypep	3.37
leucocyte immunoglobulin-like receptor,	3.37
SELENOPHOSPHATE SYNTHETASE, Human selen	3.37
Homo sapiens cD FLJ13937 fs, clone Y7	3.36

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13401	AG510175	Hs.17967	Homo sapiens cD FLJ12195 fls, clone MA	3.36
189292	AW975746	Hs.168662	KIAA1702 protein	3.36
135026	N82165	Hs.53231	ESTs	3.36
128120	N49233	Hs.46914	ESTs, Weakly similar to AA6010 X-linked	3.35
123476	AA394564	Hs.108826	ESTs	3.35
111076	N89129	Hs.20851	ESTs	3.35
111520	AB65369	Hs.301134	ESTs	3.35
133383	BE313555	Hs.7252	KIAA1224 protein	3.35
103731	AA07605	Hs.23495	gbczn70cd3.r1 Stralagene neuroepithelium	3.35
108231	AW022114	Hs.124972	hypothetical protein FLJ11252	3.35
112520	RF6854	Hs.30814	ESTs	3.35
115725	AW899053	Hs.76917	F-box only protein 8	3.35
125867	H13331	Hs.123721	ESTs	3.35
127719	AZ42163	Hs.27670	chromodomain helicase D binding protei	3.35
129663	BE379765	Hs.125872	sperm associated antigen 9	3.35
130816	M51877	Hs.1585	spectrin, alpha, erythrocytic 1 (pili)	3.35
130888	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	3.35
133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene fami	3.35
118986	HF148713	Hs.125930	bladder cancer overexpressed protein	3.35
101723	U20504	Hs.82991	gbcHuman nonmuscle myosin heavy chain II	3.34
134693	N70361	Hs.6854	Human transcription unit PVT gene, exons	3.34
102856	M26150	Hs.246177	H3 histone family, member L	3.34
105953	AA279341	Hs.174151	aldehyde oxidase 1	3.34
134746	L34039	Hs.89404	cadherin 4, type 1, Recadherin (rel)	3.34
109149	AA831179	Hs.40065	hypothetical protein MGC4825	3.33
115026	AA251972	Hs.188718	ESTs	3.33
103546	Z14244	Hs.75782	cytochrome c oxidase subunit VIb	3.33
111159	N87023	Hs.272330	ESTs, Weakly similar to G55024 reverse t	3.33
127076	AA422551	Hs.146162	ESTs	3.33
124549	AB032310	Hs.336780	tubulin, beta polypeptide	3.33
111012	AB077389	Hs.269818	ESTs, Weakly similar to Z155_HUMAN ZINC	3.33
115412	AW626660	Hs.44151	KIAA0574 protein	3.33
115351	AL133623	Hs.82991	similar to mouse Xmi1/Dhm2 protein	3.33
121633	AA417011	Hs.98175	EST	3.33
124591	N66243	Hs.152974	hypothetical protein FLJ12735	3.33
130725	AB021179	Hs.15259	HMEA-inducible	3.33
131945	NM_029516	Hs.35120	replication factor C (activator 1) 4 (37	3.33
132581	AK000031	Hs.52255	hypothetical protein FLJ20824	3.33
108726	NM_012068	Hs.9754	activating transcription factor 5	3.32
101867	M56132	Hs.52296	gt-Human MHC class II HLA-DR-beta-1*0501	3.32
105004	DE516828	Hs.153034	KIAA113 protein	3.32
100208	ALJ139103	Hs.53534	pumilio (Drosophila) homolog 1	3.32
118349	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.32
103352	H03366	Hs.78935	uracil-D glycosylase	3.30
107436	WZ1720	Hs.12450	protocadherin 9	3.30
105002	A1160541	Hs.33130	gbc244612.x1 Stralagene hNT neuron (537	3.30
103379	A1300505	Hs.15119	Homo sapiens cD: FLJ23486 fls, clone L	3.30
111221	AB037782	Hs.47111	KIAA1361 protein	3.30
117903	AA768283	Hs.15119	ESTs	3.30
122265	AA451009	Hs.15119	gbc244612.x1 Stralagene hNT neuron (537	3.30
128226	A1284960	Hs.280082	GM2 ganglioside activator protein	3.30
111545	R40663	Hs.124944	ESTs	3.30
126214	AW748336	Hs.168052	KIAA0421 protein	3.30
121073	H40199	Hs.112184	DKFZP95J0615 protein	3.30
122063	T36901	Hs.75117	interleukin enhancer binding factor 2, 4	3.30
100592	NM_007269	Hs.1238	membrane metallo-endopeptidase (neutral	3.30
134021	L13720	Hs.78501	growth arrest-specific 6	3.30
126452	R26687	Hs.42710	gbc244612.x1 Scores placenta NB2HP Homo	3.29
117195	A7780425	Hs.10340	ESTs	3.29
127663	AK000452	Hs.246112	hypothetical protein FLJ20345	3.29
115677	Z70200	Hs.16919	KIAA0788 protein	3.28
123268	AA876616	Hs.259729	ESTs, Weakly similar to AA4352 meso 2 p	3.28
105553	AL043679	Hs.2228	KIAA0556 protein	3.28
102915	X07820	Hs.19221	myosin metalloproteinase 10 (chromolysin	3.28
104348	H05405	Hs.7549	hypothetical protein DKFZp696G1424	3.28
113047	A1571940	Hs.10305	ESTs	3.28
113203	AA474563	Hs.169183	ESTs	3.28
114503	AL040600	Hs.41086	ESTs	3.28
122100	AA431220	Hs.105652	pleckstrin homology domain-containing, f	3.28
123073	AA485061	Hs.161473	ESTs	3.28
130253	A1076570	Hs.153103	phosphoglucomutase 5	3.28
133365	W65119	Hs.8938	eukaryotic translation initiation factor	3.28
130762	DB4371	Hs.46440	paraoxonase 1	3.28
132360	AW899660	Hs.52254	solute carrier family 21 (organic anion	3.28
110763	A1928445	Hs.184211	synaptotagmin-like 2	3.27
103437	AV655598	Hs.87829	peptidase (mitochondrial processing) bet	3.27
114840	AA447391	Hs.10305	ESTs, Highly similar to RB18_HUMAN BAS-R	3.27
105888	AA020964	Hs.13225	complex of binding protein	3.27
129896	BE295968	Hs.14716	UOP-GalbetaGlc beta 1,4-galactosyl	3.26
113459	T80206	Hs.320113	ESTs	3.26
134332	D86982	Hs.230113	growth factor receptor-bound protein 10	3.26
117048	H89732	Hs.268189	EST	3.26
109249	AA194730	Hs.268189	hypothetical protein FLJ20436	3.26

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	134953	W73428	Hs.8750	uncharacterized bone marrow protein BM04	3.26
	114440	AL048511	Hs.106525	hypothetical protein FLJ12567	3.25
	102196	BC266383	Hs.75728	chromatin assembly factor 1, subunit B (3.25
	109891	R45584	Hs.23025	ESTs, Weakly similar to ALLUS_HUMAN ALU S	3.25
5	120814	AW867796	Hs.96660	ESTs, Weakly similar to U38022 hypophel	3.25
	122391	AA446315	Hs.191622	ESTs	3.25
	122553	AA451254	Hs.190121	ESTs	3.25
	124755	R38087	Hs.267650	KIAA1228 protein	3.25
10	130943	U20760	Hs.272429	calcium-sensing receptor (hypocalcemic	3.25
	115185	BC296977	Hs.106481	hypothetical protein FLJ23357	3.25
	114297	AA143707	Hs.173091	ubiquitin-like 3	3.25
	106657	AW864389	Hs.33476	hypothetical protein FLJ11937	3.25
	124320	H85749	Hs.102942	EST	3.25
15	124087	H08873	Hs.288550	Homo sapiens cD FLJ11454 fs, clone HE	3.24
	110705	AB007992	Hs.32168	KIAM042 protein	3.24
	106508	A125765	Hs.30345	ESTs	3.24
	112538	A4908813		glogp77h05.s1 NCI_GSPAP_Ov6 Homo sapiens	3.24
	100130	NM_003034	Hs.103724	peripheral myelin protein 22	3.24
20	106017	AA477956	Hs.26268	ESTs	3.24
	115921	AW975530	Hs.28355	hypothetical protein FLJ22402	3.23
	121520	AA421163	Hs.164785	ESTs	3.23
	129255	A1951727	Hs.106904	H1 histone family, member X	3.23
	129569	H81306	Hs.194485	ESTs	3.23
25	119563	AA081215	Hs.58603	Homo sapiens cD FLJ14206 fs, clone NT	3.23
	111273	N10324		glc2a3305.s1 Soams field liver spleen	3.23
	102971	N116639	Hs.133805	ankyrin 1, erythrocytic	3.23
	103037	AA930503	Hs.13835	ESTs, Weakly similar to U38022 hypophel	3.23
	121773	NM_015802	Hs.278428	progestin induced protein	3.23
30	128872	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypophel	3.23
	132528	T73738	Hs.50785	SMC2 (structural maintenance of chromoso	3.23
	134835	L04569	Hs.83925	calcium channel, voltage-dependent, L ty	3.23
	103158	BC242587	Hs.118651	hypothetically expressed homeobox	3.22
	116405	AL117510	Hs.3386	KIA0573 protein	3.22
	104531	AA020844	Hs.18800	ESTs	3.22
35	114253	BE142686	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.22
	134607	A1675881	Hs.36538	ESTs	3.22
	135114	AW340483	Hs.175043	ancient conserved domain protein 4	3.22
	120191	BE407106	Hs.65507	Homo sapiens, clone IMAGE3559816, mR,	3.22
40	105029	AI122891	Hs.13268	ESTs	3.21
	128550	AA418276	Hs.170142	ESTs	3.21
	119873	A1660149	Hs.44365	lysosomal	3.21
	130715	T47284	Hs.149223	XOcs binding protein 1	3.21
	133916	ALJ08185	Hs.77555	thyroid hormone receptor-interactor 7	3.21
45	120259	AW014786	Hs.192742	hypothetical protein FLJ2785	3.21
	110721	H97678	Hs.31319	ESTs	3.21
	130362	ALJ08415	Hs.278679	a disintegrin and metalloprotease doma	3.21
	100265	D38521	Hs.112256	KIAA0077 protein	3.20
	100624	AB001026	Hs.9346	ryanodine receptor 3	3.20
50	122275	AA437124	Hs.187247	ESTs	3.20
	127099	AA347688	Hs.8172	glc-EST54026 Fetal heart II Homo sapiens	3.20
	134521	BE358382	Hs.8172	ESTs, Weakly similar to A46010 X4n	3.20
	132829	AF381444	Hs.5124	meningioma expressed antigen 5 (lysulron	3.20
	101125	A4250562	Hs.82749	transmembrane 4 superfamily member 2	3.20
55	128339	AL120387	Hs.296406	KIAA0685 gene product	3.19
	117121	H65044	Hs.321386	EST	3.19
	124760	AW403586	Hs.91052	ESTs, Moderately similar to ALLUS_HUMAN A	3.19
	132232	A1522273	Hs.42604	ESTs	3.19
	125919	W26713	Hs.256972	ESTs	3.19
60	123324	A6013352	Hs.105399	KIAA0069 protein	3.19
	103157	D14651	Hs.119	Wings (tumor 1-associating protein	3.18
	101447	M21305		glc-Human alpha satellite and satellite 3	3.18
	124345	NM_014487	Hs.120766	nuclear cysteine-rich protein	3.18
	125833	NM_012447	Hs.20132	stromal antigen 3	3.18
65	126861	AL133014	Hs.107387	CSL-20 protein	3.18
	111121	A160766	Hs.13206	ESTs	3.18
	134977	AL044963	Hs.306121	leukocyte receptor cluster (LRC) encoded	3.18
	131535	N22120	Hs.75277	hypothetical protein FLJ13910	3.18
	109950	H08280	Hs.268770	ESTs, Weakly similar to Z0045959A chromos	3.18
70	128675	A1810118	Hs.15365	hypothetical protein FLJ13320	3.18
	101654	M65296	Hs.733	erythrocyte membrane protein band 4.2	3.18
	104732	AL079294	Hs.29952	Homo sapiens mR full length insert cDN	3.18
	108887	A8037444	Hs.34952	KIAA1323 protein	3.18
	103331	AA089728	Hs.161542	ribosomal protein L24	3.18
	118042	AA52289	Hs.161465	ESTs	3.18
75	120900	AA830712	Hs.291931	ESTs	3.18
	128312	T97579	Hs.110334	ESTs, Weakly similar to T78885 sarineth	3.17
	115291	AA140377	Hs.41932	hypothetical protein FLJ21275	3.17
	113672	AA012890	Hs.181178	ESTs	3.17
	115665	BE072425	Hs.44579	hypothetical protein FLJ20199	3.17
80	127581	AK003680	Hs.265175	phosphoprotein associated with GEMs	3.17
	128644	AV559017	Hs.184325	CG3-76 protein	3.16
	106830	AA131743	Hs.103352	ESTs	3.16
	124443	AB87519	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.16

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	106290	AW061393	Hs.16364	hypothetical protein FLJ110955	3.16
	122787	AZ09093	Hs.35912	ESTs	3.16
	133112	T15495	Hs.152321	lysinepin-releasing hormone	3.16
5	115435	AA186761	Hs.334812	hypothetical protein DKFZp55660717	3.16
	109121	BE383087	Hs.49767	DH delydrotase (ubiquitin) Fe-S pro	3.16
	126721	AW579621	Hs.123539	Try-1 cell surface antigen	3.15
	105226	AA203429	Hs.79474	lysine 3 monooxygenase/histophan 5-oxo	3.15
	104512	DI1317	Hs.78715	CA-binding protein transcription factor	3.15
10	105299	AF089851	Hs.194720	ATP-binding cassette, sub-family G (WHIT)	3.15
	117842	A984505	Hs.161121	ESTs	3.15
	123049	BE040760	Hs.221169	claklapt (Drosophila lewis) homolog 2	3.15
	128639	AW529697	Hs.102697	CG-47 protein	3.15
	130343	AB040914	Hs.278628	KIAA1481 protein	3.15
	115706	AB004849	Hs.50748	chromosome 21 open reading frame 18	3.15
15	120673	AW566534	Hs.105993	ESTs	3.15
	132116	AW569474	Hs.40089	ESTs	3.15
	116217	AI070674	Hs.123178	translocase of inner mitochondrial membr	3.15
	104926	BE289809	Hs.33363	DKFZp434N093 protein	3.14
20	105297	NM_015905	Hs.193858	transcriptol intermediary factor 1	3.14
	125343	AW54585	Hs.304101	ESTs, Weakly similar to ALUT_HUMAN ALU S	3.14
	115618	H11695	Hs.322301	disruptor of silencing 10	3.14
	124883	AA830185	Hs.269680	ESTs	3.13
	106461	BES39071	Hs.65038	hypothetical protein FLJ20505	3.13
25	126165	AI741816	Hs.126597	ESTs	3.13
	100212	AJ205334	Hs.254279	Homo sapiens mR: cD DKFZp566M063 (fr	3.13
	101628	M57506	Hs.72918	small inducible cytokine A1 (i-305, homo	3.13
	107951	AI300077	Hs.61590	ESTs	3.13
	109186	AA219891	Hs.73625	RAB8 interacting, Nuclein-like (tablins)	3.13
30	117259	HT5768	Hs.57847	gh-y02007.1 Morion Fetal Cocleas Homo	3.13
	119694	AA041350	Hs.164515	ESTs, Moderately similar to IC6A_HUMAN C	3.13
	124840	R56146	Hs.290275	EST, Weakly similar to AF090530 1 PRO407	3.13
	127433	AW979195	Hs.786152	amino acid transporter 2	3.13
	128337	AI123529	Hs.166152	ESTs	3.13
35	134023	AW626996	Hs.78551	KIAA0217 protein	3.13
	134475	NM_014733	Hs.83790	KIAA0305 gene product	3.13
	128761	BE300341	Hs.104925	ectodermal-neur al cortex (with ETS-like	3.12
	124671	T23800	Hs.101001	hypothetical protein FLJ14728	3.12
	128314	T87479	Hs.291797	ESTs	3.12
40	134685	AB036329	Hs.178347	SKIP for skeletal muscle and kidney enri	3.12
	131333	BE244603	Hs.25726	transposon-derived Buxter1 transposase-1	3.12
	119781	AJ278016	Hs.55565	anlyrin repeat domain 3	3.12
	131624	U23636	Hs.32335	TATA box binding protein (TBP)-associate	3.11
	124596	AW194451	Hs.111801	arsenic resistance protein ARS2	3.11
45	116115	AL042355	Hs.70202	WD repeat domain 10	3.11
	129415	A907084	Hs.111243	MADS box transcription enhancer factor 2	3.11
	111552	T97938	Hs.191185	ESTs	3.10
	134861	NM_000937	Hs.171390	polymerase (R) II (D directed) polyp	3.10
	104971	BE311926	Hs.15530	hypothetical protein FLJ12691	3.10
50	126536	AA156151	Hs.214818	glicox48c06.1 Stralagene endothelial cel	3.10
	128246	A980512	Hs.101996	DWR1-like family C2	3.10
	108412	AA453734	Hs.61358	ESTs	3.10
	107902	AA026627	Hs.28739	ESTs	3.09
	112495	A1346487	Hs.3383	KIAA0214 gene product	3.09
55	131870	NM_014874	Hs.7457	MAGE1 protein	3.09
	105301	AW352357	Hs.112708	ESTs, Moderately similar to ZNF1_HUMAN Z	3.09
	123670	AI189144	Hs.159154	tubulin, beta, 4	3.09
	116674	AW160774	Hs.22689	Homo sapiens mR: cD DKFZp596O1318 (f	3.08
60	112064	AL045390	Hs.322149	Human clone 137303 mR, partial cds	3.08
	130625	AA361850	Hs.110653	reflexic acid induced 1	3.08
	123068	AL045390	Hs.33382	protein phosphatase 4, regulatory subuni	3.08
	102735	AF111106	Hs.190745	glyc65h12e1 Soares placenta Nb2HP Homo	3.08
	124748	R34617	Hs.31097	Homo sapiens cD FLJ21226 ts, clone C	3.08
65	120755	AA312834	Hs.315164	hypothetical protein FLJ21478	3.08
	118895	BE330497	Hs.25793	hypothetical protein similar to actin re	3.08
	107463	AW552022	Hs.125316	ESTs	3.08
	114290	R51383	Hs.151973	ESTs, Weakly similar to S33950 finger pr	3.08
	119005	AL038511	Hs.226607	hypothetical protein FLJ23511	3.08
	122676	BE512018	Hs.55075	EST	3.07
70	127765	AW223659	Hs.239370	KIAA010 gene product	3.07
	132693	BE244200	Hs.9004	DKFZP727051 protein	3.07
	106812	BE251590	Hs.25119	chondroitin sulfate proteoglycan 4 (mela	3.07
	122654	X96753	Hs.25119	ESTs, Weakly similar to YE92_YEAST HYPOT	3.06
	111636	RS5284	Hs.81008	filamin B, beta (actin-binding protein-2	3.06
75	101882	AF040045	Hs.268774	ESTs	3.06
	110004	HT0413	Hs.44666	ESTs	3.06
	117591	N64777	Hs.7589	ESTs, Weakly similar to A46010 X-linked	3.06
	110737	AA336609	Hs.61084	SEC24 (S. cerevisiae) related gene fami	3.06
80	134037	NM_010022	Hs.48827	hypothetical protein FLJ12055	3.06
	132450	AA100012	Hs.334806	KIAA1238 protein	3.06
	125556	AB033064	Hs.42744	cytoplasmic binding protein	3.06
	101811	NM_002556	Hs.23402	TCR eta	3.06
	131530	AA574309	Hs.172506	myosin VB	3.06
	105049	AB032945			

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	126614	AA701941	Hs.167555	ESTs	3.05
	130960	AF03621	Hs.21611	luciferin family member 3C	3.05
	105603	AW963624	Hs.31707	ESTs, Weakly similar to YEWL_YEAST HYPO	3.05
5	107361	U72513	Hs.159406	Human RPL13-2 pseudogene mRNA, complete	3.05
	107975	DB1886	Hs.55908	ESTs	3.05
	116999	HB4644	Hs.40707	EST	3.05
	119554	W38188		(NONE)	3.05
	120934	AA226198		gluc28a07.s1 NC_024047.1 Homo sapiens	3.05
10	125805	A116094	Hs.166656	ESTs, Highly similar to A49460 glutamate	3.05
	122263	AA331156		gH-EST159034 Embryo, 6 week, subtracted (3.05
	129025	T64877	Hs.108479	ESTs	3.05
	131090	A1143139	Hs.2289	visinin-like 1	3.05
	112197	NM_003655	Hs.5637	ESTs	3.05
15	133462	L40397	Hs.74137	transmembrane trafficking protein	3.04
	118465	AA508515	Hs.251049	ESTs	3.04
	113693	AD373741	Hs.59384	hypothetical protein MGCS3D47	3.04
	116911	AW006577	Hs.308436	ESTs, Moderately similar to KIAA0745 pro	3.04
	132533	U78525	Hs.57783	eukaryotic translation initiation factor	3.04
20	124724	H02816	Hs.112423	/Homo sapiens mRNA; cDNA DKFZ586H1420 (f	3.04
	105894	AB04740	Hs.25591	receptor (calcitonin) activity modifying	3.04
	129991	R28386	Hs.178925	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.04
	129714	T85231	Hs.179661	tubulin, beta 5	3.04
	134650	U76376	Hs.87247	haxk8a, BCL2-interacting protein (cont	3.04
25	108551	AK58923		glutathione S-transferase 1 NC_024047.1 Homo sapiens	3.04
	133445	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.04
	102691	AAU07723	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.04
	127542	AA703694	Hs.245474	ESTs	3.03
	113043	AK620709	Hs.7483	ESTs	3.03
30	134710	AA333797	Hs.6989	serine hydroxymethyltransferase 1 (solub	3.03
	119245	AB157533	Hs.114360	transforming growth factor beta-stimulat	3.03
	106391	AW950538	Hs.321214	hypothetical protein DKFZp564D0478	3.03
	114807	AF041260	Hs.123057	breast carcinoma amplified sequence 1	3.03
	111093	AA105708	Hs.44581	heat shock protein hsp70-related protein	3.03
35	130795	AT071457	Hs.38694	ESTs	3.03
	103825	A1671935	Hs.55468	ESTs	3.03
	109436	A1141031	Hs.21342	ESTs	3.03
	124459	N22508		Homo sapiens cDNA FLJ21475 fls, clone C	3.03
	126394	AA090198	Hs.4779	KIAA1150 protein	3.03
40	127995	AA970953	Hs.128709	ESTs	3.03
	127981	AA837029	Hs.157463	ESTs	3.02
	124417	K34059		gbyv28h09.s1 Scores fetal liver spleen	3.02
	124357	N22401		gbyv37g07.s1 Morion Fetal Cochlea Homo	3.02
	105437	AF151076	Hs.25199	hypothetical protein	3.02
45	101159	AA327723	Hs.76122	splicing factor, arginine/serine-rich 4	3.02
	113897	R91601	Hs.4947	hypothetical protein FLJ22584	3.02
	100159	AA281269	Hs.23468	KIAA0107 gene product	3.02
	105487	AB097340	Hs.133295	Homo sapiens clone FLB8436 PRO2277 mRNA,	3.02
	124977	F04819	Hs.190452	KIAA0365 gene product	3.02
50	131631	AA022569	Hs.29002	sirt (Drosophila) homolog 2	3.01
	102259	AL041219	Hs.62222	serpin domain, immunoglobulin domain (Ig),	3.01
	104399	AL022316	Hs.301947	luciferin-like	3.01
	116536	BE219027	Hs.89909	ESTs	3.00
	125959	AA351975	Hs.4943	hepatocellular carcinoma associated prot	3.00
55	102233	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	3.00
	102826	U90392	Hs.27112	G protein-coupled receptor 23	3.00
	112812	HS5977	Hs.35810	ESTs	3.00
	114654	AA101940	Hs.103679	ESTs	3.00
	118555	N85372		gbyv26c10.s1 Scores_fetal_liver_NHNL19W	3.00
	120035	W90105	Hs.94942	EST	3.00
	123596	AA421130	Hs.112640	EST	3.00
60	126134	AL133033	Hs.4084	KIAA1025 protein	3.00
	126194	H98755	Hs.302975	ESTs, Weakly similar to Z195_HUMAN ZINC	3.00
	129778	AK021676	Hs.12457	hypothetical protein FLJ10814	3.00
65	Table 3B:				
	Pkey:	Unique Ecd protease identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
70	Pkey	CAT number	Accession		
	123619	371681_1	AA602894 AA602894		
	124417	1642364_1	K34059 K34059		
	117299	1632596_1	N75768 N75768		
75	116845	363481_1	AA649630 AA649631 H64973		
	124748	1715060_1	R34617		
	125596	1708455_1	R35098 R35082 R50018		
	126257	182211_1	H50538 AW973759 AA328271 H90994 AA558020 AA234435 NS9599 RS4815		
	126290	1572221_1	Z19417 H20666		
	126319	1528523_1	DE1689 DE1682		
80	101172	274949_1	AA476416 AA383338 AA398747 AA476518		
	126426	110867_1	AA128894 AA127185 AA086705 AA070337 AA100017 AA078891 AA113255 AA075168 AA082768 AA083380 NB4925 AA084752		
			AA075512 AA086119 AA083018 AA088545		
			AA325606 AA089517 NB4923		
	126433	127143_1			

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	127092	177998_1	T26563 Z44165
	127099	244301_1	AA347662 AAW56810 Z44271 F07065 F37064 R13506
	126536	149206_1	AA156151 Z25109 Q25177
5	103731	112052_1	AA070545 AA131490 AA131373
	127223	222161_1	AA331156 AA331157 AA331156
	126782	111380_1	AA063531 AA128047 AA074915 AA148649
	116946	1683467_1	N02834 W25001
	127520	656170_1	TS1239
	127532	353907_1	AJ003429 AJ003367 AA564825
10	112516	174422_1	T03549 F05686
	125239	504576_1	AA098813 R70255
	112540	1605263_1	R09751 R70467 H05771 H30879 H80078
	113248	328626_1	T63657 AW571220 AA493468 T53693
	112631	1742657_1	R02040 W05934
15	126380	154028_1	F12374 T74669
	120514	25532_3	AA025335 AA259499
	127867	1511945_1	C18530 T63853
	126637	209365_1	AA811804 AA099404 AA260907 AW877624
	121481	123307_1	AA411931 AA411930
20	120554	177521_1	AJ225198 AA226513 AA383773
	106566	120368_1	BE298210 A672315 AWW06489 BE298417 AA455921 AA002537 BE327124 R14963 AA085210 AW274723 A1333684 A1369742
			AA039658 A1385095 AA476470 A1287650 A1885299 A1885381 A18552624 AW340136 A4266556 AA465390 A1310815 A4484951
25	121743	274592_1	AA397638 Z441144
	114699	135232_1	AA127086 R15844 AA127404
	106851	322947_1	AA586233 AA637008 AA484509 R22065 AA485570
	123731	genbank_AA09639	AA609839
	123973	506395_1	C14805
	116793	74964_1	T177281 AW041457 D14232 A181246 AA452599 AAG29494 N35686 AA45493 AA1201738 T77780 A1342309 A1069302 H06003
			AA0510576 H37814 W15360 A137326 A1702287 AA125405 AA119697 AW1169012 AA043053 A289511
30	109700	genbank_F09609	F09609
	118486	genbank_N6741	N66741
	111273	genbank_N70934	N70934
	116555	genbank_N06372	N06372
	111462	genbank_R05296	R05296
35	118720	genbank_N73515	N73515
	118737	362979_1	AA199686 N73661
	111826	genbank_R35975	R35975
	120376	genbank_AA227459	AA227459
40	120809	genbank_AA345495	AA345495
	120839	genbank_AA348913	AA348913
	123673	genbank_AA330915	AA330915
	115498	genbank_AA291070	AA291070
	101045	entrez_J05814	J05814
	129969	genbank_N57818	N57818
45	106407	genbank_AA075519	AA075519
	122939	genbank_AA471141	AA471141
	117031	genbank_H08353	H08353
	124298	genbank_H91679	H91679
	117099	371871_1	H93699 H97976 H80035
50	101447	entrez_X021905	X021905
	124357	genbank_W22401	W22401
	101723	2602_1	U04304 AA355800 M09181 AA375523 AA093550 AA365395 SG7247 A371761 AW351920 AW19189 H28934 W79172 AA653543
55			AA122005 W95572 AF095605 C02448 W57658 T11988 W95465 AA425179 F05724 F12205 F06285 R16384 T66222 F08515
			F07280 AA163046 H63284 T96770 H63366 AA347253 H72001 H62899 H08396 H09380 N29054 N30250 T97385 T96819
			AA463307 AL073990 T11387 AA335949 AA149133 T60613 AA022555 AA035108 AA449123 AA340297 AA211515 W95196
			AA595678 AA149134 C18426 C16097 C16587 C16138 C16107 AA021794 C16590 N30019 R55718 R60552 N84522 A1143322
			AW515024 AA490700 N02675 AW295747 C16068 D68331 C15518 A141214 N67221 C15423 C16537 C16094 C16152 H28935
			T66152 C16382 AW022425 AA602058 AA594603 H22255 W74368 C16356 A129361 A917896 A552253 A1923896 A1039007
			AA191910 A857881 C16428 A16345 A277790 R12325 A640428 A104136 A27757 C16106 F09836 T71212 AA152316
			AW009751 A0053902 T16094 AW0022915 C16556 AWK72878 T96200 AA476286 N70446 F02270 H03268 T09992 AA07463
			T34275 A1616017 H11758 A1652080 H82900 A174575 N66716 F04914 AA505470 AA983349 F01973 A112277 F04729 C16236
			A4879148 AA295754 AA887045 R08127 D57339 AA49047 A16698 H8 A1190955 AA03507 A115272 AL135029 AA258725
			AL079521 N40239 A850919 N85148 AA341165 T28492 N83749 A1302123 A006303 A1550411 A1335653 A276551 AW027482
			AW197537 A1162523 A1336930 A094939 A051400 AA425955 AA341763 AA09274 AA03570 A1123565 T72559 F05080
			AA065931 AA45824 T07180 AW084799 AA306254 T69006 W28367 F55226 W22995 AL044546 AA501890 N84045 T97274
			N87532 AL135219 AA116066 T06000 AA116057 T07181 R08126
60			R10103
			H05683
			N06132
70	126577	genbank_R01073	R01073
	110243	genbank_W06683	W06683
	101867	entrez_M06132	M06132
	101941	entrez_S77583	S77583
	113052	146538_1	R10689 R10688
	126152	239811_1	R26867 R27438
	119523	genbank_T15977	T15977
75	112040	genbank_R43286	R43286
	103657	entrez_Z73677	Z73677
	119600	genbank_T32767	T32767
	119554	NOT_FOUND_entrez_WC3818	W38186
	123130	genbank_AA487200	AA487200
	123143	genbank_AA487595	AA487595
80	121950	genbank_AA429515	AA429515
	122665	genbank_AA491209	AA491209
	114988	genbank_AA251089	AA251089
	107794	genbank_AA019255	AA019255

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123422 genbank_AA598484 AA598484
169352 genbank_A1165041 AA165041

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TABLE 4A: ABOUT 1154 GENES UPREGULATED IN GLIOBLASTOMA

Phy: Unique Ecd protein identifier number
ExAcc: Exon/Accession number, Genbank accession number
UniGeneID: UniGene number
UniGene Title: UniGene gene title
R1: Ratio of brain tumor to body atlas
R2: Ratio of brain tumor to normal brain

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Phy	ExAcc	UniGeneID	UniGene Title	R1	R2
417719	AW016610	Hs.126911	ESTs	117.8	3.3
428321	AB95894	Hs.301347	ESTs	109.9	3.9
455031	AC069880	Hs.815	SRV gene determining region Y-box 2	107.5	9.6
431917	D16181	Hs.23663	peripheral myelin protein 2	99.0	11.3
415917	U8967	Hs.73957	protein tyrosine phosphatase, receptor-t	72.0	11.3
449494	AW237014	Hs.298550	aquaporin 4	60.0	2.2
432955	AL133916	Hs.291896	ESTs	59.2	2.2
447072	D61594	Hs.12729	lysylprotein sulfotransferase 1	54.2	7.1
456759	BE259150	Hs.127792	della (Drosophila)-like 3	53.5	2.5
427343	AB93044	Hs.176977	protein kinase C binding protein 2	49.6	2.2
426983	AA663372	Hs.165355	homo sapiens cDNA FLJ12015 ts, clone HE	49.5	3.1
412569	D87455	Hs.75880	KIAA0262 protein	46.3	3.0
447004	AW26968	Hs.157538	ESTs	43.7	3.2
436973	BE465204	Hs.47448	ESTs	38.8	10.8
433551	AB55544	Hs.289048	ESTs	38.7	4.3
425842	AB587490	Hs.159623	HW-2 (Drosophila) homolog B	38.3	26.2
407034	UA5440		gbHuman dystrobrevin isoform DTN-3 (DTN	38.1	39.1
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	38.4	3.7
453392	U23752	Hs.32964	SRV box determining region Y-box 11	37.5	22.1
447197	R39075		glycylglycyl-His100.1	37.5	13.3
439415	F05538	Hs.12825	ESTs	35.4	3.1
409395	UA6745	Hs.54435	dystrobrevin, alpha	34.3	3.0
449139	W93363	Hs.58446	ESTs	33.6	33.6
408522	AA363823	Hs.31141	Homo sapiens mRNA for KIAA1966 protein,	32.9	5.9
431019	NM_005429	Hs.2714	forward box G1B	32.4	17.0
427540	R12014	Hs.20976	ESTs	32.0	2.9
425067	AA826434	Hs.90944	ESTs	31.0	2.3
431941	AB010305	Hs.272227	Homo sapiens cDNA FLJ20095 ts, clone OO	30.8	30.3
416123	AB010305	Hs.90220	catenin (cadherin-associated protein), d	30.4	2.2
420807	AA290627	Hs.57946	ESTs	30.4	30.4
444190	AB798119	Hs.10526	cysteine and glycine-rich protein 2	30.4	30.4
429486	M86935	Hs.12827	ESTs	30.2	7.2
444471	AB020654	Hs.11217	KIAA0877 protein	29.5	29.5
451673	AA374181	Hs.26789	DKFZ-55400754 protein	29.3	3.0
439979	AW600291	Hs.6823	hypothetical protein FLJ10430	27.7	3.2
433800	A034361	Hs.135150	lung type-I cell membrane-associated gly	27.1	27.1
449435	AL042201	Hs.21273	ESTs	26.9	26.9
411078	U222000	Hs.162384	ESTs, Weakly similar to 25 kDa hyalini	26.0	26.0
407868	AA663559	Hs.289109	dimethylarginine dimethylaminohydrolase	25.8	2.2
416155	AB007264	Hs.205442	ESTs, Weakly similar to AF117610 1 inner	25.5	25.5
421658	NM_014459	Hs.106511	prothocadherin 17	25.0	3.3
439132	AF040646	Hs.224149	hypothetical protein FLJ20647	24.7	24.7
433332	AB367347	Hs.127809	ESTs	24.6	24.6
452714	A1267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZ-534E082 (fr	23.5	23.5
415271	N94901	Hs.238532	ESTs	23.6	5.5
447387	BE247676	Hs.18442	E-1 enzyme	23.1	3.2
439039	AB565017	Hs.48713	ESTs	23.0	7.2
414175	AB368876	Hs.103849	ESTs	22.2	2.0
451099	R52795	Hs.25894	interleukin 13 receptor, alpha 2	22.0	7.8
410102	AW245508	Hs.273727	Homo sapiens cDNA FLJ14035 ts, clone HE	21.6	2.3
415010	U22350	Hs.78913	chromokine (C-X3-C) receptor 1	21.2	3.0
451468	AW503369	Hs.210047	ESTs	21.0	4.7
454117	BE410100	Hs.40363	adaptor-related protein complex 1, sigma	20.5	20.8
443590	AW014723	Hs.134719	ESTs	20.4	38.5
418735	AB385533	Hs.68632	ESTs	20.2	2.2
449433	AB72096	Hs.2012	ESTs	19.9	16.6
435705	W31254	Hs.7045	GLI04 protein	19.7	19.7
407182	AA609200		gfaf2f2002.s1 Soares_Tesla_MIT Homo sap	19.7	19.7
416862	L24693	Hs.30409	growth arrest and DNA-damage-inducible,	19.6	19.6
425692	BE379534	Hs.34789	ESTs	19.4	19.4
439451	AF089250	Hs.275554	heterochromatin-like protein 1	19.1	17.4
426320	W47595	Hs.109300	transforming growth factor, beta 2	18.7	5.4
412985	X31120	Hs.75110	cannabinoid receptor 1 (brain)	18.5	18.5
452106	A141031	Hs.21342	ESTs	18.6	18.6
431173	AW571193	Hs.254088	ESTs	18.5	18.5
422583	AA410306	Hs.118578	Hsapiens mRNA for ribosomal protein L18	18.5	18.5
419083	A538323	Hs.77496	small nuclear ribonucleoprotein polypept	18.5	18.5
443547	AW217273	Hs.23767	Homo sapiens cDNA FLJ12966 ts, clone NT	18.5	5.1
451592	AB05416	Hs.213857	ESTs	18.4	18.4
453133	A038989	Hs.24395	hypothetical protein FLJ10826	19.3	19.3

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	422544	AB018259	Hs.119140	KIAA0716 gene product	18.2	4.7
	403096	BE250162	Hs.83755	dihydrofolate reductase	18.0	18.0
	410027	AB037807	Hs.83293	hypothetical protein	18.0	8.2
5	414117	W98559	Hs.1787	proteolipid protein (Pelizaeus-Merzbach)	18.0	18.0
	429418	AI381023	Hs.95293	ESTs	17.7	17.9
	432527	AW915025	Hs.102154	ESTs	17.7	4.2
	447809	AW027605	Hs.164230	ESTs, Highly similar to phosphodiesterase	17.5	4.3
	419704	AA429104	Hs.45057	ESTs	17.4	4.6
	436476	AA326109	Hs.53631	ESTs, Weakly similar to enhancer-of-apl	17.4	2.1
10	445133	AIH15746	Hs.153895	ESTs, Weakly similar to AF150753.1 micro	17.3	18.8
	446659	AI35391	Hs.726376	ESTs	17.2	2.8
	409049	AI423132	Hs.146343	ESTs	17.2	3.8
	443572	AA323302	Hs.9567	butyrolactone (gamma), 2-oxoglutarate di	17.2	11.0
	407745	AI.079409	Hs.35176	KIAA0506 protein; SCN Circadian Oscillator	17.0	6.3
	435327	AI365251	Hs.143207	ESTs	16.9	16.9
	417791	AW965330	Hs.111471	ESTs	16.8	10.5
	417355	D13168	Hs.82002	endothelin receptor type B	16.4	16.4
	427897	NM_0017413	Hs.191060	apelin; peptide ligand for APJ receptor	16.3	4.2
20	418721	NM_001680	Hs.309850	angiotensin 4	16.2	4.4
	427701	AA411101	Hs.221750	ESTs	16.1	3.9
	424345	BE218886	Hs.282070	ESTs	16.1	5.7
	426809	BE313114	Hs.29706	ESTs	16.0	10.0
	407881	AW072003	Hs.401968	heparan sulfate (glucosamine) 3-O-sulfate	15.9	15.9
	400569				15.7	15.7
25	409731	AA125955	Hs.56145	thymosin, beta, identified in neuroblast	15.6	15.6
	420092	AA814043	Hs.88045	ESTs	15.6	5.4
	448605	AW113581	Hs.198416	ESTs	15.5	3.0
	422385	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	15.3	4.6
	445611	AI970394	Hs.197075	ESTs	15.2	15.2
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	15.2	5.6
30	405238				15.1	2.8
	429007	D06442	glcHJM02E09B Human fetal brain (TFujine)	15.0	3.5	
	409630	AW404020	Hs.21335	ESTs	14.9	7.1
35	445988	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	14.8	5.7
	416737	AF154335	Hs.79891	LIM domain protein	14.7	4.2
	429763	AA884766		glcra00a10s1 Scores_NFL_T_GBC_S1 Homo s	14.6	3.0
	436270	AA204219	Hs.43679	ESTs	14.6	2.6
	443191	AI033201	Hs.54548	ESTs	14.6	3.5
40	436281	AW411194	Hs.120051	ESTs	14.5	8.5
	449448	D00730	Hs.57471	ESTs	14.4	2.8
	422554	AI148006	Hs.222120	ESTs	14.4	14.4
	440743	AW363771	Hs.77496	small nuclear ribonucleoprotein polypept	14.3	2.4
	428748	AW503206	Hs.98785	ESTs	14.2	14.2
45	452576	AB023177	Hs.29900	KIAA0690 protein	14.1	8.1
	452461	U78223	Hs.108106	transcription factor	14.1	12.8
	445070	F07683	Hs.23869	Homo sapiens mRNA; cDNA DKFpZp434c2172 f	14.1	14.1
	436537	AT783629	Hs.26756	ESTs	14.0	2.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	13.9	13.9
50	419078	MB3119	Hs.89584	Insulinoma-associated 1	13.9	2.9
	451069	X51652	Hs.56744	hist (Drosophila) homolog (sercophalos	13.9	4.1
	452355	N54826	Hs.29202	C protein-coupled receptor 34	13.9	13.9
	421452	AI925946	Hs.104530	fetal hypothetical protein	13.9	13.9
	432650	AT734110	Hs.136355	ESTs	13.8	13.8
	430387	AW372894	Hs.24070	nuclear cap binding protein subunit 2, 2	13.6	13.6
	419275	AA184876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	13.5	13.5
	416795	AI487778	Hs.168053	ESTs, Highly similar to AF227948.1 HEV p	13.5	13.5
	422025	BE348774	Hs.122554	ESTs	13.3	13.3
	400892				13.3	5.5
	41174	AA723554	Hs.191343	ESTs	13.2	2.5
	425187	AW014496	Hs.22509	ESTs	13.1	8.2
60	456955	AW131888	Hs.127292	ESTs, Weakly similar to hypothetical pro	13.1	2.7
	419452	AW503756	Hs.286184	hypothetical protein dJ55102.5	13.0	2.4
	405327	L21162	Hs.53653	collagen, type IX, alpha 3	12.9	4.0
65	430519	AA837118	Hs.118366	ESTs	12.9	7.6
	438299	AK000787	Hs.5111	hypothetical protein FLJ20729	12.7	3.1
	446657	AI335191	Hs.260702	ESTs, Moderately similar to ALU7_HUMAN A	12.6	12.6
	424073	BE252922	Hs.123119	MAD (methers against decapentaplegic, D	12.6	12.6
	424778	AK000723	Hs.144517	hypothetical protein FLJ20716	12.6	12.6
70	451196	AW514021	Hs.245510	ESTs	12.6	7.0
	400960				12.5	23.1
	439579	AF096400		glcHomo sapiens full length insert cDNA	12.4	12.4
	403312	AF263613	Hs.44199	mitochondrial membrane-associated celula	12.4	12.4
75	419948	AB041035	Hs.33947	NADPH oxidase 4	12.4	2.4
	427304	AA761526	Hs.163353	ESTs	12.3	12.3
	419489	AI036591	Hs.20987	hypothetical protein FLJ10392	12.2	12.2
	428137	AA421792	Hs.178999	ESTs	12.2	12.2
	432653	AW956411	Hs.10475	ESTs	12.2	2.0
	408622	AA056000	Hs.202577	Homo sapiens cDNA FLJ12165 fts, clone MA	12.1	12.1
80	453884	AA355925	Hs.38232	KIAA0186 gene product	12.0	5.2
	441440	AB07381	Hs.30495	ESTs	12.0	3.6
	414211	AI301299	Hs.273893	Homo sapiens cDNA FLJ23165 fts, clone L	11.9	11.9
	410227	AB009294	Hs.51152	exonuclease (multiple)-like 2	11.9	2.9
	439444	AI277652	Hs.54578	ESTs	11.9	16.5

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5	433300	AA807080	Hs.128558	ESTs	11.7	9.0
	439170	AA332865	Hs.165538	ESTs	11.6	9.7
	417160	W76767	Hs.1787	proteolipid protein (Policaeus-Mercotache	11.5	7.2
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	11.5	5.8
10	410611	AW954134	Hs.20924	KIA1628 protein	11.5	28.2
	437124	AA564458	Hs.204200	ESTs	11.3	11.3
	418856	AW961605	Hs.21145	Homo sapiens cDNA: FLJ22489 fs, clone H	11.3	2.8
	423600	AB933589	Hs.20076	Homo sapiens cDNA: FLJ21841 fs, clone H	11.3	11.3
15	423933	AA383024	Hs.201603	ESTs, Highly similar to hypothetical pro	11.3	3.4
	431103	M57399	Hs.44	placitophlin (heparin binding growth fac	11.3	11.7
	452082	BE264374	Hs.27842	hypothetical protein FLJ11210	11.3	2.6
	431701	AW936490	Hs.14658	ESTs	11.2	2.2
20	423939	AA452244	Hs.16727	ESTs	11.2	27.8
	403888	AL119844	Hs.49476	Homo sapiens clone TUAB C6-de-ctat ragl	11.1	11.1
	442571	A0005668	Hs.134779	EST	11.1	11.1
	425254				11.1	11.1
25	415558	AA855143	Hs.125719	ESTs	11.0	8.8
	422390	AW450893	Hs.121830	ESTs, Weakly similar to KIA00904 protein	11.0	6.1
	419475	A1858732	Hs.30443	serpin/SLMO-specific protease	11.0	5.6
	458809	AW972512	Hs.20895	sh3-associated polypeptide, 30kD	11.0	3.3
30	410227	AJ148710	Hs.165441	ESTs	11.0	11.0
	444017	U04940	Hs.214	neuro-oncological ventral antigen 1	10.9	3.3
	437814	A068192	Hs.135474	ESTs, Weakly similar to DDX8_HUMAN ATP-D	10.8	8.0
	427194	AA359918	Hs.256335	ESTs	10.8	10.8
35	423260	AW971364	Hs.20076	glt-EST333453 MAGE resequences, MAGL Homo	10.8	10.8
	453961	A1028638	Hs.30120	ESTs	10.6	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfat	10.6	3.4
	416913	AW564714	Hs.190488	glt-RC1-DT0001-03129-011-a11 DT0001 Homo	10.6	10.6
40	418049	AA211467	Hs.75194	chitinase 3-like 1 (cartilage glycoprote	10.5	27.2
	413063	AL033737	Hs.20369	ESTs, Weakly similar to gonadotropin ind	10.5	2.0
	452264	AA353953	Hs.132596	ESTs	10.5	10.5
	434400	A1031771	Hs.257208	ESTs	10.5	6.2
45	451897	AW445774	Hs.257208	ESTs	10.3	10.3
	436754	AJ351288	Hs.133437	ESTs, Moderately similar to gonadotropin	10.3	2.9
	410290	A1693821	Hs.182185	ESTs	10.3	10.3
	412766	BE544475	Hs.54347	ESTs	10.3	10.3
50	450469	A1692275	Hs.243010	ESTs, Moderately similar to RTGCL_HUMAN G	10.3	4.5
	433551	NM_007436	Hs.44229	dual specificity phosphatase 12	10.3	4.5
	442027	AA301116	Hs.142838	Homo sapiens cDNA: FLJ23444 fs, clone H	10.2	2.1
	410386	W026187	Hs.3327	Homo sapiens cDNA: FLJ22219 fs, clone H	10.1	10.1
55	440684	A1253123	Hs.127356	ESTs, Highly similar to NEST_HUMAN NEST1	10.0	10.0
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cere	9.9	15.8
	418294	AJ431351	Hs.11417	topoisomerase (DNA) II binding protein	9.7	23.2
	419972	AL041465	Hs.264038	ESTs, Moderately similar to ALU2_HUMAN A	9.6	4.5
60	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	9.5	6.7
	434851	AA808164	Hs.116592	ESTs	9.5	6.5
	436316	AA808593	Hs.117927	ESTs	9.2	5.8
	453331	A1204865	Hs.8995	ESTs	9.0	6.2
65	414429	RS1494	Hs.71818	ESTs	8.9	16.1
	424998	US8515	Hs.154139	chitinase 3-like 2	8.9	3.6
	446936	H10237	Hs.47314	ESTs	8.8	3.8
	410276	AB545445	Hs.66301	ESTs	8.8	3.8
70	453957	AL080225	Hs.35861	DKFZP586E1621 protein	8.8	3.8
	448321	NM_005883	Hs.20912	adenomalous polyposis coli like	8.7	3.0
	414783	AW068669	Hs.75829	zinc finger protein 6 (ZNF6X1)	8.7	2.2
	414179	AW150687	Hs.107418	ESTs	8.6	4.5
75	437517	A1927575	Hs.99858	ribosomal protein L7a	8.6	12.2
	450062	AL157488	Hs.50150	Homo sapiens mRNA: cDNA DKFZp5648182 (fi	8.6	10.4
	420630	AL133101	Hs.99508	Homo sapiens mRNA: cDNA DKFZp543403921 (f	8.5	11.6
	405280	AW242407	Hs.18479	ESTs	8.4	4.6
80	422343	AA962480	Hs.129874	ESTs	8.4	7.2
	416439	AA180363	Hs.118769	ESTs	8.2	9.2
	428054	AJ949688	Hs.266619	ESTs	8.2	2.6
	421633	AF121880	Hs.136260	sorting nexin 10	8.1	3.3
85	433285	AW176944	Hs.237396	ESTs	8.0	13.4
	433226	AW903733	Hs.5414	KIAA1488 protein	8.0	2.5
	424900	AL035588	Hs.153203	MyoD family inhibitor	7.9	4.8
	425681	AK018257	Hs.159183	KIAU754 protein	7.9	3.7
90	445334	AW233376	Hs.160323	ESTs	7.8	6.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	7.5	7.8
	446985	AL038704	Hs.155827	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5	3.9
	446619	ALU76643	Hs.313	secreted phosphoprotein 1 (osteopontin	7.5	7.7
95	418522	AK020038	Hs.7148	Homo sapiens cDNA: FLJ21590 fs, clone H	7.5	2.2
	439844	AF120075	Hs.201397	ESTs	7.4	6.3
	419723	AL120193	Hs.92614	Homo sapiens growth differentiation fac	7.4	3.5
	447996	AA361124	Hs.294069	ESTs, Weakly similar to ORF2 contains a	7.3	22.1
100	404210				7.3	49.8
	439671	AW137169	Hs.146515	ESTs	7.2	11.8
	439321	AW591935	Hs.141490	ESTs	7.2	2.5
	418030	BE207573	Hs.53321	neuroxin B	7.1	6.4
105	453290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	7.0	6.7
	452669	BE499331	Hs.134012	Ctfr-related factor	7.0	4.9
	414825	X08370	Hs.77432	epidermal growth factor receptor (avian	6.9	6.4

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	420018	US6387	Hs.9K376	proprotein convertase subtilisin/kexin 1	6.9	8.6
	429600	AW83261	Hs.15356	ESTs, Highly similar to AF161358.1 HSPCO	6.9	7.7
	438380	T06430	Hs.6194	chondroin sulfate proteoglycan BEHAB/b	6.9	3.1
	402604				6.8	7.0
5	417022	NM_014737	Hs.80905	Ras association (RACGAP-6) domain fam	6.8	2.5
	402239	U85781	Hs.11568	oxidative 3 alpha hydroxysteroid dehydro	6.8	2.9
	435357	AW007090	Hs.8817	ESTs	6.6	2.6
	434629	AA789081	Hs.4029	glucan-ampified sequence-41	6.6	13.9
	413866	AW568264	Hs.103832	ESTs, Weakly similar to TRH_Y_HUMAN TRICH	6.6	2.7
10	451460	A797350	Hs.208552	ESTs	6.5	13.7
	442145	A022650	Hs.8117	erbB-interacting protein ERBIN	6.5	15.6
	437273	AL137451	Hs.120873	ESTs, Highly similar to hypothetical pro	6.5	2.4
	418365	AW014345	Hs.161690	ESTs	6.4	12.8
	421684	BE261591	Hs.106768	hypothetical protein FLJ10511	6.4	4.3
15	445456	A185678	Hs.209521	ESTs	6.4	7.3
	426413	AA377823		gb:EST190005 Synovial sarcoma Homo sapien	6.3	13.2
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	6.3	10.9
	417709	D87434	Hs.82426	KIAA0247 gene product	6.3	23.3
	445939	BE513280	Hs.259655	prothymosin, alpha (gene sequence 20)	6.2	2.9
20	444980	AW116683	Hs.154150	ESTs	6.2	19.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	6.2	12.7
	448664	AW965446	Hs.46637	ESTs, Weakly similar to cDNA EST y1289g5	6.2	4.1
	407752	A077715	Hs.39384	putative secreted ligand homologous to I	6.2	3.4
	431982	AL043035	Hs.272221	Homo sapiens mRNA: cDNA DKFZp586M1418 (f	6.1	2.6
25	424232	AB015982	Hs.143460	protein kinase C, nu	6.1	14.6
	436443	AW138211	Hs.128746	ESTs	6.1	2.8
	433547	AA063367	Hs.222294	ESTs	6.1	15.0
	445961	AW265634	Hs.131310	ESTs	6.1	3.4
30	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	6.1	6.1
	430383	AW015318	Hs.23165	ESTs	6.1	21.6
	450683	AA450461	Hs.203965	ESTs	6.1	2.2
	407346	AA126252	Hs.40483	Chap330-interacting transactivator, wit	6.0	2.4
	446117	NM_103542	Hs.13340	histone acetyltransferase 1	6.0	10.9
	440690	R41692	Hs.6640	ESTs	6.0	2.1
35	417675	A1808507	Hs.3781	similar to mouse leucine-rich repeat pr	6.0	2.4
	411083	N41340	Hs.65318	hypothetical protein FLJ20344	6.0	3.6
	407310	AA550274	Hs.41296	flavonoid leucine rich transmembrane p	6.0	6.0
	402855				6.0	2.6
	445584	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.0	11.6
40	418791	AA936633	Hs.194628	ESTs	5.9	6.7
	452682	AK000031	Hs.52239	hypothetical protein FLJ20624	5.9	2.3
	436817	AA594142	Hs.284726	ESTs	5.9	11.8
	430334	AB824719	Hs.47557	ESTs	5.9	7.5
	452034	A1638627	Hs.105685	ESTs	5.9	2.6
45	427315	AA179949	Hs.175583	Homo sapiens mRNA: cDNA DKFZp564W0783 (f	5.8	3.1
	428250	AW092928	Hs.183237	DNF ZP569P124 protein	5.8	2.0
	418506	AA084248	Hs.85339	G protein-coupled receptor: 30	5.8	2.5
	417115	AW952792	Hs.1086	small nuclear ribonucleoprotein polypept	5.8	16.0
50	436768	AW977167	Hs.153272	ESTs	5.8	3.6
	446332	AK051635	Hs.14338	hypothetical protein FLJ10773	5.7	5.1
	429463	AF163570	Hs.135756	polymerase (DNA-directed) kappa	5.7	11.1
	428190	A1129787	Hs.182874	Homo sapiens cDNA: FLJ12193 f8, clone H	5.6	7.1
	424343	AW956360	Hs.4748	ESTs, Highly similar to JN0902 pituitary	5.6	2.2
55	417318	AW958337	Hs.12881	ESTs	5.6	25.0
	423582	BE100031	Hs.23839	Homo sapiens cDNA FLJ11561 f8, clone HE	5.6	4.1
	427472	AA527538	Hs.131250	transposon-derived Baster3 transposase-I	5.4	3.6
	434701	AA460478	Hs.4095	KIAA0742 protein	5.4	21.2
	430147	R67074	Hs.23434	habyenhancer of split related with YBP	5.3	2.7
60	411919	AW969397	Hs.48617	Homo sapiens cDNA FLJ20013 f8, clone L	5.3	2.4
	424939	AK000059	Hs.153681	Homo sapiens NY-REN-52 antigen mRNA, par	5.3	2.4
	424028	AF055084	Hs.153682	KIAA0586 protein	5.3	2.7
	444534	AW271626	Hs.42294	ESTs	5.3	2.1
	426711	A1128906	Hs.301454	ESTs	5.2	3.8
65	431843	AA516420	Hs.163526	ESTs	5.2	6.2
	438204	AS589645	Hs.129690	ESTs	5.2	5.8
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 f8, clone PL	5.2	8.4
	436223	AK001184	Hs.23759	ESTs	5.2	2.4
	435849	NM_001429	Hs.297722	Human DNA sequence from clone RPI-35F18	5.2	15.3
70	416198	A1123705	Hs.106832	ESTs	5.2	2.2
	443392	A1055821	Hs.233420	ESTs	5.1	3.3
	416179	R13015	Hs.17907	MAD (mothers against decapentaplegic, Dr	5.1	16.7
	452167	NP5236	Hs.13075	Homo sapiens cDNA: FLJ20013 f8, clone L	5.1	16.7
	434001	AW955095	Hs.39357	serine (or cysteine) protease inhibito	5.0	2.4
75	458435	A1418718	Hs.144121	ESTs, Weakly similar to c337E16.2 (H.sapi	5.0	3.9
	433586	T85301	Hs.293690	ESTs	5.0	2.8
	429940	AW973242	Hs.293690	ESTs	5.0	4.5
	404029				5.0	4.3
	421141	AW117261	Hs.125814	ESTs	5.0	2.1
80	402605				4.9	4.2
	435839	AF249744	Hs.23981	Rho guanine nucleotide exchange factor (4.9	2.5
	416404	AA160138	Hs.167924	ESTs	4.9	2.4
	435615	Y15055	Hs.43975	potassium voltage-gated channel, KQT-4b	4.9	7.2
	448425	AI500359	Hs.233601	ESTs	4.9	4.9

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	445773	H23456	Hs.13299	Homo sapiens mRNA; cDNA DKFZ761M0111 (4.9	2.9
	443451	AW015994		gbl.UH-H8D-abh-g-05-4.Uls1 NCI_CGAP_S	4.9	2.2
	444839	AV051680	Hs.208558	ESTs	4.8	6.7
	452438	BE514230	Hs.29595	JM1 protein	4.8	2.7
	443898	AV084256	Hs.0959	Sred1 gamma	4.8	7.2
	452776	AA194540	Hs.13522	ESTs	4.8	3.4
	426108	AS222037	Hs.165468	programmed cell death 5	4.8	16.7
	418774	AA05169	Hs.28274	Homo sapiens cDNA: FLJ22049 fs, clone H	4.8	3.2
	427704	AW671063	Hs.295282	ESTs	4.8	23.8
	432689	AV058972	Hs.133386	ESTs	4.8	12.8
	410108	AA081659	Hs.191908	KAA1479 protein	4.7	2.1
	433656	W55321	Hs.111450	Homo sapiens cDNA: FLJ21715 fs, clone C	4.7	11.2
	419962	AW714835	Hs.271883	ESTs	4.7	2.2
	404649				4.7	3.0
	439222	AJ208737	Hs.122810	Homo sapiens cDNA FLJ11489 fs, clone HE	4.7	3.3
	425234	AW152225	Hs.165909	ESTs	4.7	3.1
	426490	NM_010621	Hs.170087	aryl hydrocarbon receptor	4.7	5.1
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	4.7	2.7
	420722	U75956	Hs.150787	issue inhibitor of metalloproteinase 4	4.6	5.7
	461989	AF169937	Hs.27413	adaptor protein containing pH domain, PT	4.6	13.4
	412450	AV080364	Hs.288850	Homo sapiens cDNA: FLJ22528 fs, clone H	4.6	18.4
	422486	AV079980	Hs.152060	ESTs	4.6	7.7
	428862	NM_002546	Hs.23347	SVY (pen-determining region Y)-box 9 (ca	4.6	4.6
	419724	AA131459	Hs.23767	Homo sapiens cDNA FLJ12596 fs, clone NT	4.5	11.9
	424265	AB184717		gbq6.6x01.x1 Soares_testis_MRT Homo asp	4.5	4.5
	403549				4.5	11.6
	458239	W00633	Hs.297792	ESTs	4.5	5.1
	421181	NM_005574	Hs.164555	LIM domain only 2 (rhomblin-like 1)	4.5	10.6
	439566	AF086387		gltc.Homo sapiens full length insert cDNA	4.4	2.6
	446329	NM_013272	Hs.14005	solute carrier family 21 (organic anion	4.4	17.2
	444886	AB077762	Hs.15116	KAA1261 protein	4.4	8.4
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	4.4	2.6
	427413	BE547647	Hs.177781	superoxide dismutase 2, mitochondrial	4.4	14.3
	424340	AA330935	Hs.7033	ESTs	4.4	3.9
	421552	AF026992	Hs.105700	secreted frizzled-related protein 4	4.3	31.1
	422353	AW046505	Hs.110953	cloudin 5 (transmembrane protein deleted	4.3	6.1
	434476	AW068020	Hs.271825	ESTs	4.3	4.5
	420582	BE047878	Hs.99033	Homo sapiens chromosome 15, cosmid R2637	4.3	3.6
	419904	AA874411	Hs.10872	ESTs	4.3	17.1
	407939	W05538		gbc285607.r1 Soares_fetal_lung_NHSL19W	4.3	5.0
	426336	AW066996	Hs.94842	ESTs	4.3	3.2
	426304	AA374532	Hs.297895	ESTs	4.3	6.6
	439553	AW021103	Hs.5531	hypothetical protein FLJ20373	4.3	2.3
	424723	BE409613	Hs.152337	protein arginine N-methyltransferase 3(h	4.3	2.5
	423094	BE467014	Hs.185146	Homer, neuronal immediate early gene, 3	4.2	4.1
	409509	AL038923	Hs.127009	ESTs	4.2	15.4
	424391	BE550112	Hs.112712	ESTs	4.2	3.8
	426246	AW567442	Hs.252766	ESTs	4.2	11.1
	410259	AA215404	Hs.137289	ESTs	4.2	10.3
	445925	BE140696	Hs.14831	ESTs	4.2	3.1
	414821	M83835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.2	34.8
	430935	AW072916	Hs.115554	ESTs	4.2	3.0
	442253	AW967146	Hs.28439	ESTs, Weakly similar to ORF2 (MLNmusculus	4.2	2.4
	415989	D28459	Hs.50512	ulivincin-conjugating enzyme EDA (RAD6 h	4.1	15.3
	437097	N45312	Hs.45905	ESTs	4.1	15.6
	428189	AA424030	Hs.45927	ESTs	4.1	3.6
	434963	AW974957	Hs.268719	Homo sapiens cDNA FLJ12142 fs, clone MA	4.1	12.2
	425530	AB011541	Hs.158200	EGF-like domain, multiple 4	4.1	2.6
	4351177	AB18174	Hs.42936	ESTs	4.1	2.1
	416357	Z44718	Hs.301010	ESTs, Highly similar to AF159551 1 Rho G	4.1	4.1
	419085	NM_000216	Hs.85591	Kallmann syndrome 1 sequence	4.1	4.1
	406857	W15573	Hs.5027	ESTs	4.0	2.1
	423598	F07286	Hs.407611	ESTs	4.0	2.2
	423905	AW579860	Hs.125150	lung type-I cell membrane-associated gly	4.0	3.6
	437095	D14661	Hs.119	Wilms' tumour 1-associated protein	4.0	10.0
	425332	AA613306	Hs.127279	ESTs	4.0	10.9
	451555	AF016028	Hs.280039	sarcospan (Vinc oncogene-associated gene	4.0	3.8
	427209	H06509	Hs.92423	KAA1566 protein	4.0	3.1
	435468	AW362803	Hs.166271	ESTs	4.0	2.2
	415773	AK000240	Hs.78826	hypothetical protein FLJ20333	4.0	2.6
	440483	AF200826	Hs.150386	ESTs	4.0	2.5
	414821	AA053654	Hs.10040	STE20-like kinase	4.0	10.4
	433873	AW155913	Hs.150476	ESTs, Weakly similar to KAA00987 protein	4.0	2.3
	420078	AB014680	Hs.8786	carbohydrate (chondroitin 6-sulfate) sul	3.9	2.8
	445706	AW007631	Hs.190488	hypothetical protein FLJ10120	3.9	3.8
	424530	AK532693	Hs.285611	ESTs	3.9	2.2
	448851	AW007332	Hs.16261	Homo sapiens cDNA: FLJ22063 fs, clone H	3.9	16.0
	424720	M89907	Hs.152292	SWHSNF related, matrix associated, acti	3.9	4.5
	409465	U34862	Hs.54473	cardiac-specific hormone box	3.9	8.0
	420439	AW070041	Hs.150353	eukaryotic translation initiation factor	3.9	7.9
	417440	AW961327	Hs.280833	ESTs	3.9	2.1
	430687	N69801	Hs.280287	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.9	2.5
	409361	NM_005882	Hs.54416	slate ocular homeobox (Drosophila) homolo	3.9	4.6

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	426509	M31166	Hs.2050	perlecan-related gene, rapidly induced b	3.9	4.0
	410079	U94362	Hs.58395	glycogenin 2	3.9	18.3
	426818	AA554827	Hs.124841	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.9	3.0
5	435292	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C(p1)	3.8	4.0
	427228	AA105170	Hs.174051	small nuclear ribonucleoprotein 70KD gp1	3.8	7.9
	443001	AW008942	Hs.253594	ESTs	3.8	3.8
	450746	D62673	Hs.169921	general transcription factor II, I, psi	3.8	2.2
	443837	A1964625	Hs.9884	spindle pole body protein	3.8	6.5
10	435780	AF231922	Hs.213004	chromosome 21 open reading frame 62	3.8	2.2
	427657	AQW05040	Hs.152905	ESTs	3.7	3.1
	443101	A1268936	Hs.129872	sperm surface protein	3.7	2.4
	440118	AB040833	Hs.6968	XOAI1460 protein	3.7	3.5
	410612	AW502698	Hs.118152	ESTs	3.7	22.5
	438069	AF756910	Hs.54569	vascular endothelial junction-associated	3.7	4.2
15	433208	AW002834	Hs.24085	ESTs	3.7	16.0
	432367	AA452806	Hs.274412	similar to yeast Upf3, variant A	3.7	2.6
	413916	N48613	Hs.79615	apolipoprotein C-II	3.7	5.4
	429786	AA512710	Hs.146140	ESTs	3.7	3.2
	431470	AL390147	Hs.194742	hypothetical protein DKFZp547D065	3.7	5.4
20	436469	T43300	Hs.35304	Homo sapiens cDNA FLJ13555 fs, clone PL	3.7	10.7
	420361	N92054	Hs.206910	ESTs	3.7	18.7
	406819	AW153463	Hs.48320	DKFZP566B1345 protein	3.7	8.8
	411960	RY7776	Hs.10163	ESTs	3.7	2.3
	435923	BE301930	Hs.50110	Homo sapiens clone 24672 mRNA sequence	3.7	2.2
25	440145	AW021433	Hs.250853	ESTs	3.7	3.6
	453740	AL112035	Hs.7579	gbt.DKFZp761M007_s1 761 (synonym: hamy2)	3.6	3.0
	443975	AW499814	Hs.106103	hypothetical protein FLJ10402	3.6	2.0
	443145	A1979331	Hs.106103	ESTs	3.6	12.4
	419687	A1038899	Hs.227699	ESTs, Weakly similar to Yhr217op (S.cere)	3.6	2.7
30	451029	AA852097	Hs.26829	ras-related protein	3.6	2.9
	414512	AL044330	Hs.8831	golgi resident protein GCP90	3.6	10.5
	410833	H04580	Hs.304049	ESTs	3.6	23.9
	419900	A149960	Hs.170698	ESTs	3.6	3.5
35	429573	AA864407	Hs.211595	protein tyrosine phosphatase, non-recept	3.6	7.5
	428290	A1932995	Hs.103475	Homo sapiens clone 25061 mRNA sequence	3.5	9.5
	444381	BE387395	Hs.285713	ESTs, Weakly similar to CASH_HUMAN COLLA	3.5	4.9
	442104	L29917	Hs.188	phosphodiesterase 4B, cAMP-specific (pan	3.6	2.1
	441269	AW015206	Hs.176784	ESTs	3.6	2.8
40	447981	W32791	Hs.170405	ESTs	3.5	4.6
	447735	AA775266	Hs.6127	Homo sapiens cDNA: FLJ23020 fs, clone L	3.5	2.1
	437680	AA710176	Hs.293667	ESTs	3.5	3.5
	447710	AL020523	Hs.151282	ESTs	3.5	3.5
	438445	AW016809	Hs.119021	ESTs	3.5	2.2
45	446412	A0219063	Hs.42532	ESTs, Moderately similar to ALUS_HUMAN A	3.5	4.1
	409712	AA167385	Hs.13533	ESTs	3.5	3.5
40	440048				3.5	3.2
	440616	S42303	Hs.151	cadherin 2, type 1, N-cadherin (neuronal	3.5	5.1
	409342	AU077058	Hs.54389	BRCA1 associated RING domain 1	3.5	10.6
50	453038	AA502764	Hs.123459	ESTs, Weakly similar to AF208855 1 BM-01	3.5	3.8
	420101	AL014901	Hs.153381	Homo sapiens mRNA: cDNA DAF22564F12 (f	3.5	32.2
	426252	A1935919	Hs.120969	Homo sapiens cDNA FLJ11562 fs, clone HE	3.5	4.6
	433864	AA610649		gbnp9503.0.1 NCL_CGAP_Thy1 Homo sapiens	3.5	3.5
	408495	W68796	Hs.237731	ESTs	3.5	6.1
	411801	AA228336	Hs.115122	ESTs	3.5	6.1
55	422493	AW474183	Hs.233616	ESTs	3.5	15.2
	428141	D50402	Hs.182511	solute carrier family 11 (proton-coupled	3.5	2.4
	414591	A088490	Hs.55902	ESTs	3.5	8.3
	439627	BE521702	Hs.28076	Homo sapiens cDNA: FLJ21641 fs, clone H	3.5	30.2
	444689	AZ033334	Hs.106928	ESTs	3.5	3.1
60	435370	A1964074	Hs.225830	ESTs	3.5	3.0
	443228	W24781	Hs.293798	ESTs	3.4	5.0
	414612	BE274552	Hs.76576	protein inhibitor of activated STAT3	3.4	4.6
	437410	AW022340	Hs.14680	ESTs	3.4	2.7
	444172	BE147740	Hs.104566	ESTs	3.4	12.9
65	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.4	2.6
	437860	AA333063	Hs.278998	Homo sapiens cDNA: FLJ23165 fs, clone L	3.4	4.0
	426716	AW010636	Hs.153487	ESTs, Highly similar to R29144 1 (H.sapi	3.4	2.5
	409403	AA386102	Hs.103462	ESTs	3.4	3.4
	432559	AW452948	Hs.257631	ESTs	3.4	6.3
70	451455	A1937227	Hs.8821	liver-expressed antimicrobial peptide	3.4	6.1
	444155	AK001510	Hs.10414	hypothetical protein FLJ10748	3.4	2.6
	42872	BE290788	Hs.167646	ESTs	3.4	2.2
	414761	AU077228	Hs.77266	enhancer of zeste (Drosophila) homolog 2	3.4	2.6
	416131	L03532	Hs.79024	heterogeneous nuclear ribonucleoprotein	3.4	9.5
75	408376	NM_003542	Hs.46423	H4 histone family, member G	3.4	3.4
	431710	BE221480	Hs.265555	S'-5' exonuclease 2	3.4	3.2
	426030	BE343933	Hs.105642	zinc finger protein 27 (KOC 15)	3.4	3.1
	422573	AW297985	Hs.28777	H2A histone family, member L	3.4	2.1
80	436065	AW880365	Hs.190488	hypothetical protein FLJ10120	3.4	7.6
	442051	AW770493	Hs.165074	guanine nucleotide binding protein (Gpr	3.4	2.9
	418899	BE396339	Hs.173350	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.4	6.5
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fs, clone H	3.4	3.9
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3.4	16.8

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42727	AA325308	Hs.18916	Homo sapiens mRNA; cDNA DKFZp666H0324 (f
410020	T96315	Hs.728	ribonuclease, RNase A family, 2 (Rn,
427272	NM_014827	Hs.17369	KIAA0553 gene product
407656	AW174796	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f
433354	AA678267	Hs.117115	ESTs
43884	U08171	Hs.22627	tyrosin receptor
44684	H15474	Hs.12214	Homo sapiens clone 23/16 mRNA sequence
431053	S40369	Hs.249141	Glutamate receptor subunit
424682	AW64804	Hs.151717	KIAA0433 protein
45572	AA13060	Hs.47448	ESTs
424752	AL119442	Hs.153684	eukaryotic translation initiation factor-1
438666	AW014493	Hs.126727	ESTs
447796	AW953622	Hs.223025	RAB31, member RAS oncogene family
426751	W62744	Hs.22964	ESTs
432251	BE515865	Hs.5002	nuclear protein (PQED repeat)
425688	AA721140	Hs.49330	ESTs, Weakly similar to B34907 hypothet
416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316
424030	X99639	Hs.135262	XAP associated factor-1
434887	AW975114	Hs.233273	ESTs
428642	NM_014889	Hs.183906	KIAA0673 protein
420372	AW960049	Hs.233660	ESTs, Weakly similar to A49610 probable
422224	NM_0113294	Hs.113294	neuregulin 2
425482	L15267	Hs.273524	cystophila myotomins-containing WD repeats
435663	AW247329	Hs.6793	glutamate-activating factor acetylcholin
428418	A368826	Hs.30654	ESTs
416728	AB024597	Hs.79553	casein kinase 1, epsilon
415224	NM_025002	Hs.79088	meliodoxin 2, EF-hand calcium bindin
422903	W61430	Hs.223025	RAB31, member RAS oncogene family
431387	A1873854	Hs.252229	v-mut muscib. aponeurotic fibrosarcoma (a
404171			
435575	AF213467	Hs.44234	trypsin receptor expressed on myeloid
426421	AW967884	Hs.169632	zinc finger protein 42 (myeloid-specific
445070	NM_000677	Hs.528	calcium A3 receptor
407047	X65965	Hs.13630	gbH.sapiens SCO-2 gene for manganese su
446006	NM_004403	Hs.2659	deafness, autosomal dominant 5
430830	X54232	Hs.2659	glycopin 1
435807	AA376417	Hs.173601	Homo sapiens mRNA for FLJ00008 protein,
430412	AW341754	Hs.183906	ESTs
442807	AL045274	Hs.8736	Homo sapiens mRNA; cDNA DKFZp554H203 (f
420253	A1656025	Hs.36200	neighbor of A-48ase anchoring protein 9
434942	AF284422	Hs.115139	calmodulin-dependent protein-interactin
423422	AC005175	Hs.128425	NY-REN-24 antigen
413020	R89736		ghytr3 tHb. r1 Soames fetal liver spleen
452877	A1259789	Hs.32478	ESTs
415113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4
421087	A1209112	Hs.125232	Homo sapiens cDNA FLJ13266 fts, clone OV
450219	A1826999	Hs.224624	ESTs
434256	A1378177	Hs.191847	ESTs
421407	T82331	Hs.127453	ESTs
451138	AW845441	Hs.11550	Homo sapiens cDNA: FLJ21127 fts, clone C
445664	AW968638	Hs.237691	ESTs
411089	AA454544	Hs.118637	Homo sapiens cDNA FLJ13365 fts, clone PL
450950	AA434708		gln. d. 9. 9. 4. s. 1 NCI_CGAP_Ov2 Homo sapiens
451440	AB040888	Hs.417038	hypothetical protein FLJ10474
417270	AA423615	Hs.38593	Homo sapiens cDNA: FLJ22233 fts, clone C
427951	A1826125	Hs.43546	ESTs
443683	A344732	Hs.5683	protein-kinase, interferon-inducible dou
413367	NM_006517	Hs.75317	soluble carrier family 16 (monocarboxylic
429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13
447752	W13700	Hs.347	lactoferricin
403949	AF189011	Hs.45163	putative ribonuclease III
419039	R06699	Hs.153172	ESTs
447343	AA355641	Hs.226894	ESTs, Highly similar to LRP1_HUMAN LOW-D
424441	X14850	Hs.147057	H2A histone family, member X
435163	AA668884	Hs.19155	ESTs
428712	AW085131	Hs.190452	KIAA0365 gene product
434542	AF769310	Hs.61269	hypothetical protein FLJ13164
428147	AW629865	Hs.234953	ESTs
415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B
422170	A1791949	Hs.112432	anti-Müllerian hormone
448861	NS7423	Hs.173898	HSPC085 protein
413542	BE239529	Hs.79424	inhibitor of DNA binding 1, dominant neg
431562	A084334	Hs.11637	ESTs
410274	AA381807	Hs.61762	hypoxia-inducible protein 2
450962	NM_005850	Hs.25190	purine-rich element binding protein A
456277	R68520	Hs.120917	ESTs
453288	AW683292	Hs.274412	similar to yeast UPL3, variant A
447471	AF003843	Hs.19676	sproy (Xrosophila) homolog 2
442554	AW467376	Hs.123940	ESTs
441486	AW673081	Hs.54828	ESTs
420297	A1629722	Hs.88329	ESTs
445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp596C1019 (f
453405	A567972	Hs.49319	ESTs

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434521	NM_002267	Hs.3896	haryophein alpha 3 [importin alpha 4]	3.0	9.3
447948	AIE20923	Hs.46679	ESTs	3.0	10.1
445756	AA290690	Hs.288493	ESTs	3.0	3.5
413243	AA769266	Hs.193657	ESTs	3.0	5.9
422845	AA317841	Hs.301838	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0	2.2
419408	AW297831	Hs.143792	ESTs	3.0	2.1
446441	AK001782	Hs.15093	hypothetical protein	3.0	2.1
427150	BE616183	Hs.173737	res-related C3 botulinum toxin substrate	3.0	4.1
421043	BE379455	Hs.89072	ESTs	3.0	3.0
427238	BE270447	Hs.174070	ubiquitin carter protein	3.0	4.1
433517	AG211331	Hs.131765	ESTs	3.0	11.0
415102	M51899	Hs.77929	excision repair cross-complementing node	3.0	6.0
414702	L22005	Hs.76932	cell division cycle 34	3.0	3.3
428773	AW601325	Hs.274472	high-mobility group (nonhistone chromoso	3.0	15.8
422766	DB461	Hs.1570	histamine receptor H1	3.0	2.1
415693	BE220445	Hs.279635	ESTs	3.0	2.3
412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.0	10.5
424005	AB033041	Hs.173507	KIAA1215 protein	3.0	3.9
440769	BE561793	Hs.174070	gub00345602F1 NH_MGC_8 Homo sapiens cD	3.0	5.1
428832	AA579229	Hs.174070	gub00345602F1 NOL_GCAP_HSC1 Homo sapiens	3.0	2.3
430293	AI419908	Hs.238272	inositol 1,4,5-bisphosphate receptor, ty	3.0	6.3
405883	NM_0013148	Hs.25619	death-associated protein kinase 3	3.0	5.6
407679	AA045484	Hs.6557	ESTs	2.9	7.0
425157	AF030922	Hs.167495	Homo sapiens cDNA FLJ11120 fs, clone PL	2.9	2.5
435281	AB029699	Hs.4854	KIAA0852 protein	2.9	3.9
432338	AW411259	Hs.25945	ESTs	2.9	2.9
440524	RT1264	Hs.15738	ESTs	2.9	9.7
430363	BE383668	Hs.42484	hypothetical protein FLJ10618	2.9	4.4
427729	AB033100	Hs.300645	Homo sapiens cDNA FLJ11744 fs, clone HE	2.9	3.1
422072	AB018255	Hs.111138	KIAA0712 gene product	2.9	2.9
438904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.9	3.6
440100	BE382656	Hs.155849	ESTs	2.9	3.5
448355	AL120637	Hs.20593	high-glucose-regulated protein 8	2.9	13.9
428905	AW302245	Hs.181390	casein kinase 1, gamma 2	2.9	3.7
403019	AA834626	Hs.55718	RAD64 (Sceviae)-like	2.9	5.8
419175	AW270037	Hs.175007	KIAA0779 protein	2.9	2.3
433502	NM_004042	Hs.3435	deleted in oral cancer (mouse, homolog)	2.9	2.3
413922	AI535995	Hs.221024	ESTs	2.9	2.8
428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	2.9	3.3
447189	DC26059	Hs.7972	KIAA0071 protein	2.9	2.1
450107	AA811881	Hs.22595	transmembrane 7 superfamily member 1 (p	2.9	2.8
448960	BE313103	Hs.23213	ESTs	2.9	3.0
425304	AA463844	Hs.31309	fibroblast growth factor 11	2.9	3.3
434845	AW295089	Hs.115798	ESTs	2.9	5.1
408146	RA5621	Hs.61057	ESTs, Moderately similar to CL3BC (Rnor	2.9	5.1
446544	NM_003272	Hs.15791	transmembrane 7 superfamily member 1 (p	2.9	2.8
448908	AA703225	Hs.15193	Homo sapiens mRNA; cDNA DKFZ5969211 (f	2.9	8.5
433017	Y15057	Hs.279514	zinc finger protein 232	2.9	2.2
428590	X7855	Hs.289114	hexabrachion (nestin C, cytotactin)	2.9	4.5
444705	AA020398	Hs.11747	hypothetical protein FLJ20321	2.9	3.6
407925	BE002320	Hs.287584	Homo sapiens cDNA FLJ14030 fs, clone HE	2.9	2.1
431790	AF208955	Hs.258122	hypothetical protein	2.9	2.5
447118	AB014599	Hs.17411	KIAA0599 protein	2.8	2.1
455496	AA442103	Hs.33084	soluble carrier family 2 (facilitated glu	2.8	7.4
425227	HB4455	Hs.49339	ESTs	2.8	2.6
455534	X91195	Hs.100923	phospholipase C, beta 3, neighbor pseudo	2.8	76.2
421465	AK001020	Hs.104527	Homo sapiens cDNA FLJ10158 fs, clone HE	2.8	6.1
405395	AW337722	Hs.235659	ESTs	2.8	34.0
424096	Z59348	Hs.112461	ESTs	2.8	2.1
432045	AL043683	Hs.271367	ESTs, Weakly similar to unnamed protein	2.8	11.9
414079	HI19184	Hs.265230	ESTs	2.8	2.1
414369	MS2194	Hs.79529	cadherin 11, type 2, OB-cadherin (osteob	2.8	3.9
438890	AA627156	Hs.135049	ESTs	2.8	4.9
430354	AA654810	Hs.230704	human homolog of Drosophila Scribble	2.8	5.2
458367	AA086470	Hs.83136	p53-responsive gene 6	2.8	4.4
412014	AK620650	Hs.43761	ESTs	2.8	4.8
428727	AF079847	Hs.191356	general transcription factor IIIk, polype	2.8	5.7
447942	F12828	Hs.155470	zinc finger protein 35 (FOX 25)	2.8	2.8
425432	AF001601	Hs.169857	paraoxonase 2	2.8	3.5
439180	AI551185	Hs.144630	nuclear receptor subfamily 2, group F, m	2.8	2.5
446756	AW028485	Hs.26136	ESTs	2.8	4.1
432148	AW954912	Hs.81907	ESTs, Moderately similar to ALU4_HUMAN A	2.8	2.5
405459				2.8	3.8
414473	BE302693	Hs.143321	gub00345602F1 NH_MGC_20 Homo sapiens cD	2.8	2.4
443839	AW139834	Hs.143321	ESTs	2.8	2.1
446804	AW512213	Hs.42500	ADP-ribosylating factor-like 5	2.8	2.7
428835	AL133415	Hs.2954	nirardin	2.8	2.8
417528	H47315	Hs.27519	ESTs	2.8	11.6
453657	W20237	Hs.296162	ESTs	2.8	3.2
432714	Y12629	Hs.279675	bromodomain-containing 4	2.8	6.7
441072	AW275480	Hs.36354	ESTs	2.7	2.7
441297	AW043084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	2.7	2.2
443849	BE566066	Hs.9893	ASB-3 protein	2.7	3.0

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408243	Y00787	Hs.624	interleukin 8	2.7	3.8
442423	BE296396	Hs.14512	Homo sapiens cDNA FLJ11761 ts, clone HE	2.7	3.3
432238	AL133057	Hs.274135	Homo sapiens mRNA: cDNA DKFp434K181s (I	2.7	3.0
433644	AL117118	Hs.3686	KIA0076 protein	2.7	3.1
411400	AA311919	Hs.69851	GAR1 protein	2.7	16.0
436240	AIW453375	Hs.132803	ESTs. Highly similar to T00367 hypothet	2.7	4.1
428281	AA194554	Hs.183434	ATPase, H+ transp., lysosomal (vacu	2.7	3.2
426340	Z97989	Hs.160370	FYN oncogene related to SRC, FGR, YES	2.7	2.0
408320	AI125867	Hs.20734	ESTs	2.7	4.7
422963	T55579	Hs.115474	replication factor C (topoisom. I) 3 (38	2.7	2.2
436440	AI471862	Hs.196708	Homo sapiens cDNA FLJ11723 ts, clone HE	2.7	4.7
408912	AB011084	Hs.48924	KIAA0512 gene product	2.7	2.1
419304	AA271326	Hs.146101	ESTs	2.7	3.4
415045	AA321559	Hs.38270	Homo sapiens cDNA: FLJ20884 ts, clone C	2.7	2.3
414772	BE567100	Hs.154538	hypothetical protein MD3005	2.7	2.3
422343	AK529633		gb377405.x1 NCI_CGAP_V3511 Homo sapien	2.7	2.5
415539	AIJ73381	Hs.72472	ESTs	2.7	2.7
434829	BE089782	Hs.9877	hypothetical protein	2.7	4.7
413881	AA328340	Hs.44670	ESTs	2.7	3.3
429155	BE242291	Hs.197340	hypoxia-inducible factor 1, alpha subunit	2.7	5.5
431319	AA673350		gzhb6402s.1 NCI_CGAP_V3511 Homo sapiens	2.7	65.9
430219	X99209	Hs.235887	HMT1 (HmRNP methyltransferase, S. cerevis	2.7	3.1
421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobulin	2.7	5.2
417259	AW903338	Hs.61800	chondrin sulfate proteoglycan 2 (vers	2.7	10.7
431747	AW979134	Hs.10700	hypothetical protein	2.7	2.9
408085	N25929	Hs.42500	ADP-ribosylation factor-like 5	2.7	7.8
425218	AF115043	Hs.158005	transcriptional intermediary factor 1 ga	2.7	4.5
434845	BE297657	Hs.4200	hypothetical protein R3216A_1	2.7	4.5
451544	N23235	Hs.30567	ESTs	2.7	2.3
428408	W74437	Hs.168157	Homo sapiens mRNA: cDNA DKFp564M113 (H	2.7	5.9
446627	AY973016	Hs.15725	hypothetical protein S68948	2.7	2.7
405167	AA446104	Hs.24523	RTF2-related export protein 1	2.7	9.9
408221	AL053885	Hs.48332	NIMA (never in mitosis gene a-related k	2.7	2.1
452068	W76412	Hs.57877	ESTs	2.7	2.1
431129	AL137751	Hs.253571	Homo sapiens mRNA: cDNA DKFp4340512 (I	2.7	6.2
429025	AX39910	Hs.4842	ESTs	2.7	2.9
421114	AW915951	Hs.253151	ESTs	2.7	8.8
428755	D67454	Hs.192955	KIAA0265 protein	2.7	3.0
416391	AI878227	Hs.79284	mesoderm specific transcript (mouse) hom	2.7	5.7
414283	AW960011	Hs.154593	ESTs	2.7	5.9
422522	D07119	Hs.152415	ESTs	2.7	3.7
447726	AL136338	Hs.10366	Homo sapiens mRNA: cDNA DKFp434J065 (fr	2.7	14.3
424623	AW953052	Hs.168089	ESTs	2.7	5.6
444772	AW450800	Hs.179839	ESTs	2.7	2.7
428419	U05406	Hs.285225	eukaryotic translation initiation factor	2.7	4.6
414049	H81803	Hs.23241	hypothetical protein FLJ22376	2.7	4.5
412758	Y07818	Hs.74555	dihydropyrimidinase-like 3	2.5	5.1
447720	AL038765	Hs.161304	ESTs	2.6	3.2
419708	AK000753	Hs.32274	hypothetical protein	2.6	3.0
445502	AW978150	Hs.12813	DKFp734A124 protein	2.6	5.0
437370	AL135667	Hs.161962	Homo sapiens mRNA: cDNA DKFp567D023 (fr	2.6	2.9
444147	AB002205	Hs.10351	KIAA0308 protein	2.6	6.8
433193	AB040881	Hs.32980	Homo sapiens cDNA FLJ13122 ts, clone NT	2.6	3.2
445439	BE243064	Hs.12715	regulator of nonsense transcripts 1	2.6	3.9
450309	W51345	Hs.4854	KIAA0802 protein	2.6	3.8
422092	AB007883	Hs.111373	KIAA0423 protein	2.6	2.3
424118	BE269041	Hs.140452	carp selection protein (mammoses 6 phosph	2.6	5.5
407518	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 ts, clone MA	2.6	2.9
445493	AK001389	Hs.15144	hypothetical protein DKFp640A043	2.6	2.2
442878	AB186848	Hs.22315	ESTs	2.6	4.7
448771	BE155131	Hs.296244	SNARE protein	2.6	5.0
416611	AA568308	Hs.192789	ESTs. Weakly similar to ALU7_HUMAN ALU S	2.6	7.7
405348	AW015385	Hs.146590	ESTs	2.6	3.6
435349	AB062698	Hs.155602	ESTs	2.6	3.2
428433	AA521410	Hs.41371	ESTs	2.6	7.9
436565	BE547674	Hs.204169	ESTs	2.6	3.0
439662	AA223559	Hs.6351	cleavage and polyadenylation specific to	2.6	2.6
425362	T24531	Hs.220478	ubiquitin-conjugating enzyme E2M (mouse)	2.6	2.3
459035	AW291109	Hs.208787	ESTs	2.6	2.6
451814	AA847992	Hs.137003	ESTs	2.6	19.1
452331	AA695939	Hs.29117	H sapiens mRNA for per alpha extended 3'	2.6	2.2
438461	AW075485	Hs.283049	phosphoserine aminotransferase	2.6	2.1
424362	AL137646	Hs.146001	Homo sapiens mRNA: cDNA DKFp566F0024 (f	2.6	4.9
423699	H41850	Hs.131846	PCAF associated factor 65 alpha	2.6	3.7
441226	BE563342	Hs.118820	ESTs	2.6	2.5
442840	AK002148	Hs.12151	hypothetical protein FLJ11285	2.6	3.4
448731	AL122272	Hs.40840	ESTs	2.6	3.2
424250	AF073210	Hs.143648	insulin receptor substrate 2	2.6	2.5
433468	AA832055	Hs.232217	ESTs. Weakly similar to ALU1_HUMAN ALU S	2.6	4.3
419925	AA159890	Hs.93765	Ippoma HMGC fusion protein	2.6	3.6
411364	AA054946	Hs.126330	ESTs	2.6	2.8
425922	AL157466	Hs.162751	Homo sapiens mRNA: cDNA DKFp761E2423 (f	2.5	2.7
445074	AA778711	Hs.4310	eukaryotic translation initiation factor	2.5	2.5

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	406392	U28031	Hs.44366	KIAA1641 protein	2.5	26.4
	432426	AW973152	Hs.31065	ESTs	2.5	10.0
	436523	AI417073	Hs.107265	ESTs	2.5	2.1
	452683	AI099575	Hs.3071	progesterone membrane binding protein	2.5	2.6
5	410282	AW067197	Hs.14562	Homo sapiens cDNA: FLJ21615 ts, clone C	2.5	3.7
	441328	AW082954	Hs.159473	ESTs	2.5	9.2
	453003	H84867	Hs.16460	ESTs	2.5	26.1
	438926	R26709	Hs.10095	hypothetical protein from EUROIMAGE 1669	2.5	2.3
	427899	AA923286	Hs.181062	serum amyloid A1	2.5	20.3
10	427620	BE222494	Hs.106919	inhibitor of DNA binding 2, dominant neg	2.5	3.5
	458333	AS30428	Hs.24763	RNA binding protein 1	2.5	3.5
	444871	U46306	Hs.12102	sorting nexin 3	2.5	2.3
	411329	AL350255	Hs.69554	hypothetical protein FLJ20552	2.5	2.9
	424074	AI902465	Hs.210761	ESTs	2.5	4.0
15	439809	H35038	Hs.107874	ESTs	2.5	2.7
	412836	AA121394	Hs.181446	ESTs	2.5	5.7
	430189	AI298841	Hs.136133	ESTs, Weakly similar to ORF YNL310c [S.c	2.5	3.0
	432841	MS3426	Hs.62	protein tyrosine phosphatase, non-ecapt	2.5	13.4
	416526	H03109	Hs.108520	HT019 protein	2.5	2.8
20	451428	AA526983	Hs.173569	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5	3.8
	416388	AA117358	Hs.73677	ESTs	2.6	4.2
	421551	Z45399	Hs.105779	protein inhibitor of activated STAT prot	2.5	7.5
	436490	AJ271643	Hs.87469	putative acid-sensing ion channel	2.5	2.6
	416273	AW575691	Hs.79123	KIAA004 protein	2.5	2.6
25	427149	H84688	Hs.173737	ras-related G3 botulinum toxin substrate	2.5	2.6
	433041	AI890737	Hs.289068	transcription factor 4	2.5	2.2
	446899	NM_005937	Hs.16426	podocalyxin-like	2.5	4.7
	447301	AW958124	Hs.142442	HF1-BP74	2.5	1.2
	447789	AW812704	Hs.48754	ESTs	2.5	2.4
30	447754	AW073310	Hs.163533	Homo sapiens cDNA FLJ14142 ts, clone MA	2.5	2.5
	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.5	2.6
	440903	AI468079	Hs.126523	ESTs	2.5	2.3
	432353	NM_116460	Hs.274411	SCAM domain-containing 1	2.5	4.1
	438196	AL034548	Hs.43827	SRP (box determining region Y)-box 22	2.5	2.5
35	411373	BE326276	Hs.8861	ESTs	2.5	3.9
	452402	AI138530	Hs.22216	paroxysmal proliferative activated recep	2.5	2.4
	426988	AA683053	Hs.57841	ESTs	2.5	2.6
	421772	Z24958	Hs.105139	zinc finger protein 212	2.5	3.7
40	42573	H83396	Hs.7567	Homo sapiens cDNA: FLJ21962 ts, clone H	2.5	2.1
	444677	AL110212	Hs.52445	purine-rich element binding protein B	2.5	1.4
	441087	AW987865	Hs.92145	ESTs	2.5	3.3
	451031	AI360187	Hs.4224	ESTs	2.5	4.8
	432450	AA90739	Hs.77868	ORF	2.5	2.4
	415680	D66051	Hs.78983	diazepam binding inhibitor (GABA recepto	2.5	4.8
45	439630	AA313607	Hs.58633	Homo sapiens cDNA: FLJ22145 ts, clone H	2.4	2.3
	428607	AB023253	Hs.168340	KIA0355 gene product	2.4	4.0
	415402	AA164687	Hs.267889	ESTs	2.4	2.5
	446888	AL030696	Hs.16411	hypothetical protein LOC57157	2.4	2.2
50	438208	AK000299	Hs.187952	dynactin p62 subunit	2.4	2.4
	452900	AA626794	Hs.230555	prethymosin, alpha (gene sequence 20)	2.4	3.4
	408657	AI752621	Hs.173528	protein phosphatase 2, regulatory subun	2.4	3.6
	438143	AI389214	Hs.179260	ESTs	2.4	2.5
	439867	AA847610	Hs.161292	ESTs	2.4	9.3
	438138	AA536740	Hs.1301967	Homo sapiens mRNA; cDNA DKFZp434M196 (lr	2.4	5.6
55	432386	RI7298	Hs.298923	seven in absentia (Drosophila) homolog 1	2.4	2.4
	417289	D86982	Hs.81875	growth factor receptor-bound protein 10	2.4	2.2
	435288				2.4	3.1
	439734	AC030513	Hs.149	cAMP response element-binding protein CR	2.4	3.6
	445378	AV553564	Hs.226946	ESTs	2.4	2.4
60	454016	D62418	Hs.29626	ESTs, Weakly similar to unknown [D.melan	2.4	22.0
	427354	TS7896	Hs.191095	ESTs	2.4	3.6
	452906	BE267039	Hs.75821	serine (or cysteine) proteinase inhibito	2.4	2.2
	450065	AL050107	Hs.301558	DKFZ55881419 protein	2.4	3.6
	451091	AA810832	Hs.131890	ESTs, Weakly similar to coded for by C.	2.4	2.7
65	414639	X63692	Hs.77452	DNA (cytosine-5)-methyltransferase 1	2.4	2.6
	420303	AA258282	Hs.278436	KIAA1474 protein	2.4	2.9
	437058	AA743943	Hs.291427	ESTs	2.4	2.6
	417446	AL119371	Hs.52163	monocamine oxidase B	2.4	4.4
	421454	AI660389	Hs.286108	chlorionic serotonin/norepinephrine home	2.4	3.5
70	434943	AI929819	Hs.320	xeroderma pigmentosum, complementation g	2.4	6.4
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp5640016 (lr	2.4	3.0
	452847	AB000857	Hs.30783	hypothetical protein FLJ20950	2.4	2.1
	422505	R20909	Hs.117815	sarcosin	2.4	2.2
	405204				2.4	4.3
75	419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFZp58611524 (f	2.4	11.7
	442283	AW292634	Hs.150398	ESTs	2.4	2.1
	451484	AV449096	Hs.28481	hypothetical protein	2.4	2.0
	430545	AB032977	Hs.5239	KIAA1151 protein	2.4	2.1
	442724	AA355625	Hs.1599304	cystathionine-beta-synthase	2.4	2.8
80	405917				2.4	6.6
	413822	R09560	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	3.8
	445579	AA133968	Hs.58800	Homo sapiens cDNA FLJ12488 ts, clone NT	2.4	2.1
	406936	BE294926	Hs.46680	CG-12 protein	2.4	8.3

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409142	AL136877	Hs.50755	chromosome-associated polypeptide C	2.4	2.4
422043	AL135849	Hs.115963	Home sapiens mRNA; cDNA DKFZ-454A138 (h	2.4	2.1
446837	J05070	Hs.151738	multicatalyticproteinase B (cathepsin B	2.4	2.6
442560	AA365042	Hs.228598	ESTs	2.4	4.9
418126	T91451	Hs.86539	ESTs	2.4	11.7
413313	NM_002047	Hs.75280	glycyl-tRNA synthetase	2.4	2.1
415167	AA160784	Hs.26410	ESTs	2.4	4.4
400040	BC219431	Hs.300713	ESTs	2.4	3.4
442695	AF169312	Hs.9613	PPAR(gamma)-angiopoietin related protein	2.4	10.7
439977	AA60206	Hs.29626	ESTs	2.4	2.8
452065	AJ772149	Hs.163079	ESTs	2.4	5.4
428900	AB15585	Hs.184641	delta 6 fatty acid desaturase	2.4	2.2
409503	AW119059	Hs.63163	ESTs; Weakly similar to UDP-GalNAc:polyp	2.4	2.7
433401	AF039988	Hs.284217	serologically defined colon cancer antigen	2.4	4.8
412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 430D (con	2.4	2.2
453753	BE222865	Hs.350386	ubiquitin specific protease 1	2.4	2.9
424050	AA211218	Hs.138381	farnesyltransferase, CAAX box, alpha	2.4	3.9
440225	BE295782	Hs.159	tumor necrosis factor receptor superfamily	2.4	76.7
439512	AF162294	HA241578	UR snRNA-associated Sm-like protein LSM8	2.4	12.3
415156	284906	Hs.79050	phosphorylase kinase, beta	2.4	10.4
435975	AL118990	Hs.41997	alpha-1-8-glycoprotein	2.4	7.7
429831	AA554406	Hs.137526	ESTs	2.4	4.1
407373	AA035176	Hs.143812	Home sapiens cDNA FLJ12556 fs, clone NT	2.4	3.3
422221	AJ330648		glnEST177556 Jurkat T-cell VI Home sapi	2.4	3.0
418131	AW092924	Hs.166213	ESTs; Weakly similar to ALU1_HUMAN ALU S	2.4	3.3
410082	AA081694	Hs.153311	MusaeH (Drosophila) homolog 1	2.4	2.5
433034	AL122071	Hs.238927	Home sapiens mRNA; cDNA DKFZ-434H1235 (f	2.4	6.5
418083	AL156743	Hs.25566	ESTs	2.4	5.2
440414	BE391620	Hs.21145	Home sapiens cDNA FLJ22489 fs, clone H	2.4	3.7
423351	AJ001701	Hs.183779	Home sapiens cDNA FLJ10590 fs, clone NT	2.4	6.2
425750	AL090276	Hs.159465	zinc finger protein 266	2.4	5.1
426295	AW367263	Hs.75839	zinc finger protein 6 (ZNFXT1)	2.4	113.6
403772	N68532	Hs.294652	ESTs	2.4	2.3
426307	F24670	Hs.294094	ESTs	2.4	4.0
405203				2.4	2.5
453637	AA036755	Hs.283691	ESTs	2.4	3.6
431427	AC000401	Hs.252748	Home sapiens cDNA FLJ20394 fs, clone KA	2.4	6.2
450021	A885190	Hs.156059	ESTs; Weakly similar to KIAA1139 protein	2.4	4.5
453028	BE222199	Hs.143851	ESTs	2.4	2.6
446863	AV056030	Hs.87627	disrupter of silencing 10	2.3	9.7
441626	AA581167	Hs.111911	ESTs	2.3	23.0
446138	AW654102	Hs.13000	KIAA8700 protein	2.3	2.2
452568	AA095634	Hs.3337	transmembrane 4 superfamily member 1	2.3	22.2
417665	AW852958	Hs.22962	ESTs	2.3	8.0
420038	AC006486	Hs.289033	Home sapiens cDNA; FLJ22295 fs, clone H	2.3	5.1
421456	AW578642	Hs.104557	hypothetical protein FLJ10567	2.3	2.5
412093	BE242691	Hs.14947	ESTs	2.3	31.4
428172	U08367	Hs.182828	zinc finger protein 136 (clone pHZ-20)	2.3	4.9
450447	AF212223	Hs.25010	hypothetical protein P15-2	2.3	2.3
439601	AW903549	Hs.173040	HUEL (C-ort)-interacting protein	2.3	4.1
414705	AJ216402	Hs.240980	ESTs	2.3	2.1
459284	AF195560	Hs.34401	mitochondrial solute carrier	2.3	2.9
452701	NM_005110	Hs.30332	glutamine-fructose-6-phosphate transamin	2.3	2.6
440320	AF126245	Hs.147871	acyl-Coenzyme A dehydrogenase family, me	2.3	3.9
446669	AW972832	Hs.28468	ESTs	2.3	3.8
434616	D78635	Hs.229720	CCR4-NOT transcription complex, subunit	2.3	3.6
452136	AA02175	Hs.301805	ESTs	2.3	2.3
408996	AW959157	Hs.16542	ESTs	2.3	2.8
453175	AL121422	Hs.150413	ESTs; Highly similar to unnamed protein	2.3	3.2
419713	AW968059	Hs.92381	multicatalytic dipeptidase linked mol	2.3	17.0
414197	WA4877	Hs.55501	ESTs	2.3	11.8
445270	A1762164	Hs.54982	Home sapiens cDNA FLJ14014 fs, clone HE	2.3	4.2
412247	AF022375	Hs.73793	vascular endothelial growth factor	2.3	5.1
426404	AL119526	Hs.170098	KIAA0372 gene product	2.3	4.4
405687				2.3	2.2
417410	AF063020	Hs.82110	PC4 and SFRS1 interacting protein 1	2.3	2.0
450747	AJ064821	Hs.48306	ESTs; Highly similar to EWS_HUMAN RNA-BI	2.3	3.8
433680	AB063566	Hs.199846	ESTs	2.3	6.7
420025	AF184539	Hs.94362	LDL receptor EC protein	2.3	2.4
413407	AI356293	Hs.75339	inositol polyphosphate phosphatase-like	2.3	3.1
452909	AB001451	Hs.30965	neuronal Shc adaptor homolog	2.3	3.0
424414	AJ361002	Hs.94814	Home sapiens cDNA FLJ12168 fs, clone MA	2.3	2.0
435791	AJ433086	Hs.25204	chondroitin 4-O-sulfotransferase 2	2.3	2.4
457635	AW660976	Hs.35569	hypothetical protein	2.3	6.9
427985	AJ770170	Hs.65583	ESTs	2.3	2.3
454548	AW654019	Hs.180402	Home sapiens cDNA; FLJ23605 fs, clone L	2.3	2.3
410310	J02831	Hs.92192	coagulation factor III (thromboplastin,	2.3	4.1
453098	AL077158	Hs.24930	tubulin-specific chaperone a	2.3	3.5
444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	2.3	2.6
449607	AL042606	Hs.21599	Home sapiens cDNA FLJ10107 fs, clone HE	2.3	2.8
447975	BE378418	Hs.127240	ESTs	2.3	2.2
429767	AW783022	Hs.216320	hypothetical protein	2.3	11.5
408977	AA479033	Hs.130315	ESTs	2.3	2.3

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448481	W15284	Hs.74932	ESTs	2.3	3.3
452833	BE599681	Hs.30736	KIAA0124 protein	2.3	2.8
421057	T58293	Hs.42679	ESTs	2.3	11.0
46855	C02741	Hs.48712	hypothetical protein FLJ20736	2.3	4.6
427015	BE41007	Hs.17891	CG-52 protein	2.3	4.5
448681	ALD49591	Hs.22370	Homo sapiens mRNA; cDNA DKF2p564O0122 (j)	2.3	6.3
430154	AW533058	Hs.234726	serine (or cysteine) proteinase inhibitor	2.3	34.6
426494	AA234349	Hs.146534	hypothetical protein FLJ20005	2.3	10.2
422987	AW401887	Hs.3811772	histone H2A	2.3	3.2
408216	AA741036	Hs.6670	ESTs	2.3	3.3
407862	BE548267	Hs.50724	Homo sapiens cDNA FLJ10934 fls, clone OV	2.3	5.7
432215	AU079609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.3	2.1
410086	A125845	Hs.13467	Homo sapiens BAC clone RP11-1248 from 7	2.3	2.2
444653	AW676245	Hs.148740	Homo sapiens mRNA for FLJ00328 protein,	2.3	4.5
413284	AU077055	Hs.269107	baculoviral VP repeat-containing 2	2.3	4.8
445547	D88181	Hs.273	galactosyltransferase (Krabbe disease)	2.3	2.5
420228	AA477514	Hs.95247	transferrin-associated factor X	2.3	3.5
437223	C15105	Hs.107094	ESTs	2.3	2.7
437353	AA749195	Hs.143746	ESTs	2.3	2.5
462224	BE085960	Hs.168075	karyopherin (importin) beta 2	2.3	38.1
402575	Z23024	Hs.138860	Rho GTPase activating protein 1	2.3	3.1
435912	AW044647	Hs.196284	ESTs	2.3	2.4
452036	NM_003996	Hs.27521	sema domain, seven thrombospondin repeat	2.3	2.4
425190	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.3	4.3
441646	H05734	Hs.305559	ESTs	2.3	2.1
424130	ALJ50135	Hs.140945	Homo sapiens mRNA; cDNA DKF2p596L141 (r	2.3	2.9
414602	AU021154	Hs.76864	inhibitor of DNA binding 3, dominant neg	2.3	12.2
428114	AF105020	Hs.132899	putative protein C-mannosyltransferase	2.3	3.7
421641	A1638104	Hs.106334	Homo sapiens clone 2335c mRNA sequence	2.3	2.3
427882	AA400867	Hs.193767	ESTs	2.3	10.2
442169	AW153390	Hs.8173	chromodomain homolog 3 (Drosophila HP1 gemm	2.3	4.4
447517	BE009396	Hs.74002	nuclear receptor coactivator 1	2.3	2.4
447217	BE465754	Hs.17778	neuropilin 2	2.3	3.0
452336	AA906961	Hs.29147	hypothetical protein FLJ11015	2.3	4.1
423913	NM_016435	Hs.301025	hepatocellular carcinoma-associated anti	2.3	3.4
411737	AW150339	Hs.71791	hypothetical protein	2.2	3.0
412276	BE262621	Hs.73798	macrophage migration inhibitory factor (2.2	2.4
456974	M12520	Hs.169401	apolipoprotein E	2.2	2.6
416033	NM_012201	Hs.78979	Golgi apparatus protein 1	2.2	10.4
405720	A1556709	Hs.182425	ribosomal protein S2	2.2	115.3
449546	AU077149	Hs.21704	transcription factor 12 (HTF-4, holo-iso	2.2	4.2
437371	AK000868	Hs.5570	hypothetical protein FLJ10006	2.2	3.6
451413	AA448974	Hs.26367	PCS-96 protein	2.2	6.2
408955	T88345	Hs.112220	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2	3.2
437546	AW101596	Hs.121562	ESTs	2.2	3.0
452063	A1507575	Hs.173603	nuclear factor IIA	2.2	3.3
428303	AW974476	Hs.183601	regulator of G-protein signalling 16	2.2	3.4
441376	H94227	Hs.65592	ESTs, Weakly similar to salivary proline	2.2	2.5
413399	BE251033	Hs.122564	gla-L2 OT0731-265400-076-F04 BT0731 Homo	2.2	2.1
449913	AA194422	Hs.22564	myosin VI	2.2	2.4
439093	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.2	3.1
428025	A1634046	Hs.107313	ESTs	2.2	3.5
423846	AA152274	Hs.153629	myosin IXB	2.2	7.1
426404	AA373707	Hs.273138	ESTs	2.2	3.2
423464	NM_016240	Hs.128856	CSR1 protein	2.2	2.1
438135	D65390	Hs.5057	carboxypeptidase D	2.2	9.1
450476	ALJ45265	Hs.246849	ESTs, Moderately similar to ALU1_HUMAN A	2.2	2.5
420798	W53774	Hs.95935	keratin 10 (epidermolytic hyperkeratosis	2.2	2.2
433530	BE349534	Hs.281789	ESTs	2.2	2.1
435297	A1064582	Hs.5106	hypothetical protein FLJ10569	2.2	2.4
433058	H86965	Hs.280568	Homo sapiens chromosome 19, contig R3219	2.2	3.2
433294	AW022933	Hs.191982	ESTs	2.2	2.3
417125	AW181998	Hs.81248	CUG triplet repeat, RNA binding protein	2.2	2.3
445338	H73444	Hs.394	adrenomedullin	2.2	18.3
445065	AA085191	Hs.6949	ESTs, Weakly similar to T2D3_HUMAN TRANS	2.2	3.1
410668	A1319194	Hs.65493	hypothetical protein	2.2	2.5
429002	AW290093	Hs.96918	Homo sapiens cDNA; FLJ21551 fls, clone C	2.2	10.8
430821	AA613866	Hs.5846	Homo sapiens mRNA; cDNA DKF2p56L222 (r	2.2	2.5
412491	W31589	Hs.73967	RAB5A, member RAS oncogene family	2.2	3.4
445382	AF142419	Hs.15020	homology of mouse quaking QKI (p1) domain	2.2	2.4
453603	R32917	Hs.25042	Homo sapiens mRNA full length insert cDNA	2.2	5.2
432476	T94344		glyoxylate 10.1 Sirtosone lung (372110) H	2.2	2.6
424251	AA677465	Hs.143696	coactivator-associated arginine methyltr	2.2	5.0
450519	AW647917	Hs.107153	inhibitor of growth factor, member 1-lik	2.2	2.6
435411	A165866	Hs.40094	ESTs	2.2	2.7
424714	A1144530	Hs.208334	Homo sapiens cDNA; FLJ21874 fls, clone H	2.2	2.1
416326	AF186780	Hs.79219	RafGDS-like gene; KIAA0969 protein	2.2	2.2
407966	A0697340	Hs.76549	ATPase, Na(+)-K(+)-transporting, alpha 1 pol	2.2	6.5
449589	BE118658	Hs.141003	Homo sapiens cDNA; FLJ21091 fls, clone C	2.2	4.4
414765	X07854	Hs.77269	guanine nucleotide binding protein (G s	2.2	6.2
407136	T64895	Hs.267420	Homo sapiens cDNA FLJ11533 fls, clone HE	2.2	2.8
453965	AA628250	Hs.181165	eukaryotic translation elongation factor	2.2	2.3
439068	AW340005	Hs.164485	ESTs	2.2	2.1

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47646	BE619752	Hs.66053	ESTs, Weakly similar to S22126 finger pr	2.2	4.1
433139	AB028626	Hs.47648	3-methylcrotonyl-CoA carboxylase biotin-	2.2	11.7
413433	NM_001989	Hs.28868	transcription factor 4	2.2	2.2
421535	AB002369	Hs.105478	phosphoribosylformylglycinamide syntha	2.2	2.2
428591	BE313029	Hs.185807	Homo sapiens clone 24758 mRNA sequence	2.2	4.8
417248	AA329448	Hs.247302	twisted gastrulation	2.2	2.5
403966				2.2	5.2
437112	AA744692	Hs.168539	ESTs	2.2	3.0
414799	AJ752416	Hs.77326	insulin-like growth factor binding prote	2.2	4.9
4131049	AA646576	Hs.103267	hypothetical protein FLJ22548 similar to	2.2	4.4
422100	AB069880	Hs.111554	ADP-ribosylation factor-like 7	2.2	2.5
426543	AW950198	Hs.170313	heterogeneous nuclear ribonucleoprotein	2.2	2.2
423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fa, clone C	2.2	4.2
443804	AL135352	Hs.255883	ESTs	2.2	2.2
435980	AJ831760	Hs.155111	ESTs	2.2	2.5
452683	AF244135	Hs.303678	hepatocellular carcinoma-associated anti	2.2	2.1
433934	AW273261	Hs.216292	ESTs	2.2	2.1
432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.2	4.4
452518	AA280722	Hs.24758	ESTs	2.2	3.0
409600	AJ011679	Hs.55099	Homo sapiens mRNA; cDNA DKFZp596D2123 (f	2.2	2.3
448965	AF092134	Hs.22879	COI 2d protein	2.2	4.0
444854	AW247078	Hs.12163	eukaryotic translation initiation factor	2.2	5.3
458894	AW292171	Hs.23978	scaffold attachment factor B	2.2	2.5
402269				2.2	2.2
423798	AF047033	Hs.301617	Homo sapiens mRNA full length insert cDN	2.2	4.0
413836	W92003	Hs.70514	ESTs	2.2	3.6
432231	AA339977	Hs.274127	CLST 11240 protein	2.1	2.1
412204	A1125507	Hs.130829	ESTs	2.1	3.0
433807	AA848011	Hs.124570	ESTs, Weakly similar to reverse transcri	2.1	2.2
404170				2.1	41.6
434858	AW979012	Hs.134462	ESTs	2.1	2.2
426982	AA148707	Hs.173081	ubiquitin-like 3	2.1	2.1
421939	BE168531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.1	26.5
424232	BE083288	Hs.38178	Homo sapiens cDNA: FLJ23495 fa, clone H	2.1	3.7
424950	AA602917	Hs.156974	ESTs	2.1	19.9
418123	AA698830	Hs.83350	hypothetical protein	2.1	4.6
404657	AK001519	Hs.7194	CG-74 protein	2.1	5.3
437092	AA744292	Hs.181244	major histocompatibility complex, class	2.1	3.3
421579	NM_002975	Hs.105927	stem cell growth factor, lymphocyte secr	2.1	10.2
428953	AA306100	Hs.194676	DKFZP434C013 protein	2.1	5.0
457313	AF047002	Hs.241520	transcriptional coactivator	2.1	3.5
420570	AA535665	Hs.238078	ESTs, Weakly similar to S23650 retroviral	2.1	2.1
446918	AL135105	Hs.13813	KIA1577 protein	2.1	2.7
427567	N24236	Hs.179662	nucleosome assembly protein 1-like 1	2.1	2.8
446363	AL117440	Hs.301967	Homo sapiens mRNA; cDNA DKFZp434M195 (fr	2.1	4.0
428462	AJ290352	Hs.184582	KIAA0344 gene product	2.1	2.8
455559	AJ383673	Hs.102546	glucocorticoid receptor DNA-binding fac	2.1	2.3
442819	BE822721	Hs.301766	ESTs, Weakly similar to hypothetical pro	2.1	29.1
428808	AA436007	Hs.188780	ESTs	2.1	5.0
414693	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	2.1	15.9
447023	AA355794	Hs.17109	integral membrane protein 2A	2.1	3.0
422250	AW655272	Hs.20252	novel Ras family protein	2.1	4.2
429652	AF080158	Hs.128573	inhibitor of kappa light polypeptide gene	2.1	7.9
420006	H14429	Hs.94300	serologically defined colon cancer anti	2.1	5.6
407316	AA331963	Hs.28802	centaurin-alpha 2 protein	2.1	4.4
417139	M69043	Hs.81326	nuclear factor of kappa light polypeptide	2.1	4.4
414774	X02419	Hs.177274	plasminogen activator, urokinase	2.1	29.9
430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	2.1	2.1
428680	U98199	Hs.50259	ESTs, Weakly similar to alpha 1 (H) asple	2.1	2.5
448501	AA332519	Hs.4273	hypothetical protein FLJ131519	2.1	2.0
422552	N39729	Hs.118243	deoxyribonuclease II, lysosomal	2.1	2.9
419476	AW550300	Hs.59425	Homo sapiens cDNA: FLJ23323 fa, clone H	2.1	3.1
404681	AW935363	Hs.292833	ESTs	2.1	3.9
417263	AA375762	Hs.75362	general transcription factor IIA, 2.1 (2k	2.1	4.1
422070	AF149785	Hs.111126	pharyngeal transforming 1 integrat	2.1	4.9
422711	AF151073	Hs.8645	hypothetical protein	2.1	7.2
450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ10976 fa, clone PL	2.1	2.4
428997	BC060608	Hs.89223	ESTs	2.1	4.2
429147	AB885208	Hs.17283	hypothetical protein FLJ10890	2.1	4.6
433028	A1199144	Hs.283737	AD-D17 protein	2.1	2.6
407831	BE613377	Hs.15580	Homo sapiens cDNA: FLJ22276 fa, clone H	2.1	8.5
417871	AA521368	Hs.24252	ESTs	2.1	2.9
428754	AS21102	Hs.301374	ESTs, Moderately similar to ALU5; HUMAN A	2.1	5.3
430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit,	2.1	4.3
426222	NM_005435	Hs.8546	Notch (Drosophila) homolog 3	2.1	8.5
414242	AA749230	Hs.22666	ESTs	2.1	2.8
433323	AA805132	Hs.30701	ESTs	2.1	5.0
439222	AA356590	Hs.173804	ESTs	2.1	6.4
443357	AW016773	Hs.75815	apolipoprotein C-II	2.1	2.0
449103	T24968	Hs.23038	HSPC071 protein	2.1	2.7
427512	AB018322	Hs.179507	KIAA0779 protein	2.1	2.0
426728	NM_007118	Hs.171957	zinc functional domain (PTPRF) interact	2.1	2.8
440112	AA099014	Hs.231629	ESTs	2.1	2.3

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	448920	DE387549	Hs.31257	Homo sapiens cDNA FLJ13634 fs, clone PL	2.1	4.8
	428459	D44950	Hs.194411	gene with multiple splice variants near	2.1	2.9
	438442	AWB74093	Hs.276525	hypothetical protein PRK2605	2.1	2.3
	438829	AA825825	Hs.204214	ESTs	2.1	2.7
5	411442	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fs, clone NT	2.1	2.2
	409423	A196793	Hs.43071	ESTs, Weakly similar to AF151900.1 CGI-1	2.1	2.2
	458804	AA421645	Hs.139851	caveolin 2	2.1	15.2
	34536	H14486	Hs.3983	Cdk-2 effector protein 4, binder of Rho	2.1	2.8
	447126	AW150632	Hs.62954	fertilin, heavy polypeptide 1	2.1	25.0
10	442328	A1952430	Hs.265237	ESTs	2.1	2.1
	444469	AW159879	Hs.164796	ESTs, Weakly similar to PET2_HUMAN OUGO	2.1	2.8
	438074	H02789	Hs.137223	gdy1411.1 L1 Scores placenta M2HP Homo	2.1	10.5
	412805	AW954569	Hs.295287	ESTs	2.1	4.6
	446334	US2427	Hs.14839	polymerase (RNA) II (DNA directed) polyp	2.1	2.3
15	427201	AB037660	Hs.179393	nuclear factor IIA	2.1	5.1
	436997	AA411151	Hs.137223	ESTs	2.1	3.0
	426369	AF134157	Hs.169497	Kmt1ar (mouse) maf-related leucine zip	2.1	2.3
	453613	F08838	Hs.14763	ESTs	-2.1	2.4
	413276	Z24725	Hs.75260	mitogen inducible 2	2.1	5.5
20	422950	AA302741	Hs.25766	ESTs	2.1	4.0
	424797	AA622394	Hs.153177	ribosomal protein S28	2.1	2.1
	437365	AW955771	Hs.91065	hypothetical protein DKFZp76102423	2.1	3.0
	412482	AI499830	Hs.181043	KIAA0788 protein	2.1	2.7
	418652	AB010598	Hs.151600	ESTs	2.1	2.1
25	404030				2.1	2.1
	437902	AI475995	Hs.1222610	ESTs	2.1	3.8
	441130	AI150734	Hs.283429	SMC (mouse) homolog, X chromosome	2.1	3.5
	416004	116991	Hs.77006	deoxythymidylate kinase (thymidylate kin	2.1	7.4
	409944	DE297925	Hs.57687	four and a half LIM domains 3	2.1	6.3
30	425421	111690	Hs.157445	lauricic acid transporter-like protein	2.1	7.1
	428399	NM_006275	Hs.184167	splicing factor, arginine/serine-rich 7	2.1	2.7
	421313	NM_014923	Hs.103329	KIAA0870 protein	2.1	2.6
	445229	DE275013	Hs.172364	Homo sapiens mRNA for FLJ006096 protein,	2.1	4.7
	410101				2.1	14.7
35	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.1	7.2
	438855	AW948275	Hs.6441	tissue inhibitor of metalloproteinase 2	2.1	4.9
	433369	Z42924	Hs.3254	mitochondrial ribosomal protein L23	2.1	25.0
	433282	F28212	Hs.284247	KIAA1491 protein	2.1	5.1
	445392	AA057478	Hs.23272	ESTs	2.0	2.3
40	433891	AA813792		glnco6/hh3.0.1 NC1_CGAP_P2 Homo sapiens	2.0	2.5
	432672	AI658040	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN III	2.0	2.9
	448474	AT192014	Hs.13809	ESTs	2.0	12.1
	427045	H85904	Hs.173328	protein phosphatase 2, regulatory subuni	2.0	2.9
	444916	AD028956	Hs.21244	KIAA1033 protein	2.0	4.2
45	439177	AWB20275	Hs.78511	ESTs	2.0	3.3
	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.0	5.0
	430057	AW465303	Hs.2534	bone morphogenetic protein receptor, typ	2.0	2.3
	424429	US3830	Hs.145847	TRAF family member-associated NFkB activ	2.0	12.7
	428385	AF112213	Hs.184062	putative Rab5-interacting protein	2.0	4.6
50	458946	AA009716	Hs.42311	ESTs	2.0	16.4
	444816	Z46533	Hs.283742	H.sapiens mRNA for retrotransposon	2.0	4.9
	428029	AF915241	Hs.301719	ESTs	2.0	2.4
	433619	AW956276	Hs.284288	hsp6255 protein	2.0	4.4
	421985	AK001779	Hs.110445	CGI-97 protein	2.0	3.8
55	433995	AD037773	Hs.5762	hypothetical protein FLJ10595	2.0	2.2
	449188	AW072359	Hs.23290	myoblastin related protein 1	2.0	2.2
	404820				2.0	2.7
	425811	AL039104	Hs.159567	karyophorin alpha 2 (RAG cohort 1, impor	2.0	2.5
60	422163	AF027208	Hs.297332	Homo sapiens cDNA: FLJ21471 fs, clone C	2.0	3.7
	431172	AI125539	Hs.250866	haly (Drosophila)-homolog	2.0	10.2
	415200	ALJ04328	Hs.301912	Homo sapiens cDNA: FLJ22920 fs, clone K	2.0	2.1
	458176	AI951619	Hs.140309	ESTs, Weakly similar to KIAA0691 protein	2.0	5.0
	407895	R44203	Hs.265540	HSPC042 protein	2.0	4.6
65	449816	AI701467	Hs.30554	ESTs	2.0	2.0
	422076	AI878667	Hs.1900	see-51 homolog	2.0	5.4
	430220	BE378277	Hs.152230	ESTs	2.0	11.7
	435445	AA882305	Hs.133288	ESTs	2.0	4.2
	431031	AA930335	Hs.105273	ESTs	2.0	14.1
70	428233	Z17861	Hs.165218	EB1-95Hds-associated protein 5	2.0	1.6
	426458	DB9332	Hs.165984	nuclear protein	2.0	5.9
	421965	AA301100		glt-5/14123 Testis tumor Homo sapiens cD	2.0	2.1
	421728	AW301984	Hs.173685	Homo sapiens cDNA FLJ12519 fs, clone NT	2.0	6.3
	449722	BE280074	Hs.23960	cyclin D1	2.0	2.1
75	450016	BE271927	Hs.87385	ESTs	2.0	2.4
	453507	AF083217	Hs.33085	WD repeat domain 3	2.0	13.1
	422801	AF125672	Hs.287994	nuclear receptor co-repressor 2	2.0	3.5
	418178	AA043661	Hs.83715	Sjogren syndrome antigen B (autoantigen	2.0	3.9
	417919	AF253112	Hs.135540	ESTs	2.0	4.0
	414787	AL045332	Hs.173711	BTG family, member 3	2.0	4.0
80	447082	AK000310	Hs.17138	hypothetical protein FLJ20303	2.0	7.0
	431742	NM_010952	Hs.295281	CGI-201 protein	2.0	2.5
	448431	BE513261	Hs.300897	ESTs, Weakly similar to CA13_HUMAN COLLA	2.0	6.5
	456444	AA854517	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.0	2.5

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419178	NM_006284	Hs.89657	TATA box binding protein (TBP) associate	2.0	6.0
446437	AW014360	Hs.202119	ESTs, Weakly similar to A48010 X-linked	2.0	2.2
449910	A074585	Hs.58440	ESTs	2.0	2.1
435963	AF271212	Hs.87627	disrupter of silencing 10	2.0	2.1
421283	A760018	Hs.205071	ESTs	2.0	2.6
414482	S57498	Hs.76252	endothelin receptor type A	2.0	2.4
450960	AB013897	Hs.25722	Homo sapiens mRNA for HKR1, partial cds	2.0	2.1
438644	A1126162	Hs.129037	ESTs	2.0	2.1
448343	A044775	Hs.205091	ESTs, Weakly similar to WW domain bindin	2.0	12.5
412514	BE410731	Hs.742650	follicular lymphoma variant translocation	2.0	6.4
430709	A1796870	Hs.54277	ESTs	2.0	3.8
450582	AS139732	Hs.13144	HSPC160 protein	2.0	2.8
409936	AK001691	Hs.57655	hypothetical protein FLJ10829	2.0	3.1
426365	D63476	Hs.172813	PAK-interacting exchange factor beta	2.0	3.3
446430	AA345837	Hs.15075	hypothetical protein DNF2p43ME2216	2.0	2.0

Table 4B:

Play:	Gene cluster number	Unique Eos probe/est identifier number	
CAT number:	Accession:	Genebank accession numbers	
20	477197 477192 429007 429163 436799 423240 413513 428413 433586 443451 442495 439566 407939 453740 433954 413020 485060 447069 428032 414473 422343 431319 422221 413389 432476 433874 433891 421965	217685s_1 2200202_1 327976s_1 1238297_1 24302_1 1235950_1 924456_1 372468s_1 32508_1 7532_32 928718_1 23929_1 600367_1 612139_1 899720_1 146658s_1 61684_1 21430_5 113706s_1 35761_3 786037_1 122030_1 319_18 1511159_1 1237465_1 52147_1 647290_1 1663_13	R39075 R36167 A356546 AA50264 AA60200 AA44145 BP958169 AW904500 A119105 D30642 AW574271 AA592975 AA447312 AA584766 AF066400 W73990 W79232 AA305021 AW871394 AA50759 AW334714 AW749854 AW749902 BE162439 BE161006 BE162499 BE161005 AA190449 AW513406 BE162500 BE161037 AW554494 AA377823 BG219617 BG196665 BG616269 A022888 BC211154 AW517087 AA601064 T85512 A030087 R39698 AW816984 AB50202 BF62 H479 A552106 A154717 AW518855 AF121175 AF066387 W27711 W7784 AW118352 AW192515 W06508 ALT12395 BG291394 T38779 BG475161 H63559 AW92444 AA610649 AB937812 BE46113 R98736 Z42004 AK058784 AW901381 AW901380 AW730240 T50211 AA528756 AA834708 BG419454 BF924037 R13764 AW763200 BE551793 BG698295 BE270077 BG06887 AA461363 AA364542 B006686 AA578229 AA461375 BC302366 BE302693 AW961833 AA309282 AA561780 AB628633 AA551995 AW378461 BG435498 BG942765 AW716636 AA873350 T82428 T82429 AU1155416 AA658442 B3010369 BE326714 BF935312 AA306649 Z40922 W76533 BE391833 BE301674 BE301671 AW873259 AA545913 T34344 AA834900 AA574492 AF075017 R65779 R22463 H02780 AW132228 AA613792 T05304 AW88385 BC223244 AT42511 BE575249 AT42341 AW572776 A1566256 A538553 BG37905 AA301100 AA620903 A142367 AW082310 A147387 BF509145

TABLE 4C:

55	Play: Ref: Strand: NT_position:	Unique number corresponding to an Eos probe/est Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons.			
60	Play Ref Strand NT_position	403859 405238 403992 403860 402524 404210 402604 402955 404029 402605 404049 403540 404048 404171 405649 405268 405204 405517 405203 405587 403966 402269 404170	Ref 9757499 7249119 6396026 9757499 9798518 5006246 9909420 9662953 7671252 9908420 3658074 8081591 3658074 9930793 4296908 4156151 7230116 9454624 7230116 4268968 8568881 3128156 9930793	Strand Minus Minus Plus Minus Minus Plus Plus Minus Plus Minus Minus Minus Plus Minus Minus Plus Plus Plus Minus Plus Minus Plus	NT_position 91388 92013,98131 98294,99474-99570 51728-51836 140390-140522 151830-152104,152649-152744 20529-21096 169926-170121 20363-20767 57953-58009 108716-111112 47680-47973 75765-76155 137150-137692 54421-55003 173667-173783,176876-177055 50032-50102,50624-50764 24404-24521 125659-126754 114757-114577 125295-125493 54787-54891,55844-55917 158193-158277,160116-160290 1168-1324,5492-5611,23445-23851 168836-169248

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TABLE 5A: ABOUT 43 GENES UPREGULATED IN GLIOBLASTOMA THAT ENCODE PREDICTED MEMBRANE PROTEINS

Protein	Exon	Accession	Gene	Ratio of brain tumor to body sites	R1	R2
404030	7571252	Plus	149362-151749			
401901	722886	Minus	113631-113762			
404820	4678240	Plus	20475-20185			
15	41517	U88967	protein tyrosine phosphatase, receptor	72.0	11.3	
447072	D61534	hs.17275	lysoglycophosphatidylcholine 1	54.2	7.1	
451095	RS2735	hs.26954	interleukin 13 receptor, alpha 2	22.0	7.6	
415910	U20350	hs.78913	chemokine (C-X3-C) receptor 1	21.2	3.0	
412986	X81120	hs.75110	cannabinoid receptor 1 (brain)	18.6	18.6	
417355	D13108	hs.82002	endothelin receptor type B	16.4	16.4	
417921	NM_001650	hs.268650	oxytocin receptor 4	15.2	4.4	
452355	N54926	hs.25202	G protein-coupled receptor 34	13.9	13.9	
410227	AB009284	hs.61152	evxostoses (multiple)-like 2	11.9	2.9	
419723	AL120133	hs.52614	Home sapiens growth differentiation factor	7.4	3.5	
414525	X03370	hs.17432	epidermal growth factor receptor (avian)	6.9	6.4	
413598	AW804296	hs.5950	Sec1 gamma	4.8	7.2	
422033	AW245805	hs.110903	claudin 5 (transmembrane protein deleted)	4.2	6.1	
414621	M63835	hs.77424	Fc fragment of IgG, high affinity Ia, re	4.3	3.8	
431555	AF116028	hs.260338	sarcosin (Kos) oncogene-associated gene	4.0	3.8	
435599	AF256910	hs.54550	vascular endothelial junction-associated	3.7	4.2	
440516	S42303	hs.161	cadherin 2, type 1, N-cadherin (neuronal)	3.5	5.1	
428141	D50402	hs.182611	solute carrier family 11 (proton-coupled)	3.5	2.4	
428484	AF104032	hs.184001	solute carrier family 7 (cationic amino)	3.4	2.8	
431053	S40385	hs.245141	glutamate receptor subunit	3.3	2.4	
445070	NM_000977	hs.258	adenosine A3 receptor	3.2	7.5	
430890	X54232	hs.2699	glycophorin 1	3.2	4.3	
423422	AC009175	hs.128425	NY-REN-24 antigen	3.2	4.0	
413667	NM_005577	hs.75317	soluble carrier family 16 (monocarboxylic)	3.1	3.5	
447471	AF039843	hs.18676	sproy (Drosophila) homolog 2	3.0	4.1	
427150	BE616183	hs.173737	ras-related G3 botulinum toxin substrate	3.0	4.1	
422676	D28481	hs.1570	histamine receptor H1	3.0	2.1	
430253	A416988	hs.236272	inositol 1,4,5-trisphosphate receptor, ty	3.0	6.3	
453486	AA42103	hs.33894	solute carrier family 2 (facilitated glu	2.8	7.4	
428291	AA194554	hs.183434	ATPase, H ⁺ transporting, lysosomal (vacu	2.7	3.2	
417446	AL118671	hs.82163	monoamine oxidase B	2.4	4.4	
412676	NM_000165	hs.14471	gap junction protein, alpha 1, 43-D (con	2.4	2.2	
440225	DE395792	hs.159	tumor necrosis factor receptor superfam	2.4	78.7	
450447	AF212223	hs.25010	hypothetical protein P15-2	2.3	2.3	
410310	J02931	hs.62192	coagulation factor III (thromboplastin,	2.3	4.1	
452035	NM_003666	hs.27621	sema domain, seven thrombospondin repeat	2.3	2.4	
447217	BE465754	hs.17778	neuropilin 2	2.3	3.0	
447023	A3556794	hs.17169	integral membrane protein 2A	2.1	3.0	
422070	AF149795	hs.111126	plurality tumor-transforming 1 interact	2.1	4.9	
456804	A421645	hs.138651	caveolin 2	2.1	15.2	
430057	AW450303	hs.2534	bone morphogenetic protein receptor, typ	2.0	2.3	
422163	AF222028	hs.297332	Home sapiens cDNA FLJ21471 fls, clone C	2.0	2.4	
414482	S57408	hs.76252	endothelin receptor type A	2.0	2.4	

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TABLE 6A: ABOUT 397 GENES DOWNREGULATED IN GLIOBLASTOMA

Protein	Exon	Accession	Gene	Ratio of normal brain to body sites	R1	R2
435440	AB032436	hs.6535	iron-specific Na dependent inorganic ph	4.47	71.2	
426846	AB077324	hs.1832	neuropeptide Y	4.49	55.32	
428874	W32133	hs.194366	transferrin (transferrin, transferrin)	7.06	45.64	
416836	D54745	hs.80247	cholesterol oxidase	9.45	44.59	
401412	E1463_2958	hs.209715	ESR1, weakly similar to ALU1_HUMAN ALU S	3.20	32.55	
451835	T39443	hs.26239	ESR1	3.21	28.93	
412768	AW998044	hs.852	solute carrier family 10 (sodium/potassium)	3.16	28.12	
415448	T68455	hs.852	solute carrier family 10 (sodium/potassium)	3.27	27.04	
411305	BE241596	hs.69547	myelin basic protein	13.80	26.92	
42654	A1776026	hs.52163	ESR1	3.59	3.9	
410837	BE145698	hs.154679	glycyl-L-histidine 23118-145-e07 H10205 Homo	3.05	24.43	
425121	A1797511	hs.154679	synaptobrevin 1	6.92	23.67	
456763	AJ271351	hs.128180	B cell translocation gene 4	3.29	23.32	
429565	X05509	hs.211564	neurofilament, light polypeptide (58kD)	8.03	22.56	
451682	A1821302	hs.167834	ESR1	4.12	21.82	

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424922	BE386547	Ha.217112	ESTs, Weakly similar to Similarity to Ye	4.41	21.28
411666	AF106564	Ha.71346	neurofilament 3 (150KD medium)	5.27	21.20
432247	AA531287	Ha.105805	ESTs	3.25	21.14
435812	AV226067		gbcUH-H-8W0-agg-g-09-0-ULs1 NCL_GCAP_Su	3.02	21.10
422234	AF115916	Ha.113287	glics, large (Drosophila) homolog-associ	3.32	20.52
435708	AA62949	Ha.75169	ESTs	8.79	20.45
423135	N67655	Ha.26411	ESTs	6.82	20.28
440600	AB07691	Ha.126351	ESTs	3.56	20.09
425230	clp1_7656		exon	3.31	19.95
425915	N65640	Ha.78026	ESTs, Weakly similar to similar to ankyr	3.14	19.40
429130	AA448208	Ha.99163	ESTs	3.53	19.20
416812	H91010	Ha.44940	ESTs	3.54	19.00
454171	AV854932		gbcQV2-CT0261-201099-011-405 CT0261 Homo	3.78	19.04
457443	AB187031	Ha.272321	Homo sapiens cDNA FLJ12571 fls, clone NT	3.13	18.91
454589	AV080969		gbcARA-ST0124-241199-026-a12 ST0124 Homo	3.17	18.60
418104	T05726	Ha.177130	ESTs	3.11	18.41
419357	T82050	Ha.268907	ESTs	3.11	18.13
414683	S78296	Ha.76888	Interneurin neuronal intermediate filamen	5.55	18.13
447694	AA200983	Ha.170003	ESTs	3.56	17.79
427627	R87582	Ha.179915	guanine nucleotide binding protein (G pr	4.65	17.65
428010	AA806554	Ha.185375	ESTs	3.03	17.40
417159	R01761		gbcg81110.s1 Soares fetal liver spleen	3.23	17.28
435788	AA765008	Ha.259047	ESTs	3.16	17.01
459349	AW749381		gbcQV3-8T0381-170100-060-e02 BT0381 Homo	3.26	17.01
450214	BE439763	Ha.227571	regulator of G-protein signaling 4	3.86	17.04
438088	AF927209	Ha.283089	HMT1 (histone methyltransferase, S. cerevi	3.54	16.48
437268	AF154647	Ha.227571	regulator of G-protein signaling 4	5.83	16.32
435315	AA70240	Ha.165402	ESTs	4.95	16.12
442440	AB023185	Ha.143535	calcium/calmodulin-dependent protein kin	4.69	15.92
412446	AF768015	Ha.92127	ESTs	5.44	15.75
449714	AB033015	Ha.230941	KIAA1189 protein	4.59	15.43
435832	AA426888	Ha.41414	thano (Drosophila) like 4, RNA binding	4.63	14.97
437397	AA439847	Ha.4221	hypothetical protein DKFZp7611039	5.93	14.81
435502	L13266	Ha.105	glutamate receptor, ionotropic, N-methyl	3.29	14.51
414187	BE312141		gbc01145962f1 NH_MGC_19 Homo sapiens c	3.37	14.46
417868	AB78534	Ha.122692	ESTs	7.57	14.22
428536	AI143139	Ha.2268	Vali-like 1	5.16	13.98
402125	c18p3_155		exon	3.11	13.94
440503	NM_006539	Ha.7235	calcium channel, voltage-dependent, gamma	3.49	13.92
419090	T05201	Ha.186468	ESTs	3.25	13.79
437665	AA765417	Ha.220503	ESTs	3.07	13.79
457113	AI734016	Ha.270508	ESTs	3.59	13.69
424933	AW909974	Ha.5181	proliferation-associated 2G4, 38d	3.59	13.48
443489	AF073512	Ha.133916	ESTs	3.24	13.20
404289	epb3_5921		exon	3.99	13.12
406534	pk2_4616		exon	3.85	12.87
423280	AA324037		gbcEST25901 Cerebellum II Homo sapiens c	3.38	13.03
454241	AW537681	Ha.288324	Homo sapiens cDNA FLJ13283 fls, clone OV	3.04	12.93
437225	AF063569	Ha.283919	Homo sapiens clone HQ0117 PRO0117 mRNA	3.71	12.85
416660	RS8905	Ha.36592	ESTs	3.92	12.74
407593	AW044083	Ha.237008	ESTs	3.85	12.67
451734	NM_006176	Ha.26944	neurogranin (protein kinase C substrate,	7.41	12.59
419365	A267569	Ha.25214	hypothetical protein	7.89	12.50
405348	clp5_13716		exon	3.45	12.42
424338	AI761976	Ha.156080	ESTs	3.69	12.35
424458	M29273	Ha.1780	myelin associated glycoprotein	4.72	12.31
431400	AA504807		gbcas63a02.s1 NCL_GCAP_GCB1 Homo sapiens	4.42	12.29
417754	R13027	Ha.268703	ESTs	3.35	12.18
440184	AB002297	Ha.7022	dedicator of cyto-kinesis 3	3.35	12.18
431339	AA506294	Ha.267266	ESTs	6.15	12.11
422265	BE501518	Ha.114772	ESTs	3.82	11.96
419237	AA446240	Ha.59640	Homo sapiens cDNA: FLJ21069 fls, clone C	3.16	11.86
424991	AA775471	Ha.241467	ESTs	3.03	11.64
431988	AC002302	Ha.77202	protein kinase C, beta 1	3.28	11.61
450967	AA017202	Ha.32794	ESTs	3.11	11.60
454565	AA584559	Ha.192097	ESTs	3.26	11.54
454565	AW807605		gbcARA-ST0098-126109-001-406 ST0098 Homo	3.44	11.51
442000	H38671	Ha.8071	KIAA0735 gene product; synaptic vesicle	3.16	11.46
437948	AA772920		gbcaw73c02.s1 Stratagene scabin scabin S1	3.18	11.35
401081	cl1p3_321		gbcEST391224 MAGE resequences, MAGP Homo	4.16	11.35
430919	AW979114		gbcARA-ST0118-261099-012-c07 ST0118 Homo	3.02	11.27
454578	AW809370		C-type lectin-like receptor-2	11.13	11.13
422279	H69644	Ha.114231	ESTs	3.21	11.07
453101	AW952776	Ha.34943	gbcMR9-HT0208-101299-103-a12 HT0208 Homo	3.61	10.83
453536	BE145795	Ha.75294	cardiotropin releasing hormone	3.72	10.71
413324	Y09571	Ha.26133	ESTs	3.80	10.60
412266	N59006	Ha.26133	ESTs	7.24	10.56
436887	AW953157	Ha.193235	ESTs	3.05	10.53
454598	AW649546		gbcL3-CT0214-150300-085-H05 CT0214 Homo	3.07	10.50
418162	T11588		gbcAR028-Hest Homo sapiens cDNA clone A	3.07	10.46
425537	AB007913	Ha.158291	KIAA0444 protein	10.45	10.45
436230	AI248723	Ha.177711	ESTs	3.02	10.43
431169	AW971240		gbcEST383329 MAGE resequences, MAGL Homo		

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	447359	NM_012093	Hs.18268	adenylate kinase 5	5.91	10.40
	457187	AA443927	Hs.144360	EST	3.30	10.39
	407539	X91163	Hs.144360	glycylsapiens mRNA for Hs-M protein.	3.02	10.36
	452585	R17746	Hs.84469	ESTs	3.02	10.26
5	440352	AB92322	Hs.65373	ESTs	3.03	10.20
	456116	Z26526	Hs.172004	blin	3.11	10.17
	456172	BE007237		gbl:PAD-BM0139-053500-003-g08 BM0139 Homo	3.32	10.14
	445891	AJ263029	Hs.210689	ESTs	3.04	10.11
	454059	NM_003154	Hs.37048	stathurin	3.27	9.97
10	402624	c1p1_2680		exon	3.05	9.94
	441539	A4337200	Hs.192599	ESTs	3.27	9.82
	412172	N78794		gbcy45g07.r1 Soares fetal liver spleen	3.03	9.78
	427942	AA417856		gbcz01036.r1 NCL_GCAP_GCB1 Homo sapiens	4.09	9.73
	436867	BE041837	Hs.120316	ESTs	3.25	9.73
15	454688	AW814472		gbl:M3-ST0203-010200-109-b06 ST0203 Homo	3.41	9.73
	446122	A1952750	Hs.181801	ESTs	3.43	9.71
	420480	AL137361	Hs.98173	hypothetical protein	3.03	9.66
	433447	U28195	Hs.3281	neuronal pentraxin II	3.72	9.54
	407178	AA195551	Hs.104106	ESTs	3.89	9.47
20	415614	F12526	Hs.155988	DKF ZP564M2-423 protein	3.06	9.45
	450518	BC245175	Hs.270893	ESTs	3.59	9.39
	455675	BC365984		gbc:RC3-BT0319-120000-014-a06 BT0319 Homo	3.46	9.32
	456459	AA253074	Hs.146251	ESTs	4.08	9.30
25	423420	A1571364	Hs.128382	Homo sapiens mRNA; cDNA DKF7p7611224 (f	5.18	9.23
	455444	BC364621		gbc:RC3-BT0311-253000-014-b02 BT0311 Homo	3.02	9.23
	419800	AA282302	Hs.191525	ESTs	3.28	9.16
	430964	U10929	Hs.248167	zinc finger protein 186 (Kruppel type)	3.04	9.00
	409716	AL117454	Hs.55027	Homo sapiens mRNA; cDNA DKF Zp586J17.1 (f	3.02	9.00
	412262	AW839578	Hs.18150	Homo sapiens cDNA FLJ11550 fs, clone HE	3.33	8.99
30	443400	AA444534	Hs.195929	ESTs. Weakly similar to gm-carrum-carrum	6.50	8.96
	424617	AW603407		gbc:LR-HF-BM0-akw-d-11-Q-UJr1 NIH_MGC_50	3.17	8.94
	444194	AA344151		gbc:ESTS0059 Gall bladder 1 Homo sapiens	3.25	8.91
	441914	AA871496	Hs.128495	ESTs	3.42	8.88
	405320	c9s_1_12168		exon	3.36	8.84
35	440179	A0533785	Hs.195551	ESTs	3.43	8.04
	400335	Y13187	Hs.240066	Homo sapiens dmd gene, Intron 11	3.13	8.78
	454962	AW847645		gbl:L3-CT0213-280100-056-AD CT0213 Homo	4.16	8.74
	407603	AW681681	Hs.269064	ESTs	3.09	8.73
40	456260	AW781517		gbc:MR3-OT0007-260300-206-a09 OT0007 Homo	3.78	8.70
	431096	AA324356	Hs.249227	Homo sapiens DNA, cosmid clones Tm62 and	4.01	8.67
	424481	R19453	Hs.1787	proteolipid protein (Pulitzer-Merzbach)	8.12	8.63
	407618	AW504549	Hs.246851	ESTs. Weakly similar to CRKS_HUMAN VOLTA	3.08	8.53
	434369	AF147383		gbl:Homo sapiens full length insert cDNA	3.25	8.51
	438239	A031540	Hs.235331	ESTs	5.78	8.46
	410926	AW810708		gbl:MR2-ST0129-051099-007-g07 ST0129 Homo	3.34	8.47
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	4.26	8.45
45	429623	AW449105		gbc:LR-HF3-akg-e-35-D-LJLs1 NCL_GCAP_Su	3.32	8.43
	420156	AW445258	Hs.6187	ESTs	3.40	8.38
	411555	AF113537	Hs.70669	HMP19 protein	5.85	8.34
50	408509	AA497035	Hs.110502	ESTs	3.17	8.34
	442368	AB98577	Hs.202481	ESTs	3.02	8.33
	457870	AA732217	Hs.294054	ESTs	3.04	8.32
	437254	AA831258		gbcz7304s.1 NCL_GCAP_GCB1 Homo sapiens	3.35	8.24
	415508	R39236		gbcy91003s.1 Soares infant brain INB H	3.07	8.22
55	404883	U43879	Hs.54506	diacylglycerol kinase, epsilon (840)	3.31	8.20
	435229	AA476558	Hs.269516	carbonic anhydrases XI	3.21	8.19
	458120	W21398	Hs.54525	ESTs. Weakly similar to cytochrome P-450	3.22	8.17
	444613	H29627	Hs.79092	ESTs	3.78	8.16
	417050	N39540	Hs.108029	ESTs	4.06	8.14
60	426507	U30960	Hs.158333	proteinase, serine, 7 (tertiololase)	3.68	8.06
	412623	BC075191		gbc:PMH-BT0565-110200-003-g03 BT0565 Homo	3.40	8.04
	424549	A0873205	Hs.183114	Homo sapiens cDNA FLJ14236 fs, clone NT	3.27	8.03
	452689	F33868	Hs.284176	transferrin	3.03	8.01
65	405475	cNpL_19940		exon	3.28	8.00
	403932	csp_1_538		exon	3.59	7.99
	407095	AF011757	Hs.105937	RAGE binding protein	3.32	7.96
	415967	H11124		gbl:ym148.07.s1 Soares infant brain INB H	3.10	7.96
	417555	H63566		gbcy67c10.r1 Soares fetal liver spleen	3.05	7.95
70	448985	AA324805	Hs.22777	carboxic anhydrases XI	7.75	7.93
	428689	NM_014351	Hs.185810	sulfotransferase-related protein	7.74	7.91
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	4.68	7.74
	441099	AW339393	Hs.126573	ESTs	3.08	7.74
	446599	AF017090	Hs.21554	KIAA1107 protein	3.10	7.73
	406112	p01_24243		exon	3.12	7.73
75	458439	AV547220	Hs.282889	ESTs. Weakly similar to strong similar/	3.22	7.69
	428859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor I	3.15	7.65
	412090	AW355626	Hs.12396	ESTs. Weakly similar to ALL6_HUMAN ALL S	3.01	7.67
	415547	BC141440		gbc:PMH-BT0239-000100-015-019 BT0239 Homo	3.68	7.61
	447772	A024558	Hs.181399	ESTs	3.04	7.63
80	411132	AW819191		gbc:CM1-ST0283-071299-051-d08 ST0283 Homo	3.72	7.61
	425490	NM_002248	Hs.158173	potassium intermediate/small conductance	3.15	7.60
	454568	BE141434		gbc:MR0-BT0079-051099-002-d01 BT0079 Homo	3.16	7.59
	439999	AB337830	Hs.8462	KIAA1379 protein	3.40	7.57

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	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	5.71	7.57
	428175	AJ310774	Hs.98376	ESTs	3.04	7.55
	413162	BE088115	Hs.129368	gb:CM-B10368-051299-060-g07 B10368 Homo	3.49	7.54
	415161	AA053854	Hs.235090	Homo sapiens mRNA; cDNA DKF2p7610101 f-	3.11	7.53
5	442527	AF150289	Hs.205436	ESTs	3.31	7.53
	450407	NM_008010	Hs.24969	gamma-aminobutyric acid (GABA) A receptor	5.24	7.53
	456566	AJ585659	Hs.190032	ESTs	3.13	7.47
	441799	AA252276	Hs.127072	ESTs	3.38	7.41
	424185	AA275752	Hs.142670	Homo sapiens clone 24629 mRNA sequence	3.16	7.40
10	429793	AA811957	Hs.125779	ESTs	3.13	7.38
	429268	AA205336	Hs.156481	RAR-related orphan receptor B	3.48	7.38
	403705	c1p1_1_1252		ESTs	3.33	7.35
	402598	BE314624	Hs.3128	polymerase (RNA) (DNA directed) polyn	3.04	7.33
15	455377	AW950347	Hs.116530	gb:CV2-NN1073-220400-159-046 NN1073 Homo	3.03	7.33
	435070	AJ821270	Hs.116530	ESTs	3.03	7.33
	405427	c1p3_1_1762		ESTs	3.03	7.25
	455146	AW951879	Hs.116530	gb:CMO-CT0341-260100-160-h12 CT0341 Homo	3.55	7.24
	402816	c1p3_2531		ESTs	3.13	7.21
	422850	243784	Hs.79713	solute carrier family 25 (mitochondrial	3.40	7.15
20	422297	AW961250	Hs.155615	ESTs	3.44	7.10
	412686	AA939458	Hs.155615	gb:R02-NN0005-160300-011-c06 NN0005 Homo	3.51	7.09
	436383	BE065178	Hs.155615	gb:R1-CT0314-022020-012-h01 CT0314 Homo	3.09	7.09
	412290	DE069037	Hs.155615	gb:CV3-BT0379-161299-040-e12 BT0379 Homo	3.04	7.08
25	415466	U112214	Hs.13284	ESTs	4.22	7.07
	407728	AAW01502	Hs.175551	ESTs	3.05	7.06
	455448	R13205	Hs.21413	solute carrier family 12, (potassium-chl	5.93	7.05
	417275	XG5578	Hs.81849	parvalbumin	4.08	7.04
	418425	AJ871247	Hs.6282	ESTs	4.10	7.04
	440553	AA839574	Hs.177511	ESTs	3.28	7.04
30	411427	AA946080		gb:MR3-CT0176-081099-002-b09 CT0176 Homo	3.11	7.03
	422272	AJ482421	Hs.77565	CK-associating RS-cyclophilin	3.39	7.03
	110816	AW806175	Hs.94389	gb:MR1-UM0105-130400-003-a05 UM0105 Homo	3.30	7.02
	418375	NM_003581	Hs.94389	synaptonemal-associated protein, 25kD	9.53	7.01
35	421827	AJ133851	Hs.97318	ESTs	3.10	7.01
	447258	DE947911	Hs.97318	gb:R2-Ma05-1 NCL_CGAP_Bm52 Homo sapien	3.09	6.99
	455547	AW954078	Hs.97318	gb:R3-BN0035-090200-011-b02 BN0035 Homo	3.35	6.98
	432209	AW971278	Hs.97318	gb:EST383367 MAGE resequences, MAGL Homo	3.49	6.92
	404541	c0p1_5409		exon	4.52	6.93
	451539	AA054647	Hs.218633	ESTs	3.01	6.89
40	429954	AJ515130	Hs.21374	ESTs	3.82	6.87
	411138	AW819500	Hs.201897	gb:R05-ST0293-190100-012-C07 ST0293 Homo	3.08	6.87
	447464	AAW44657	Hs.201897	ESTs, weakly similar to ALU4_HUMAN ALU 5	3.33	6.85
	454713	AW815111	Hs.78748	gb:CM4-ST0212-081499-023-c06 ST0212 Homo	3.16	6.84
	415734	NM_014747	Hs.78748	KIAA0237 gene product	5.00	6.84
45	425667	AA456275	Hs.44941	ESTs	3.09	6.80
	403008	c21p3_2374		exon	3.04	6.78
	448079	T56522	Hs.154030	ESTs	3.11	6.75
	441965	NM_003947	Hs.126860	histarginin-associated protein interact	4.49	6.75
50	437804	AA828257	Hs.124234	ESTs	3.42	6.73
	436454	AA757615	Hs.231509	ESTs	3.01	6.72
	418334	H53139	Hs.36271	ESTs	3.12	6.70
	452960	BE167014	Hs.175285	gb:CM2-HT0502-140200-088-038 HT0502 Homo	3.06	6.68
	445095	AJ585285	Hs.175285	ESTs	3.19	6.66
55	445611	AW419467	Hs.154679	ESTs	3.61	6.66
	437762	T78026	Hs.154679	synaptobasmin 1	7.21	6.68
	416268	HA6111	Hs.45773	gb:CV21c07-r1 Soares adult brain NZLGH05	3.02	6.67
	445766	AW869690	Hs.45773	ESTs	3.25	6.64
	445100	AJ033198	Hs.45773	gb:aw0408-s1 Soares_fetal_liver_spleen_	3.07	6.64
60	408070	AW148852	Hs.60857	gb:av0505-x1 NCL_CGAP_Bm35 Homo sapien	3.12	6.60
	451602	AA008546	Hs.126860	ESTs	3.05	6.59
	441447	AA934077	Hs.4775	junctional protein 3	4.06	6.59
	445078	AJ865975	Hs.194152	ESTs	4.25	6.59
	434501	AF143878	Hs.24974	Homo sapiens clone IMAGE:115304 mRNA seq	3.25	6.59
65	415960	RA5020	Hs.24974	ESTs	3.34	6.58
	403395	c2p1_11541		exon	3.29	6.57
	403061	c2p1_10450		exon	3.06	6.56
	419232	AJ382037	Hs.87421	ESTs	3.28	6.56
	425954	AW936277	Hs.165636	hypothetical protein DKFZp761C07121	6.50	6.56
70	402317	c4p1_3133		exon	3.53	6.52
	452178	AW043676	Hs.171529	ESTs	3.38	6.53
	455758	R15709	Hs.284231	Novel human gene mapping to chromosome 22	4.42	6.52
	433858	N65243	Hs.152974	Homo sapiens cDNA FLJ12735 fs, clone NT	3.58	6.52
	425440	AA357518	Hs.90297	gb:EST86256 LNCAP cells 1 Homo sapiens c	6.45	6.49
75	418412	AW161053	Hs.7947	synuclein, beta	5.60	6.47
	423678	AW963357	Hs.35758	ESTs	3.47	6.47
	416625	R97839	Hs.194096	ESTs	3.10	6.46
	451864	T52636	Hs.194096	ESTs	3.28	6.46
	405732	AA497229	Hs.202129	nm23a1	3.71	6.44
	434619	HA3163	Hs.32510	ESTs	3.05	6.44
80	413797	BE167274	Hs.55956	ESTs	3.23	6.44
	438612	AW973960	Hs.202129	ESTs	3.39	6.42
	412317	AW951579	Hs.153406	gb:R01-BN0014-210100-012-b05 BN0014 Homo	3.46	6.42
	422189	N7567	Hs.153406	ESTs	3.03	6.41

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	453100	AW068871	Hs.224796	ESTs	3.30	5.49
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	3.24	5.48
	454935	AW045075	Hs.142442	gblMF3-CT0176-081989-002-b02 CT0176 Homo	3.26	5.48
	435447	AW02932	Hs.142442	HP1-BP74	3.89	5.47
5	402963	c26g1_3451		exon	3.28	5.47
	458233	AA203339		gluc255a01.1 Scores_fetal_liver spleen	3.02	5.47
	407716	AW007084	HL243243	EST	3.30	5.45
	417429	AW050629	Hs.286237	Homo sapiens cDNA FLJ11941 f1, clone HE	3.31	5.38
	446406	A079169	Hs.203456	ESTs	3.07	5.37
10	441192	AW073535	Hs.143962	ESTs	3.19	5.35
	430661	AW052160	Hs.320114	ESTs	3.70	5.35
	433832	AW054599	Hs.169330	neuronal protein	6.78	5.33
	427002	AA524093	Hs.231558	ESTs	4.00	5.32
	428741	AA461366		gluc270H05.r1 Scores_tkoi_fetus_Nb2H-F8_	3.10	5.32
15	448383	T05616	Hs.525111	ESTs	3.39	5.30
	442988	AK061930	Hs.131683	ESTs	3.07	5.29
	426713	AW055299	Hs.130055	ESTs	3.33	5.29
	421294	AA713466	Hs.180291	ESTs	3.44	5.28
	406452	glt_21861		exon	3.20	5.28
20	423508	AW040921	Hs.129711	hepatitis A virus cellular receptor 1	3.26	5.27
	442114	BE217975	Hs.157021	ESTs	3.32	5.26
	432508	AW080915	Hs.190201	ESTs	3.46	5.26
	425604	U94320	Hs.158330	neuropeptide Y receptor Y5	3.26	5.23
25	417325	R26789	Hs.23595	ESTs	3.08	5.23
	444448	H68317	Hs.143660	ESTs	3.61	5.22
	413024	AF036268	Hs.75149	SH3-domain GRB2-Ric-2	3.71	5.22
	437911	AA549010	Hs.124250	ESTs	3.11	5.18
	435406	Z78698	Hs.4894	calcium/calmodulin-dependent protein kin	4.95	5.17
	407131	R88679		gluc31d03.1 Scores_fetal liver spleen	3.30	5.16
30	435776	AW37182	Hs.263986	ESTs	3.14	5.13
	455532	AW084628		gblRC1-HN0015-120400-C21-h11 HN0015 Homo	3.14	5.13
	457352	AA488059		gluc2a56H02.a1 NCL_GAP_GCB1 Homo sapiens	3.48	5.12
	428870	AA413682	Hs.134832	ESTs	3.17	5.12
35	445962	AD66410	Hs.201386	ESTs	3.14	5.12
	418153	R13696	Hs.112830	ESTs	3.16	5.10
	440695	AW103823	Hs.131586	ESTs	3.08	5.10
	451146	AW024029	Hs.255369	Homo sapiens cDNA FLJ110265 f5, clone HE	3.42	5.09
	456036	BE355554	Hs.75839	zinc finger protein 6 (ZMPK1)	3.21	5.09
40	420683	A0735488	Hs.111436	ESTs	3.17	5.08
	455628	AW084757		gblRC1-HN0015-040400-C11-g10 HN0015 Homo	3.35	5.08
	408442	R05636	Hs.21435	ESTs	3.10	5.07
	446093	AW066489	Hs.145096	ESTs	3.30	5.05
	403489	c3p1_2255		exon	3.43	5.05
	402078	cNp3_1070		exon	3.05	5.03
45	412604	H18857	Hs.22547	ESTs	3.63	5.03
	458407	V03022	Hs.186809	ESTs, Highly similar to LECT2 precursor	3.52	5.03
	407367	AA130773		gluc2130d1.r1 Stratagene c/on (937204)	3.51	5.02
	439106	AW163034	Hs.6467	synaptogyrin 3	5.63	5.01
50	445336	A1220339	Hs.166775	ESTs	3.21	5.01
	435404	A1240681	Hs.124935	ESTs	3.99	5.00

TABLE 6B:

Pkey: Unique Eox probeast identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
	410537	282574_1	AW060917 AW066409 BF890475 BF890476 AW066540 AW066614 BE145666 AW066575
	436812	559772_1	AW078773 AW078607 AA016101 AW194180 AA731645 AW08073
60	464171	1045940_1	AW054832 AW054736 AW054857 AW054816 AW054834 AW054817
	454569	28039_5	BG074750 BF374578 AW010801 AW010106 AW010084 BF374755 AW009521 BF374734 BF374590 BF374534 AW096959 BF374588 AW10437
	417159	207568_1	AW010151 AW009682 AW010151
	450349	102722_1	R01760 N49787 R01761
65	414167	315279_1	AW743081 H53337
	423280	801045_1	BE259777 BE312141 BF942960
	431400	1233916_1	AW055178 H66635 AA324037
	454656	164604_1	AW059394 AA504607 AA504705
70			AW070525 AW070380 AW070772 AW07752 AW067673 AW067900 AW067956 AW067679 AW067615 AW067917 AW067849 AW067632 AW067821
			AW067842 AW067827 AW067754 AW067830 AW067829 AW067825 AW067819 AW067769 AW067805 AW067833 AW067763 AW067812 AW067840
			AW067908 AW067684 AW067689 AW067596 AW067595 AW067593 AW067597 AW067902 AW067646 AW067756 AW067687 AW067685 AW067633 AW067632
			AW067170 AW067753 AW067669 AW067678 AW067666 AW067680 AW067688 AW067647 AW067957 AW067674 AW067674 AW067602 AW067617 AW067821
			AW067657 AW067652 AW067616 AW067670 AW067760 AW067760 AW067956 AW067608 AW067693 AW067839 AW067601 AW067622 AW067698
			AA772901 B68670 BE1151 AW051331 BF940996
75			AW079114 AA226060 AW037606 AA252003
			BE150647 AW071143 AW080924 AW050921 BF753820 AW060220 AW080178 AW080150 AW080915 AW0809175
			BE145800 BE145921 BE145873 BE145871 BE145800 BE145797 BE145736
			AW048279 AW049030 AW047866 AW047557 AW049046 AW046516 AW049034 AW049033
			117156 T20135 T13723 T11958 T11616 RA5874
80			AW071240 AA493723 AA483043
			BE007237 BE546311 AA984811 B12568810 W19919 BE007263 BG000032 BF327011 AA809159 BE007496
			1121172 AW061336 H54221
			BE514561 AA417636 AW756446 BG000004 BM00307 BG460993 BG613293
			BF375123 AW081447 AW0814474 AW0813343 AW081615 AW081338 AW0813300

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5	459675_1	493763_1	BE065984 BE066085 BE065942 BE065965
	459684_1	1408581_1	BE064521 BE064441 BE064426 BE064525
	451496_1	85420_1	AA046579 BF32758 AW503407 AA015131
	424617_1	895912_1	AW563059 AA344151 AA344472
	451962_1	323094_1	AW583345 AW54063 BF962818 AW847791 BF035483 AW847645 BF961514 BF963464 BF952264 BF963521
10	455260_1	231032_1	BE161805 AW817037 BE161759 BF970032 BF869598
	434893_1	146176_1	AF147353 147219 147216
	410206_1	1064369_1	AW510708 AW810806 AW810771 AW810924
	430623_1	830636_1	AW449665 BE220971 AW448105
	432754_1	123876_1	AW576161 AA512293 AA769857 AA747712 AT94019
15	415509_1	167142_1	FA5579 F1022 F05206
	413263_1	1497122_1	BE075132 BE075131 BE075130 D60035 BF080035
	415967_1	1859490_1	HA9130 H11230 BF363185 HA9061 H11124
	417555_1	1978200_1	AA203678 AL597743 HA5306
	413547_1	1505005_1	BE147456 BE147560 BE147708 BE147440
20	453377_1	154707_1	AW819177 AW819302 AW819191 AW819175 AW819252 AW819244 AW819265 AW819269 AW819190 AW819268 AW819183 AW819246 AW819194
	454568_1	1061859_1	AW819249 AW819186 AW819180 AW819168 BE158470 AW819251 BE152602 AW819263
	413162_1	1402365_1	AW837509 AW807824 AW807826 AW807903 AW807786 AW807750 AW807811 BE141434 AW807611 AW807837 AW807699 BF374481
	453377_1	154707_1	BE089104 BE086096 BE08198 BE086115 BE086102 BE086154 BE086103
	453377_1	154707_1	BF947516 AW805291 BF947512 BF952006 BF952716 BF952525 BF952524 BF952619 BF947500 BF952608 BF952523 BF952532 BF952344 BF746516 BF947614 BF746511 BF952358 AW930540 AW930300 BF947617 AW905349 BF952531 AW905403 BF952528 BE081655 BF746513 AW905286 BF952658 BF947513 BF947510 BF947618 BF947619 AW905347
25	435149_1	1099403_1	AW861879 AW861948 AW833447 AW861873 AW865045 AW866167
	412896_1	1243154_1	AW864508 AW864677 AW864902
	436383_1	46787_1	AE227675 BE065176 BE065320
	412290_1	163352_1	BE066037 BE066175 AW933034 AW936025
	411427_1	1083097_1	AW846080 AW846074 AW846118 AW846130
30	410816_1	108261_1	AW868175 AW868176 AW868170 AW868166
	447256_1	1485710_1	BE017316 BE047391 AA394167
	455647_1	1245954_1	AW994078 BE176183
	432209_1	1235790_1	AW971278 AA528270 AA553447 AW971281
	411138_1	1071173_1	AW819500 AW819503 AW819481 AW819459 BF375618
35	450713_1	1067686_1	AW819111 AW819394 AW819218
	455565_1	1555933_1	BE167014 BE167059 BE167062
	416268_1	1959926_1	H41554 HA9111 HA6317
	443100_1	1418955_1	BE004743 AW804074 BE069437 BE069439 BE069378 BE069438 BE004795 W02375 A033168 BF332422 BF332418 BE178660
	409070_1	632213_1	AW140522 BG594152
40	425440_1	1228151_1	AW926960 AA357518 AA360531
	412317_1	1164038_1	AW951979 AW951961 AW951983 AW933585 AW991977 AW991971 AW936652
	453039_1	3206957_1	AL138417 AL138418
	415392_1	215662_1	W25573 W27416
	412218_1	147109_1	BE148133 BE148132 BF736564 BE148152 BE148159 BF83700
45	411206_1	1074383_1	AW834895 AW834717 AW834714
	412734_1	1245451_1	AW993458 AW993484 AW993490 BF512874
	412694_1	1243393_1	AW984388 AW984392 AW984373 AW984351 AW984381 AW984377 AW984366 AW984348 AW984391 AW984372 AW984373 AW984353 AW984362
	411532_1	1089952_1	BE143305 BF374184 BF374190 AW850286
	411167_1	107140_1	AW820223 AW820314 AW820321
50	413118_1	1489780_1	BE066075 BE066539 BE065956
	454751_1	1070838_1	AW819132 AW819122 AW819018 AW819135 AW819125 AW819024 AW819012 AW819141
	452861_1	319757_1	BE177863 AW9394738 A0323735 BF945431 BF946329
	455574_1	1161013_1	AW954025 AW954030 AW954039 AW954031 AW954032 AW954046
	454935_1	1063098_1	AW846075 AW846103 BF333876 AW846077 AW846122 AW846123 AW846095 AW846076 BF333879 BF333878 AW846092
55	428741_1	1384359_1	AA033339 AA06160 AA929005
	455532_1	1384359_1	AA61386 AA633841 AA433845
	455532_1	1384359_1	AW846023 AW846017 BF959406 AW846017 AW846026 AW846022 AW846073 AW846076 AW846023 AW846076
	457352_1	1233795_1	AW968968 AA809599 N72933 AA809184
	455528_1	1243660_1	AW846734 AW984757 AW984677 AW984675
60	407367_1	4907_1	AF065963 H72500 H72511 AA130773
	TABLE 6C.		
	Ref.		
	Unique number corresponding to an Ecos probedet		
	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA		
	sequence of human chromosome 22" Dunham, et al. (1995) Nature 402:459-495.		
65	Strand:	Indicates DNA strand from which exon was predicted.	
	NT_position:	Indicates nucleotide positions of predicted exons.	
	Phy:	Ref	Strand
	401412_1	7941013_1	Minus
70	406230_1	7249032_1	Minus
	402125_1	4033680_1	Plus
	404289_1	2789644_1	Plus
	406534_1	7711477_1	Plus
	405348_1	2914717_1	Minus
75	401081_1	3478647_1	Plus
	402624_1	7885063_1	Minus
	405320_1	3478667_1	Minus
	406476_1	2121229_1	Plus
	403932_1	7454203_1	Plus
80	406112_1	9133145_1	Plus
	400708_1	7245204_1	Plus
	405427_1	7243901_1	Plus
	402816_1	6723302_1	Minus
	404541_1	8318559_1	Plus

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403008	6070306	Plus	94906-94785,95006-95233
403395	9430353	Minus	144847-145075
403361	6594192	Plus	143075-143098
403717	7259747	Minus	75166-79750
401313	9212516	Minus	150842-191090
405961	8190197	Plus	45132-45254
404403	7272157	Minus	72053-72238
405332	5165141	Minus	70483-71207
400710	7249204	Plus	156753-157120
402953	9408724	Minus	122603-122743
404542	5960362	Minus	75322-76427
403449	7331314	Minus	39897-39212
405278	6139075	Minus	3953-3965,4823-4891,5420-5529,6043-6170

TABLE 7A: EXTENDED GLIOBLASTOMA SEQUENCES: This table includes sequence information for 21 DNA and protein sequences

DNA sequence 1

Gene name: Protein tyrosine phosphatase, receptor-type, Z polypeptide 1

Unigene number: Hs. 78867

Protein Accession #: P53426

Nucleic Acid Accession #: NM_062851

Coding sequence: 148-7092

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	CGCGAGAGGG	CGCGAGACCG	CTCGGAATG	CGAATCTGTA	AGGTTTCTCT	CGCTTGACTT	180
	CGACTCTCTCT	GTGTTTGCGC	CTCGGATGAG	CGTAATGAGT	ACTACAGACA	AGAGAAATTA	240
30	CTGTTTGAGG	AGATGATCTG	GTGTCATATC	GGAGGACCTA	ATCAAAAAAA	TGGGGGAGAG	300
	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCTATCA	ATATTGATGA	AGATCTTACA	360
	CANSTAAATG	TGAATCTTAA	GAAACTTAAA	TTTCGAGGTT	GGGATAAAAC	ATCATTTGAA	420
	AAACATATCA	TTCTATACAC	TGGGAAACAA	TGGGAAATTA	ATCTCAGTAA	TGACTAACGT	480
	GTCCAGCGAG	GAGTCTGATG	TGAGTCTGAA	AGATTAAGTT	TCTCTGGGGA		540
35	AAGTTCGATA	TGTCACTCTG	TGATATCAGG	CATAGTTTGA	AGGACAAAA	ATTTCCAGCT	600
	GAGATTCGAA	TCTACTGTCT	TGATCCGGAG	CGATTTTGA	GTTTTGAAGA	AGCATCTCAA	660
	GGAAAGAGGA	AGTTTAAAGC	TTTATTCAGT	TTGTTTGGGG	TGGGGACAGA	AGAAAATTG	720
	GATTTTCAAG	CGATCTCTGT	TGAGTCTGAA	AGATTTAGTC	GTTTTGGGCA	CGAGGCTGCT	780
	TTTAAATCAT	TGCATCTGTT	GAACTCTCTG	CCAAATCTGA	CTGACAGATA	TTACATTTAC	840
40	AATGGCTCAT	TGACATCTCC	TGCTCTGACA	GACACAGTTG	ACTGGATTGT	TTTAAAGAT	900
	ACAGTATACA	TCTCTGAAG	CCAGTGTGCT	GTTTTCTTGT	AAGTCTCTAC	AATGCACACA	960
	TCTGTTTATG	TGAGTCTGAT	GGACTACTTA	CAAAAGATAT	TTGAGAGACA	ACGATACAG	1020
	TTTCTGAGAT	CGATCTCTGT	CTCACACACT	GGAGAGAGAG	AGTTTATAGA	AGGCTTTTGT	1080
	AGTTCCAGAC	CGAGAAATGT	TCAGGCTGAC	CCAGAGAAAT	ATACAGAGCT	TCTGTATACA	1140
45	TGGGAAAGAC	CTCGATCTGT	TTATGATACC	ATGATTTAGA	AGTTTGCAGT	TTTGTACACG	1200
	CGTTTGATAT	GGAGAGACCA	AACCAAGCAT	GATTTTGTGA	CAGATTTGCA	TCAGAGTCTT	1260
	GTGTGCAATC	TCGATAATTT	CTCAACCAAT	ATGATGATTA	TTTCTCAGAT	AGTAGGCATA	1320
	TGCACTAATG	GCTTATATGG	AAATATACAG	GACCAACTGA	TGTGCAACT	GCTTACTAGT	1380
	AATCCTGAAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAAGCT	AAGAAATAT	CAAGGAGGAG	1440
50	GAGAGAGGGA	AGAGCATATG	AAGAGGCCCT	ATTGTGAATC	CTGTTAGAGA	CAGTGTATACA	1500
	AGCCAAATCA	GGAAAGAGGA	ACCCGCAATT	TCGACAGACA	CACATCTACA	TCCGACAGAG	1560
	AGCAAAATCA	ATGAAAGCCA	GACTAAACGA	TOCCCAACGA	GAGGAGATGA	ATTCTCTGGA	1620
	AGGGGTGATG	TGCCCAATAC	ATTCTTTAAAT	TOCACTTCCC	AACCAAGTAC	TAAATTAGCC	1680
	AGAGAAAGAG	AGATTTCTTT	GACTCTCTAG	ACTGTTGACTG	AACCTCCACG	TCACATCTGT	1740
55	GAGATGATAT	CGATCTCTTT	AAATAGATGG	CTGTAAGAGT	TTCTTAGAGT	TCCGACAGAT	1800
	AACCTTTGCG	GGATCTGAGA	ATCTCTTAAT	ACGTTTCTCA	TAMCAAGATA	TGGGAGGAGG	1860
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	GAAACCCGAG	AGACATACAC	ATATAGATCT	CTATATACAG	AACCTCTGAG	TAAGTCTCTC	2040
60	GAGATCTCAA	CTTCACTCAG	TCAGAGAGGA	TCATTAAGAG	ATCCTTCTAT	GGAGGGAATAT	2100
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	AGCTTTCTCC	AGATCAATTA	CAGTCAGATA	GGTGTGATG	AATCTGAGGA	GACACACAGG	2220
	TCTCTTTTCC	CAGACCCAGT	ATGCTCAAGG	ATCTCTCTCG	CTTCTAGAGT	GGAAATGCCA	2280
	CTATTATCTA	CTTTTGCTTA	CTCTCAACT	GGATCTAACG	CTCATGCTT	TACCCCATCC	2340
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	GTATACAAATG	GTGAGACACC	CTCTCAACTC	TCTCAAGATA	GTGAGTCTT	TCTCTATGTC	2460
	ACCCCTTTGT	TGCTTGACAA	TGAGATCTTC	AAGCTTACCC	CTGCTGCTTC	AATTAATGAT	2520
	TGGGCTTTGC	ATATCTAGCC	TGTATTTTCC	AGTGTGGAGG	TGTCTCTGAT	ATCATCTCTG	2580
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	GAGTAGGTGC	TTGCGATGCG	TTTCTGCGCA	GTGGCTGGGG	GTGATTTGCT	ATTAGAGGCC	2760
	AGCTCTTCTC	ATATCTCTCA	CTTCTCTCTC	CTACTACTGT	CTGCTGAGCA	GACTCTGCGA	2820
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	AGCATGTGATG	CGATGATGCA	TGACAGTTCT	TGAGGCGCTG	AACTTCTCTA	TGCTTGTGCT	2940
75	GATAATGAGG	GCTCCCAATCA	CATCTCTCAG	GTTCCTTACA	GTTCTGCAAT	ACCTTGAGAT	3000
	GATTTCTCTG	TTATTTAGTA	TGTATTTTCC	AGTGTGGAGG	TGTCTCTGAT	ATCATCTCTG	3060
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	GGGCTGACAG	CCCTTAAATC	TCTCTTCACT	GTTCCTGAGG	CTGAAATTAC	ATATACACAA	3240
80	TCTCTGTGTTG	GTATATATTA	TAGGCGCTCT	CTGTAAGAGG	AAATCATATA	TGGGATAGAG	3300
	ACTGTAAGCTC	AATCTCTCTT	TTTCAAGGAG	ATGTTTTCAG	CTTCTGTAAG	CATCATCTCT	3360
	CCCAACATGT	ATGATTAATGT	AAATAAAGTTG	AATGTGCTCT	TACAGAAAC	CTCTTTTCTC	3420
	ATTTCTAGCA	CCAGAGGAGT	GTTCCTCAGG	TCCCTTGCTC	ATACACACAC	TAGTGTTTTT	3480
	GATCTAGAGA	TGATTCAGAT	TCCAGAAAT	AACTTTTGG	TTTCACTTAC	ACATACCTGC	3540
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 5 CCGAAGTGT ATAAATAATG TTCTCAAGAT TTGCATCTCA TTGTATCAAA TTCTCTCTCA 3840
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 70 TTTAAACACT TCTCATATG CTAACAGAAA ATGATGAAA TTTTACTGT TTTACTGTCT 7560
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 GTTCTTATC CAGGAATG CAAATATAA TATTAATAT GCATTAAAA AAAAAAAA 7920
 AAAAAAAA AAAAAAAA A

Protein sequence 1

Gene name: Protein tyrosine phosphatase, receptor-type, Z polypeptide 1

Unigene name: Hs.7886

Protein Accession #: NP_002842

Signal sequence: 1-20

Pfam domain: carb anhydrase [38-300]

Transmembrane domains: 1639-1661

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 1 11 21 31 41 51

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MLRLKPLAC IQLCLQCRID WANKYRQRQ KLVBRIGWY TGAIDQRWNG KEYTCHSKP 60
 GSPVINDLH TGVVIVLDEL KPDZKDKSL RNTDTHARKV TGVHLEBDY PVQGVSDHW 120
 FIASKITFW KQNMSSSDGS EHLERQKFP LMQVYCPDA DPFSPFEAV KIKKLRKALS 180
 ILFVQTEEN LDFKALIDGV ESWSPFKQA ALDPFLLAK LFNSTDKYI YNGSLDTPPC 240
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 LIGTEIIEK EREGKDIIEG AIVMPGRSA TWIKRKEKP ISTTHVNR IGTKNEAKIN 480
 KPSFPROFES QGDVVPFSL NSTSQPVTKL ATEKDISLS QTVELPFHT VSGTASLAD 540
 GSKTVLARI MLKSLGTADL MYVLEITEP ESSLTSEKLD TWARDSGSS PATSAIPFIS 600
 ENISQYIFPS SNFPTTTO VLUPESAMA SEDTSSGSE TSLADPQMW NMFVPSSTI 660
 TAQDVGSGR ESFLQITNTE IAVSESEKT KFSQAPVMS QGVSPTOLEH PLYSTFATP 720
 TEVTPUAPT SSQQLDVST VNVVYSQTO PVYINGTELO PSYSSVFPFL VTPLLADWYI 780
 LNTTPASSS DSALBAPTVP PSVUSPFES LSYVIGAPLL PFSASFPSSE LPEHLEATYQ 840
 LQVQTSAT SDVPLRLSL PVQGDLLLE PLQALQSDV STETAASBLT DPFSSGVLT 900
 KTLMPQVPE PSDAMHAGR SSGPEPSYAL SDNDSQHIF TVEYSALPV HSWGVNTQG 960
 SLFSPSHIP IPKSSLITPT ASUQPTHAL SDGSGMGAS SDSEFLPADT DCLTALNIS 1020
 PVSAPLPTT TSVFGDNIA LSHSEIYGN SELQIPESN DMVPSSESTV PMHMDHNVK 1080
 DIASLQEVV SLSSTCHMP DSAHMTTKV FHEIISQVVE HNFVSQVDT VQASQSTSL 1140
 KPLNSANSE ASDPASEEM LSPSTOLLYP ETSASFSTEV LLQFSTQAD VDTLLTLP 1200
 AVPSDILVE TPVKDKIST MLHLVNSA SSEHMLSTS VPFVDSPTS IMHISASQL 1260
 TISVASEKE PVLKSESH QVVGELYSND ELVOTANLEI NQMPFKGR VPATVPLSID 1320
 EPLATLNLH HSDLEIST ESYTGKVA OLPYVSDTF VSTHVSFVIG NQVATVAVS 1380
 PHKDSVSTL KLFPSKATS ELHSAKEDA GVQGGSDGQ TQVDDGSD SDLSQDNKRS 1440
 CMSCSYRES QKVWSDSDT HENSINDQNI FIVSLSEHS EEDNRVTSV SDGTONKRS 1500
 KQKSPRANGL SQHWDKES NDIQTGSALL PLSPEKAMA VLTSDEESGS GOOTSDSLAE 1560
 HESTSTPFA DFNKQADGI LAJESSEITP QPKSPFSSV TSNGEVFHV SDAPASNSH 1620
 ESKQLAQLL ESEKAVIFL VYGAATITL LAYVLELIT MRCPCFAM VLESTSENV 1680
 ISTPTTPIFP ISDVQAIPI KHFPRKVALD HASGFTPEE ELUKEVQV QSTCVLQIT 1740
 ADSRHFDRK HKRNYINIA VHSRVLKAL LAEKDKLTD INIMNVQVY NPFIAYIAQ 1800
 QFLKASTAR HNMHEWREY VPMHNLVE KORKKQDM FADGSSEYQ FLVTRGVRG 1860
 LAYTVRIFT LNKYGLKGS QKQPSRIVY TQYVTKLQ WQFVSLAV VPFKXAKA 1920
 KXHAHVSVV HCSAGVORT TYVLDMLQ QIQSEVTNI PGLKHRSQ RMLQYLEDQ 1980
 VYVHDTLVE AILSKETEVL DSHIHAYNA LLIPGPAOK KLEKQFLLS QNIOQSDYS 2040
 ALLQKCNREK NHTSIPFV ESHVSIHSE GSGDTYNAS YIMYQSNIE FITYHPLN 2100
 TIKPWFHPE VQKCNASIE GQKQKQVYV LKESFKVTL MABEIKLEN 2160
 EEKLIQDPI LEATQDHYL BRFHGFCKFM PHFDSPIKT FELISVKEE ANNDGMIV 2220
 HDEHGVQAT TFCALTILAH QLEKNSVDV YQVAMNIML RQGVFADIQ YQFLKRVLS 2280
 LVSTRQENP STSLDSNGAA LFDGNIAEL ESLV

DNA SEQUENCE 2

Gene name: tyrosylprotein sulfotransferase 1

Unigene number: Hs.110903

Protein Accession #: D45894

Nucleic Acid Accession #: NM_003596

Coding sequence: 82-1194

1 11 21 31 41 51
 | | | | |
 GTACAGTCT CATGCGCTGA ACATTITCOO AAATCATTT TGACAAAAAT ACTGTTTAA 60
 TACACAATA ACCACATGAA GATGTTTGA AGCTGAAGC AGAACTTACT ATTGCATGT 120
 CCGTGATTA OTCTGTGAC TGTGTTTTC CTGGCGCAGC ATGCCATGGA ATCCATCAC 180
 CCGTACAGG AACCTACGAC GCGATCTAAA TGTGAGACCA CAGACACCA TGTAGAACAT 240
 GCGTGAACC TCGACAGCA CAAGACCTT GATCATGCA AGATATACC TTATATATT 300
 ATTGAGTGT TGCTCTCGAG TGGACACCA CTCATGAGG CCACTCTGGA CGCAGACCT 360
 GACATTCCCT GTGAGAGGA AACAGGGTC ATTCOCOGA TCTGTGCCCT GAGACGATG 420
 TGCTACGCT CAGTAAGA GAGACGCC CCGATGAGG CTGTGTTTAC TGATGAGTG 480
 CGGATGCT CAGTCGAC CTCCTACTA TGAAGATGCT TGAAGATGCT GAGACGAC 540
 CTTATTATT GATAAAGA TCTTGTGC CGAAACTCT TAACCTACT TTCTGTTTA 600
 TTCGCCATG CCAATTTCCT CCGATGCTC CGAGATGCC GCGACTGAG CATTCAGTG 660
 ATTCTCGAA AGGTTACTAT GCGTGATT TT GATCTGAACT GCTATGAGCA CTGTGTGCA 720
 AAGTGAGCT GACCTGAT GACCTGTAT GACCTGTGTA TGGAGTTGG TATAAAGA 780
 TCGATGTTG TTACATAGA ACACTGTGC TTACACTCT ACCTGTGCT GAGAGACTC 840
 TAAAGTTC TCGAGATCC ATGAGACAC TCGATTATG ACCATGAGA GATGATGGG 900
 AAAGCTGGG GAGTGCTCT CTCARAAATG GAGAGATCTA CAGACCAAG ATTCAAGCA 960
 CTCATGTC GACTGTATC AATAGGGT GAGAGATAC CCGCAGATC CCGACGAC 1020
 ATGCGATGA TCTGCTCAT GCTTCCAGG CTGSGATG ACCATATGC CACCTCAC 1080
 AACCAAGAA AACCTGATCC CAAATATAT GAAACACTC CAAGGTCTA TAGGCGAA 1140
 TTCAACTAC CTGACTTCT TAAAGAAAA CCGACACTG AGCAGATGGA GTAGCAGAC 1200
 CAGAGGCTC GAGAGATCT GAGAGAGAT TCTGCTCT TCGAGGAG GGAATTCCT 1260
 AGATGTGCT GTCCCTCCG ACCTAGAGA TCGAGGTGTC CCGACACTC CCGCGCTCT 1320
 GCATTGACA GTTCTCTCC CAGAGAGGA TCGAGGTGTC CCGACACTC TCGAGGTCT 1380
 GAGGATCTG CTTCTCGAC AAGAGGCTCT TGATCCGAT TTCACTACA GCTCTGAGT 1440
 AAGAGACCA GAGAGACAT GTTITCTCT TARAACCTC TCTGTGTTCT TTTTCTGA 1500
 TATAGCTT TCTTTTCTG GAGAGATCT AAGAGATCT TCTGTGTTCT TTTTCTGA 1560
 AGTCTCTTT TGAATAGT TGTCTGTACA TGTCTTACT TTTGTAGA CAGTGTCTC 1620
 TGTTAGTG TATTGATGT AATATATTA AATATCTTA TTATTTAAT CATGTATTG 1680
 TTTCTGAGA GTTGGAAAT TACCATTTA CATTTACAC CTAACTACT TTGTATTTA 1740
 TTTTCTAAA TAAAGCTTT CATGTGA

Protein sequence 2

Gene name: tyrosylprotein sulfotransferase 1

Unigene number: Hs.110903

Protein Accession #: NP_003587

Signal sequence: 1-21

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PCT/US02/29560

Transmembrane domains: none found
Cellular Localization: plasma membrane

	1	11	21	31	41	51	
5	1	11	21	31	41	51	
	NVGLKQKQLL	LACLVISSTV	VFTLQGHAME	CHRIEERSO	PVKLESTRRT	VRKGLDLKAN	60
	ETPAYKIDMP	LPIQGVPR	GTILMRALMD	AIIDPDCGR	TRVTPRIAL	KQMSSESRK	120
	ETRLDERGPT	DEVLGSDR	FLBLIVFGR	EPAPLQND	FLALGLTYL	SRLEPNAVL	180
	LMWEDRQSV	HWKLSVFTT	AGFDANRSD	CLTKGHRLE	DMYQCMQGV	YKQNLHAYR	240
	QLVLEPERNM	RTLLKFLQIP	MNHSVLHRE	NIGKAGGVSL	SKVERSTQV	IKPFWGALS	300
10	1	11	21	31	41	51	
	ENVKGLPDDV	LQDMVLAPM	LAKLQVDPYA	NPNYGKDDP	KIIRNTRKV	KSEPLDPLD	360
	KEKPQTQGV						

DNA sequence 3
Gene name: interleukin 13 receptor, alpha 2
Unigene number: Hs.25954
Probeset Accession #: R52795
Nucleic Acid Accession #: NM_000640
Coding sequence: 94-1236

	1	11	21	31	41	51	
20	1	11	21	31	41	51	
	CGDGTGAGG	CTATTGAG	TGCCATAAC	CTGTCAGAA	GTGTGCGCTG	CGCGGGGAG	60
	AGAGCGAATA	TCAAGTTTT	AAATCTCGA	GAAATGCTT	TGTTTGCTT	GGCTATCGA	120
	TGCTTATATA	CCTTTCTGAT	AAGCAACA	TTTGCGTGA	CTTCATCTT	AGACACCGG	180
	ATAAAGTATA	ACCTCTCTCA	GGATTTCGG	ATATGATG	CGGATCTT	AGCTATCTT	240
25	1	11	21	31	41	51	
	TATTTCGAT	GGCAACCCC	ACTCTCTTG	GATCATTTA	AGGATGCGC	ATGTGATAT	300
	GACTAAAT	ACCGAATAT	TGTTAGTGA	ACATGAGAA	CCATCATTC	TAGATATCTA	360
	CATTACAAG	ATGGGTTGA	TCTTACAAAG	GGCATGAG	CGAGATACA	CACGCTTTA	420
	CTATGCAAT	CGCAATGAT	ATGAGATTT	CAAGTTCTT	GGCGAGAAC	TACTTATCT	480
	ATATCGCGC	AGGATATTC	AGAACTGAA	GTTCAGATA	TGATTTGCT	ATATTACAT	540
30	1	11	21	31	41	51	
	TGGCATATT	TACTCTCTT	TTCGAAACCT	GGCATAGGT	TACTCTTGA	TACCAATTC	600
	AACTGTTTT	ACTGATAGA	GGGCTTGAT	CATGATCAT	ATGTGTTGA	TTATCAACG	660
	GGTATGAGC	AAATATAGG	ATGACGATT	CCCTATTGG	AGGATGAGC	CTATACAGT	720
	TTCGATATT	GTGATCTG	ATCATCTGC	ACAGAGCTA	TGATGATCT	TATTTCACT	780
	TTTCACTGC	AAATATAGT	TAAACCTTG	CGCGAGCTC	ATCTTACTT	TACTCGAGC	840
35	1	11	21	31	41	51	
	AGTTCAATG	AAATTAAGT	GAATGTGAG	ATACCTTGG	GACCTATTC	ACGAGGTTT	900
	TTTGATATG	AAATGAGAT	CAGAGAGAT	GATACACTT	TGTGATGCT	TACGTTGAA	960
	ATADACAT	AGCATGAA	AGCAACAT	GAACCGGAC	AAATATGCT	TGTGTAGA	1020
	AGCAAGTGA	ATATTATTG	CTCAGATGC	GAATTTGGA	GTGATGAG	TGATAACAA	1080
	TGCTGGGAG	GTGAGACCT	ATCGAAGAA	ACTTTGCTAC	GTTTCTGCT	ACCATTTGCT	1140
40	1	11	21	31	41	51	
	TTTCACTTAA	TATTAGTAT	ATTGTATAC	GGTCTGCTT	TGCTATGAC	AAACCATAC	1200
	CCAAATATG	CTGCTGAT	ATCATGAGC	TTTCTATG	ATCATGAGC	AGGATGAGC	1260
	GTATTTGCT	ACAGCTGCT	ATCATGAGC	AAATGTTCA	TATGATCTC	AATAAAGTA	1320
	ATTTTCTGT	CGAAAAAAA	AAAAAANA	AAAAAANA	AAAAAANA	AAAAAANA	1380
	AA						

Protein sequence 3
Gene name: interleukin 13 receptor, alpha 2
Unigene number: Hs.25954
Probeset Accession #: R52795
Protein Accession #: NP_000631
Signal sequence: 1-23
FN3 domain: 155-322
Transmembrane domains: 340-362
Cellular Localization: plasma membrane

	1	11	21	31	41	51	
55	1	11	21	31	41	51	
	MAFVCLAIGC	LYTFLISTFL	GCTSSDSDEI	KNPPQDFSI	VDFGYLYLY	LQWPLSLD	60
	HFPECTVETV	LYTVISGRT	HWRTITAMK	YDGFGLNG	IEKHITLPL	NQCMNREY	120
	SSMAETTTM	SPQGPSTKV	QMDQCVYNN	GYLLCSWPK	IGULLDNYN	LFWVSEGLR	180
60	1	11	21	31	41	51	
	ALQCVDTYKA	DQNGICRFP	YLEASDYDF	YICVMSHHN	KPISRSYPT	QLQNIKPELP	240
	PVYLTFRES	SCEIKLWSI	PLGPIPARCT	DYIEIRED	TLTATVAVN	STYTKATME	300
	TROLGVFRS	KVITCSGSD	WESNDRQC	WESDLAKT	LAKPLPFG	ILLILVIFVTG	360
	LLLRKNTVP	KHIEPFDZ					

DNA sequence 4
Gene name: chemokine (C-X3-C) receptor 1
Unigene number: Hs.78913
Probeset Accession #: U20350
Nucleic Acid Accession #: NM_001337
Coding sequence: 46-1113

	1	11	21	31	41	51	
70	1	11	21	31	41	51	
	GGGCGAGTC	CAGATTCCT	TTGAGTCCA	CGCCAGGCT	TCACCATGA	TGATTCCTT	60
	GAATCAGTGA	CAGAAACCT	TGAGTACAT	GATTTGCTG	AGGCTCTTA	TATGSGGAC	120
75	1	11	21	31	41	51	
	ATGCTGGCT	CTGCTGCTC	GTTCCTGTC	ATATCTACT	CGTCTACTT	TGCAATGAC	180
	CTGTGGGAA	ATTGTTGAT	AGTTCTTGC	CTACCAACA	GCAAGAGGC	CAAGATGTC	240
	ACGACATTT	ACTCTTGAA	AGGCGCTTG	TCTGATCTG	TGTTTATAG	CACTTTGCC	300
	TTCTGAGCTC	ACTATTGAT	AAATGANAAG	GGGCTCCACA	ATGCTATG	GAATTTCACT	360
	ACGCTGCTC	CTCTGATG	CTTTTGA	AGATGATCT	TCTATGCT	CGATGCTT	420
80	1	11	21	31	41	51	
	GATAGTACC	TGGCATCTC	CTGCGTCCG	AACCTCATGA	ACAAACGGAC	GTGCGAGCT	480
	GGGCTCACCA	TGAGCTAGG	GGTCTGCGCA	CGACCATTT	TGATGCGAGC	ACCCAGATC	540
	ATGTTCAACA	ACGCAAGAA	AAATGATGCT	CTTGATGACT	ACCCGAGCT	CCTCTGAGAA	600
	ATGCTCCGCG	ATGCTGCGA	TGTGGAAGA	AAATCTCTG	GCTCTGACT	CCCTCTCTC	660
	ATTATGACT	ATTCTACTT	CGATATCTC	CGAGGCTGT	TTTCTGCA	GAGCCAGAG	720

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PCT/US02/29560

5
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AAGCCCAAG CATTAAACT GATCCTCTCG GTGTCATCG TGTTTTCTCT CTCTGGACA 780
CCCTADACD TTGATGATT CTGGAGAGC GTTAGCTCT ATGACTCTCT TCCAGTCTT 840
GACATAGAGA AGGATCTGAG GTGCGCTCT AGACCTCTCT ATTAGCTCT 900
TCTCTCTGTA ATCCCTCTAT CTATGCAATT GCTGGGAGCA AGTTCAGAGT ATACTCTTAC 960
GACGCGTATG GGAATAGCCT GCGCTCTCG TGTGGGCGCT CATCTCAAGT TGATTCTCTC 1020
TACTCGAAT CACAAAGAGG CAGCATGAGA AGTCTCTTGA GCGACAAATT TACTTACCC 1080
ACGAGTATG GAGATGCAAT GTCTCTTCTC TGGAGGGAAT CCGAAGGCT TGTCTTACA 1140
GNGAACCTCG AGTCTCGAA CCGATGCTCG ACTAGTAGG AGGATTTTGT TGTATTCTC 1200
TTACAGGCA AATATGATGG ACCCAATGCA CACAARACA CCTTAGAGTG TTGTGAGAA 1260
TTTGCTCTCA AATTGTGAGA ATGACCAAAAT TGAACCTTT GAAGCAAAA GAGTAGACAT 1320
TTCTCTTACT ATGATGAGD FFSCDMECT TTGTCTTGA GATCAAAA ATTCACATA 1380
GACTATTTTA GTTAAATGAG GGTGTGATAT ATTTCTTATA TTGTGACACA AGCAAAAGG 1440
GTGTCGTAGC CCTCAAAGTG AGGGGAACA GGGCTGAGC CAGCTA
  
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Protein sequence 4

Gene name: chemokine (C-X3-C) receptor 1

Unigene number: Hs.78913

Protein Accession #: NP_001328

Signal sequence: 1-44

Pfam domain: 7tm_1 [48-293]

Cellular Localization: plasma membrane

1 11 21 31 41 51
 MDQFFSEVTE NFEVDLLAEI CTIGDIWVFG VFLGLIFTVS FAIGLWGL LVYFALTNSK 60
 KFKSVTDIYL LMLALSLLFL VATLGFWTHY LNEKGGLNHA MCKFTTAFVF IGFPGSIFPI 120
 TVISIDIRYLA VLAAHNSBN RTVGGVTHIS LGVVAAILLV AAPQPMFTQG KENECLGDYF 180
 EYLQIWEFVL RVNETHFLQF LMLLLCHMYC YFLIQTDLFS CQNKIKATAT KULILWVVF 240
 FLFTYDYMV IFLTALGLD FFLSCDMECT TTGTCTTGA GATCAAAA ATTCACATA 300
 KRYLHLYGK CLAVLCURSV HYDFSSESGS RSRAGSVLSS MFTYHSDGD ALLLL

DNA sequence 5

Gene name: cannabinoid receptor 1 (brain)

Unigene number: Hs.75110

ProbeSet Accession #: 412985

Nucleic Acid Accession #: NM_001840

Coding sequence: 92-1510

1 11 21 31 41 51
 TGGCTTATTT TTTTTTCCCT CACTTAGGA TTGCCCCCTG TGGGTCACTT TCTCATCAT 60
 TTGAGGACCA CCTATACAA AGACTTAGGG TATGAGTGG ATCTTAGATG GCGTTCGAGA 120
 TACTACATCT CCGATACCA CTCTGACACT CTCTGATGAG GCTCATCAATG CAGTCTGATA 180
 CAGAGCACTC AAGGCTGACA TGGCATCCAA ATTAGGTATC TTCCACAGAA AATTCCCTTT 240
 AACTCTCTTT AAGGGAAGTC CACTTCAGAA GAGATGACTC GCGGGAGACA ACCCCAGACT 300
 AACCCACAGA GACCAAGTGA ACCTTACAGA ATTTTACAA GAGTCTCTCT GGTCTCTCAA 360
 CSGAGATGAG GAGACATCC AGTGTGGGGA GAACTCTGVS GACATAGATG GTTCTCATGT 420
 CCTGAACCCC AGCCAGCAGC TGGGCATTCG ATCTCTGTCC CTCACGTGG GCACTCTCAC 480
 GGTCTGGGAG AACCTCTGVS TGCTGTGGGT CATCTCCAC TCCCGAGCC TCGCTCTGAG 540
 GCGTCTCTAC CACTCATATG GCGACCTGGC GGTGGCAGAC CTCTGTGGGA GTGTCTATTT 600
 TGTCTACAGC TTCTATACCT TCGCATGGTT CCGACCGAAA GATGACCGCA AGGTGTCTCT 660
 GTTCAACTCG GGTGGGGTCA GCGCTCTCTT CACTGTCTCC GTGGCGAGCC TGTTCTCTAC 720
 AGCATATGAC AAGTACATAT CATTATACAG CGCCCTGGCC TATAGAGGA TTGTCAACAG 780
 CGCCAGAGCC GTGTGTGGCT TTGCTCTGAT TGGACACATA GCACTTTGTA TGCGCTGTCT 840
 GCGTCTCTG GCTGTGAAT CCGAGAAACT GCAATCTGTT TGCTGACATA TTTCCTCAGA 900
 CATTGATGGA ACCTACCTGA GTCTCTGATG GGGGTCTCAC AGCTACCTGT TCTCTCTCAT 960
 CGTGTATGCG TACATGTATA TTCTCTGGAA GGTCTCAGC CAAGCGCTCC GATGATTTCA 1020
 GGTGTGACCC CAGAGAGACA TCATCATCCA CAQCTCTGAG GATGGGAAGG TACAGGTGAC 1080
 CGGCGCAGC CAGACCGCCA TGGCATATMG GTTACCAAG ACCTCTGTCT TGATCTGGGT 1140
 GGTGTGTATC ATCTGCTGAG GCGCTCTCTT TCGACATG TGATATGATG TCTTGTGGGA 1200
 GATGAACAGC CTCATTAGA GGTGTTTTGC ATTCCTCAGT ATGCTCTGCC TGCTGAACCT 1260
 CACCGTGAAC CCGATCATCT ATGCTCTGAG GAGTAGAGAC CTGCGACAGC CTTTCTGGAG 1320
 CATGTTTCCC TTTTGTGAAG GCACTCTGCA GCTCTTGAT AGACAGATGG GGGATCTGGA 1380
 CTGCTGACG AAGACGGA ACAAATGAG CAGTGTCC CAGGCCAGC AAGCTCTCAT 1440
 CAGAGACACA GTCAAGATTG CCAGAGTAA C CATCTCTGTG TCCACAGACA GGTCTGCGGA 1500
 GGCCTCTGCA GCGTCAATGC TGGTGTGGCA CACAGAAAA GAATTTTTTT TTTTATCTCT 1560
 AAAATCTAGA AGAGTCTTAT GTCCTCTTGT TTATTTTITT TTAACCTTAC CATCTCTAG 1620
 GAAAGGCTGA TTCTCTTCTT GATGCTCTAT CAGTTTCTTA ATGCTCTCT AGGTGAGGA 1680
 CTCAACTCC ATTCCTCAGG GGTTTACAGT GAAGCAAGCC TGTGTTTAA GTGACTGAC 1740
 GATCTCTCAA AGTCTCAATG AATATAGAG GAAACCTTTG GCTACACAT TGAAGTCTTA 1800
 AGAACCCATG GAAATATGCC ATCAATATGA TATGCTCTT GTAGACACAT CTTTCACTAT 1860
 AATTTGATAT TATGATGAG AGATCTCTAT TTTTACATCT TTTTACATCT TTTTACATCT 1920
 GAGCATATTT GTAAATATGA TTATGCTCTG TGAGATGTGT ATACAGTGT TATGCTCTAT 1980
 AATATTTCCT TAGTTCAGCC AAATCGAAG GTAGACTTTT ATGAGAACCA TGAGACAACT 2040
 GTGAGTAAGT GTCAATGTGT GCACTTTTTT TCTATATAT TGGCCATGAT ATAACCTTAG 2100
 AATAAAGCT TAAATTTCTT TCCAAAAA AAAA

Protein sequence 5

Gene name: cannabinoid receptor 1 (brain)

Unigene number: Hs.75110

Protein Accession #: NP_001831

Signal sequence: none found

Pfam domain: 7tm_1 [133-397]

Transmembrane domains: 121-143, 156-178, 195-217, 237-259, 276-298, 344-366, 378-400

Cellular Localization: plasma membrane

1 11 21 31 41 51

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PCT/US02/29560

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1  MSKILGLAD  TFRITITDIL  LTVGSHDIOY  ERIKEDWASK  LOYFFQRFPL  TSPRGSPFOR  60
2  HTAGBNPLG  VDAQVQVITE  ENGHGHCDS  WPMUICITW  LPSQXALIA  120
3  VLSL/LGTTT  VLEBLL/LCN  ILMSRSLRCR  PSYHIGSLA  WDLLOSVPF  VYSPDIFPV  180
4  IRKSDSRUFL  FKLGQVTSF  TASVGSFLT  AIDRYSIHR  PLAYKRIVTR  PKAVVAFCLN  240
5  KTAIVIAVL  PLGHCNCKL  QSVKSDIFPH  IDKTYLPMI  GVSIVLLFI  VIAYMILWK  300
6  AHSBVMHQ  RGTGSI  LHI  TSDCKQVIT  RPDQBMDIR  LAKTLLILW  VLICKWPL  360
7  AMYIVDFKC  MKLLKTVFA  PCSGLCLMS  TWPIITAIR  SKDLRIAPRS  MFPSCBGTQ  420
8  PLKNSGQSD  CLKHANNAA  SVHRAANSCI  KSTVITAKVT  MSVSTDSAR  AL  480

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DNA sequence 6

gene name: endothelin receptor type B

Unigene number: Hs.82002

Probeset Accession #: D13168

Nucleic Acid Accession #: NM_000115

Coding sequence: 238-1556

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1      11      21      31      41      51
20  GAGCATTCC  GTTGGGGGAC  TCTGGCGAGC  CCGAGCGAGC  TGGATCTCTA  GAGCATTCC  60
3  AGTTAGTCT  TTTGGTGGTT  GGAACCCCTT  OCCGAGCCAG  TGTGTGGGAG  GCTCCCTCAA  120
4  AGCATCAAC  CAGTGGCTGA  ACACTGGGAA  GGAACATGTA  CTTGGAGTCT  GGCACATCTA  180
5  AACTTGGCTC  TGAAACTGGG  GAGCGGGCAC  CGAGCGCCCT  CTGGAGCAGG  TAGCAGCAIG  240
6  GAGCGCCCTC  CAGTCTGTGG  GAGACGGGCC  CTGTTTGGCC  TGTTTCTCTG  CTGGCGCCGG  300
7  CTGGGATCT  GGGAGAGAAA  GAGAGCTCTC  CCGCTGTGCA  GGGGACATCC  GCTTTTCCA  360
8  ACCGACAGAA  TAAAGACGCC  ACCCACTAAG  AACTTATGSC  CAAAGGTTTC  CAGCGCCAGT  420
9  CTGGCGCGTT  GATGGGCACC  TCGGAGAGTG  CCTAAAGAG  ACAAGACGSC  AGATCTCCG  480
10 CAGACACCA  TCTCCCTCTC  CCGCTGCCAA  GAGCCCATCT  AGATCAAGGA  GACTCTCAAA  540
11 TACATCAAC  GZTGTGCTC  TTGTGTCTGS  GACATCATCA  GACACATCA  GACATCAAA  600
12 CTCTCAAGAA  TTATCTAAG  GAAACATGTC  ATCCGAAACG  GTCCCATAT  CTGTAGTCCG  660
13 ACTTGGCTCT  TGGGAGACCT  GCTCGACACT  GTCACTACAA  TCCCTATCAA  TGCTACAAG  720
14 CTCTCTCGAG  AGATCTGGCC  ATTGTGAGCT  AGATGTGTA  CAGCTGTGSC  TTTCATACAG  780
15 AAAGCTCCG  TGGAGATTA  CTCTGAGAT  CTAATGCTCT  AGTGGTCTTG  CAGTATGTA  840
16 CTTGTGCTT  CTGGAGATAG  AATTAAAGCA  GTTGGZTTTC  CAAAGTGAC  AGCATAGAA  900
17 ATTGTTTGA  TTTGGTGAGT  CTCGTGGT  CTGGCTGTCC  CTGAAGCAT  AGGTTTGTAT  960
18 ATAAATACA  TGGACTACAA  AGAAGATTAT  CTGGGATCT  GCTTGTCTCA  TCCCGTTCCG  1020
19 AGACAGCTCT  TGTCTCGATT  TTAAGAACCA  CCAAAAGATT  GGTGGTCTTG  CAGTTCTACT  1080
20 TCTCTCTG  TGTCTCTGAT  TTTATACAT  TTTATACAT  TATGACTCT  TGAAGATTT  1140
21 AGAAGAAAA  GTGGCATGCA  GATTCCTTTA  ATGATCACC  TAAAGCAGG  AGCGGAGTG  1200
22 GCGAAACG  TCTTTTGGT  GGTCTTGTCT  TTTGCCCTCT  GCTGGCTTCC  CCTTCACTCT  1260
23 AGCGGATTC  TGAAGCTCAC  TCTTTATAT  CMAATGATC  CMAATAGAT  TGAATCTAT  1320
24 AGCTTCTCT  TGTCTCTCAT  AGCTAGATG  CATACATG  CTCTACGAA  TCTCTCAT  1380
25 AACCCATGT  CTCTGTATT  GGTGACGAA  AGATTCAAAA  ACTGCTTTAA  GTCATGCTTA  1440
26 TGTCTGTGT  GCGATCAT  TGAAGAAAA  CAGTCTTGG  AGGAAGAGCA  GTGCTGCTTA  1500
27 AAGTCAAG  CTAATGATCA  CGATATGAC  AACTTCGTT  CAGTATATTA  ATACAGCTCA  1560
28 TCTTCAAG  AGACATATC  ACGTATATC  ATTCTCTTA  TATGAGCCG  AATGACATTA  1620
29 AACCAATGA  AACATTGCC  AAACCAAC  AAAAACTAT  GTATTGAC  AGCACATAT  1680
30 TAAATATTA  AGTATATTA  TTTTACAT  CAGACATCA  TATGACATT  TATGAGCT  1740
31 TTTGCGAT  GAAGAAGAA  CAGTGGAT  TAAAGAGCC  TGTCTGTA  AGCTATAT  1800
32 TTTTACAT  TACACATCA  AATACATCT  TAAACATCT  CAGATATCT  AGCACATCT  1860
33 TAGCTTAA  AATGACCTA  CTGGAATTT  CTATCTTTC  TAAAGAGG  TTTATTTTA  1920
34 ATCAATGG  ACTCTGAT  AAAGGAGAA  TATGCTACTG  TAAACAGAA  CTTTAAATG  1980
35 AGCTTAAT  TACTCAATT  AAAATTTTA  ATCTCTTTA  AACACATT  CAATTAAT  2040
36 TATCACTA  TATCAATG  GTATATGAT  CCAATGAG  GAGCATTTA  GTTGTTCAT  2100
37 TTTTGGCA  CTGAGATTA  TTAAGATCT  AGGAGGAT  AACAGACA  CCAAGCTCT  2160
38 TTTTGAAT  CATTACAT  TCACTAGAG  CCGCAACCTC  AGCATCTCG  AATATATAC  2220
39 CAAATGTA  GAACAGCA  GATGTATCA  GACTGACCA  TGTCCAGCT  GATTTTAA  2280
40 TATAATCT  TAAAGAGAA  AATTATACA  TCTTTTACT  TCAATTAAG  TCAACCTCA  2340
41 CAAAGAGAA  TGAATATTA  CAGACACTAT  CTTTGTGAT  TTTTGTGAT  CTCTCTCA  2400
42 CTACCTGT  GAGACAAAT  CTATCTACA  TTTTTCAG  ATATATAAA  TCTCTTTT  2460
43 TCACTATGT  AGCTTAACT  CTGTTGGT  TGTGACTG  TAAATACTA  CTAATACATA  2520
44 CTGATGAT  ATGATTAAT  GAGGCGAG  CBTGTCTCA  TACTTTTAC  ATGAGAGAT  2580
45 GCTGTGAC  TCTATATTA  GCTGTGAT  AGTGTGAT  TTTTGTGAT  CTCTCTCA  2640
46 GCGAGTAGCA  CCTCTCTCA  CCTATCTGT  GGTATAAATG  GTTCTAGCA  TATGATATAT  2700
47 GCTATGTTA  AATATATTT  TCTTAAATC  ATACAGTTA  GTACATTTA  CAGCTATCT  2760
48 TAAAGCTAT  TACTATATTT  TGTATATTT  TGTATATAT  CCAATAGAGA  AGTTTCTGT  2820
49 AGATGTTGT  TGTATATTT  CTAGAGGCA  AGCTCTTAT  TGAAGACTAT  AGAACCTCT  2880
50 AGCTTTGTC  GTTCTGCT  AATTTTTATA  TCTCTTACG  AAAGTCCCT  AGATACCTT  2940
51 GGGATGAGT  GTGTGTGAA  GTATGTACA  GNGAAACGG  AGAGAGGAG  AATGAGGAG  3000
52 GGGTTGAG  AAAACCAAG  GAGACATCT  CACTCTAG  CTAACGTC  GTCATGTCT  3060
53 CTCACTCA  ATGCAAGG  TCTGATTTT  GTTCTGCA  AACAGCTG  AATGTTCT  3120
54 GATTCATCT  CCAATTAAT  TGGGCKAG  AGCTTTTAC  GGTCTTTAA  AATGCTCA  3180
55 ATTTTACT  TTTTTTCT  TTAATAGCT  GGCACATCT  TTTGAAATA  GCTAGTAACT  3240
56 TTTTTTCT  TCAATATGA  ATGTGATGT  ACAGTAAC  AAACCCAG  AATGTGCA  3300
57 GAGAGAGGA  CCAATATTA  TTAATTACA  CACATATGT  ATTTCTTTA  TAAATCACC  3360
58 AAACCTCT  TCTTATTT  CACTGACCT  ACTTTTTCG  AGCTCTTA  TCAATAGAT  3420
59 CATTTTAC  TCTCAATTT  AAATTAAT  TGAATACTA  ATATTTCAT  AGATTTTAA  3480
60 TATATTAAT  TCAATTTAA  ATTTAGAT  ATTTTTATA  CAGTGTACTG  AATTTTACA  3540
61 TCTGATAC  CTTCCTTCT  CAGTCTGCT  ATCATCTCT  CTAATATCT  TCAATATCT  3600
62 TAAATCTCA  CAGATAGAG  ATATCTGAT  TATTTATTA  AAATTTACA  TGTGCTCT  3660
63 TTAAGAAAA  AGTTTGTAT  CAAATCTTA  ACATCTGAT  AGTAAGAA  CAATTAAT  3720
64 TCTTTACAT  ACTCAAAAC  AGATAGAAA  AAGTCTAT  GCTTCACT  CAACATCT  3780
65 TCTTATAT  TAAAGACTT  AATATACCA  CAGCAAAAT  TATTTTAT  ATGATGTTA  3840
66 CACTCAAA  GATTAATTA  AGATTTCT  CATTCTCT  CCTATTATC  CACTGATAT  3900
67 GTGATGAT  GTTCAAAAC  CTTTATAT  TATGATCTA  CATATGCCA  AAGSATAA  3960

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5 GTTTATAGCA AACATGGGT ATGCTCTAOC TAACITTTATA AAGGTGTAT ATACAACATG 4020
AAAAAATTAT ATATCTGGGA GGATTTTTTG GTTGCTCTAA CTGCTCTATG TTAGCATTT 4080
TTTATATGT AGCAAAACCT AACAAAAAT TAAAGTTTT TAACACTACT CTATTTTTC 4140
ACTGTACAGA CACTTAATCA TAAATACTA ATTCATGTT TAAAGAANT ATAAATGGA 4200
CAATGGGACA TTTATATGT TAAATACATA ATATCAAGC AGATATGAG TTTATCAAT 4260
AAATGCCAC ATTCTGTCT TCTGGG

Protein sequence 6
Gene name: endothelin receptor type B
Unigene number: Hs.42002
Protein Accession #: NP_000106
Signal sequence: 1-27
Pfam domain: 7cm1 [118-386]
Transmembrane domain: 100-122, 138-160, 173-195, 221-243, 277-299, 325-347, 358-380
Cellular Localization: plasma membrane

11 21 31 41 51
1 | | | | |
NQPPFSLGCR ALVALVLACG LSRIMGERR PFPORATFLA GTASIMPTPT KILWKGSGNA 60
SLARSAPAR VPKGDRTAGS PRITISPPC GQPIRIKFT KYINTVSCIL VFLDILGNS 120
20 TLRIIYKHK CHRGPHILI ASLALGDLHL IVIDIPIINV KILAEWVFG ARMCKIVPFI 180
QKASVGTIVL SLSCALSDRY KAVASWSRIK GIGVPMWAT KIVLIWVSV VLAUFRAGF 240
DIITWYKGS YLRICLLIPI OKTAPHFIE TAKDMLFSF YFCLPLAITA PFTITATGEM 300
LKRKSGMOIA LNDHLQKSR VAKTVPCLVL VDALCQPLHL LKRLILALY KQWDEKGL 360
25 LSLPLLYDIY GINMASLNSC INPIALVLVS KRFKCNFKSC LQWQGFSE KQSLKQSGC 420
LKFKAHDGY INFPSNKYS SS

DNA sequence 7
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
ProbeSet Accession #: Hs4926
Nucleic Acid Accession #: AF019686
Coding sequence: 79-1224

11 21 31 41 51
1 | | | | |
35 AAAAACCTGA AGCATAGA ACTACACATG AGGAATATGT CATTTAGCAC TTTCACTTT 60
TGATCTCCAC AGAGACATAT GAGAGATCAT ACCATAACAA TGAGAGACAC TTCATGTAGC 120
AGCTGGCTTT ACTCTGCCA CAGRATGGGC TTATTAACCA ATCATAGOGA CCACACCCCA 180
CAAACTCTCT CAGACACACC AAGAGTACTT ACTGTOTCCA TGGATGAAAA ATTGTATCT 240
40 GCTCTATGA CGATCTTATG TCTACTGTGG TACTCATGTG GACTGTGTGG GACATATAC 300
GCCCTCTATG TATTCTGGGG TATTCACTCT AAAGAAATCT CACTCTAAT TTTACTACT 360
AACGTAGCCA TTGCAGACCT CACTACTCAT TCTGTCTCC CTTCGGNAT CATGTATCAT 420
TTATACCAAA AACTAGTACC ACTAGGTGIG ATTCTGIGCA AGGTTGTGGG AACACTGTT 480
TATATAAGA TGTACATGAG CATTAATTTG CTGAGATCCA TCAGTTTGGG TCGCTAGATA 540
45 AAAATTAATC GGTCTATACA GCACGCGAG CCAATACACA CCACACAGAG TACTTATGTC 600
TGTGTATAG TATGATGGT TGTCTGTGGT GGATTTCTAA CATAGATTAT TTTACACTT 660
AGAAAGGAG GGCATATTC CACATGTGT TTCCATTACA GAGATAGCA TAAAGCAAAA 720
TTATACCAAA TTTTAACTT CATCTGTGTG GTAAZGTGCT GGCATATTTT TTTACTAATA 780
ATCTCTTACT ATTTACTAT TGGTACAGAT CATATTGAGC TTTCATAAAG GAGGTCAAAA 840
50 TTTCTTAAT CTGGTAAATA TGCCATACA GCTCGTAAT CTTTATGCT ACTATCAT 900
TTTACTATAT GTTTGTTC CTATCATGCC TTTCAGTTCA TCTCAATTC TTCAAGCTA 960
AATATATCAT CTCTCATCT GAAGAAATTT GTTCACAAAA CCAATGAGAT CATGCTGTT 1020
CTCTCATCT TCAATGTTG CTGAGTCCA GTCAGTATT TCTGAGTGC CATAGACTT 1080
CGCAAAATAA TGTGCCAAT CTCTTTTGA GANTTTCAAG GTGACCAAG TGGAGTGA 1140
55 AGCACTTCAG AATTAAAC AGGATACTCC CTGCAATGA CATCTGTGGC AGTGAATAA 1200
CTCATGTTT GTAAAGTAG TCGAGTAAA CATACTAAAA TGAATATAT ATATGACGCT 1260
CTAATCTCT TCGATAGA AATATAGG CAACAAGTT CTACACTTA CAAAGCTCAG 1320
ATCTCAAGC TCTGCTGTA TTTGTGATAT TCACTTCT TACTGTAAA CACT

Protein sequence 7
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
Protein Accession #: AAD50531
Signal sequence: none found
Pfam domain: 7cm2 [71-327]
Transmembrane domain: 90-112, 126-148, 171-193, 217-239, 263-285
Cellular Localization: plasma membrane

11 21 31 41 51
1 | | | | |
70 MRSHITMTT TSVSWPYSY HRMFITNS POPONFSAT PHTTCEDE KLSGLVLT 60
YSVIFVGLV GMLIALVFL GHRKRNISQ IYLLNVAID LLLPLCLR INWHIKW 120
TGLVLCRVV GLTFPMNVI SILLGFISL DYKINKSI QKRAITTEK SIYVCIVWM 180
VALGFLNVI LITLKEGNS STMCNFRUK HWAGGAEIN FILVPMWLI FLILISLYK 240
IGNLLIKR HRSRQWCK VATTARNSI VLIITFCV PHAPFTIY SGLNWSKY 300
75 WETVHKINE EMIALVSPS CLDFVWFIL SMIRKINQ LLLWRPQGF SRSSTSYK 360
PQYSLHDSV AVIKQSSNS T

DNA sequence 8
Gene name: exostoses (multiple)-like 2
Unigene number: Hs.61152
Nucleic Acid Accession #: NM_001439
Coding sequence: 288-1280

11 21 31 41 51
1 | | | | |
80 CACTTTGCGG CGGCACITT TTCCAGGTG TTAATCCAGC TAATGAGAGA GATAGATGC 60

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5
 10
 15
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 25
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 35
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 45

ACGCTACTTG GTTTAGAAJA AAAACAAAAA ATGAGCAAAAC GAGAGCGCCC TTCCCTTTTA 120
 TGATAACTAA GCTGCGAGGA AATTAATCGG CGCGCCCTAC TGCATCTCAG TGCATCTCAG 180
 AAACACACGA GAATATCTCT TGAATTTATCT TAATGTGTGAG AAGTGAGTCT GCTTCTCTGA 240
 ATTAATCGAG CTAAAGACAG ATTTTITPAA AATTAJAATCT CAAGACAAAG AGGTGTGTCC 300
 ACATCTGCGA ACTCTCGGG AGAATTAAGG GGAATGAGT GCTTCAATTA TCTTTGTGTG 360
 TGACCTCTGT ATTATPACTG GTAGCTGTGTG CTTTGACTGC CTACTCTCC AGTGTTPAAG 420
 AGACACAT GCTCATGTGT GGTAGGAGAA TAAATCCCA GCGCAAGTCC ACCATGAGT 480
 CTTTACTCT CATTAAGCAG ACCTACACCA GAACGAGTCT CTATTTGAA TCTTTAATC 540
 ATTATCAGG TGTAACAAAT CTCACAAAG TGATTGTGT ATGGAACAT ATTGGAGGA 600
 AGGCACAGA TGAATATGTG AATTTCTCAG GCGCCCAACC TATCCCTGTG ATCTTCAAG 660
 AACGACAGC AAACAGATG ABAATTCGAC TCCAGTCTCT TCCGTACTGT GAACCATATG 720
 CAGTGTAT GTTATGAGT GATCACTCTA TCGAGTCTCC AGACTCTGT TTGCTCTCT 780
 CAGTTTGCCA CCAATTTCTT GATCAAAATG TAGGATTTGT TCGTAGAAG CAGTCTCTA 840
 CTTCTCAGG TATCTACAGT TATGGAAGTT TGTAAATCCA AGCAGCGGG TCGGAATGT 900
 GTACACAGTA CTCTATGTG CTGATCTGAG CACTATCTCT CATAGCAAA TACTTGTAT 960
 TATTTCAAG GCACTCTCA GCTGTCTAG CTGTATAGA TGATATCTGA AACGTGATG 1020
 ATATTGCCAT GAATTTTATC ATTCGCAAG ATATGTGCGA CACTTCAGG ATATTGTGA 1080
 AGCCTGTAAA CATGACAT TGTGAAAAG AAACCAACAG TGCTATTCTT GGAATGTGGC 1140
 ATCGACCTGA CCACTCTCTG CACAGGTCTT ATGTATATA TACGCTGTI AATATCTATG 1200
 ATATACATA CTGATATAC TCGAAGATA TGAATTCGA TTGTGTTCT CAGATATCCA 1260
 ACTACAAAG AAAATATAA AGATATAACA AACAAAMCA ACCCTGAANA CTGCTTCCA 1320
 TTTGAGTACG TTCTCATCGT TATGTATTTT TTTAAGCAAC ATCATGATAT TTATCTACTC 1380
 CAGAGTCTC TACATATAGA AAAAAGTGG AGTGTCTCTA GGAATATAAA TTCACTATAC 1440
 TTTTGAAGC CAGACATGTT GTCTATATCA ATGATGCTCT TTTATAGAGA GTTTTCACTC 1500
 AGGATATAA CTCTCTGTC AGTGAATTTA TTGTTTACAT CCTGAGACGT TTCTACAGTT 1560
 TCTTGACTC CTGSCATTTC CTTTAAGGAC CTATAGCAG CTGTTCTTAG GATCGAAGAC 1620
 TCAAGAGAGT CATTTCTCTT CTTTTCATCT AAGGTCCAGT TGTTTAAAT TGAACATCTGA 1680
 AAGCTCTCT TACGAAAGCT GTTGTATGTG GTTAAAGCCA TGTAAAGAGA GAATATCTC 1740
 AGTCACTAT GAGAGGAA ATTTGCACT GCGATGCTT TCTGTGTCC CTTGCTGACC 1800
 AGCTCTCTCA GAGCAGCTAG AGTGCAGCAT GTTITTCAT TACCATCCA TCGTITTTAT 1860
 TTTTAAAT CTTTTGTGAC TGAGTGAATC AATTTAGTA GCTGAGAAC GCTAGTGTGT 1920
 TGCTTGATA TTTGTGACA TTTACTGTG GATCACTATC GATATATCT CTGATTTCT 1980
 TACACCCAC TTATGTCAG CAGAGTAA ATGTGTACT AGATTCGAT AGTCACTAT 2040
 GTCATGAAT CTGACCTTGA GAGTGTACAT TAATTTCTAT ATTTTACATA ATGTATGTGT 2100
 TGTTTAAGA ATGTATATAA AACCTGAAA AATGAGTAA GAACCTGCCA AGTTPAANA 2160
 CCGTGTATC AAAAGTCTT TATGTGTAGA GCACTGTTTA TCTTCTGAT ACTAANAAT 2220
 TATATACGA AGCTGACCA ACTTGAABA AAGAGTCCA GAACTATCT 2280
 ATATATGA GAATTTCACT ACATCAAGG AGGAGAAAT AAGAACCCAG TCATATCAGA 2340
 GGAATCTAT AGGATCTGAC ATCATATCAT TCTTAAAGTT GCTACTCTC TGTATGTGA 2400
 ATTAGGCTC GTGTTGACC CATGTCTGT GTTTATCTCT TGTTCACAC TAAAGCAGG 2460
 AATCTTATC TATGCTTCACT TATGCTCTC CCGTCTTCT GTATATCT TCTTATCT 2520
 CTTCTCTCT TCTCTCTTA TAAATCTCA TGAATCTCC AAATATGCA ACCGTGTGCA 2580
 ATATTAAT AATCAAGCT AGGTTCCTCA TAATCAAGTC TTGTGCAAT TATGTCOCA 2640
 TATATGZT TTTTITTTAC ATTAAGAGT ATATGTCTCT TAATGCACT AGATGTAAA 2700
 AAACAAAC AAGAACTA AGATCTTAC TAAATATGA TATATGATC TATCTTTT 2760
 GTCAATAT GTATGACTT TTTGTCTCT TATATCTCT CTAGACATA AATAAAGAA 2820
 ACTTTGCCA TCC

Protein sequence 8

Gene name: exo70osess (multiple)-like 2

Unigene number: Rs.61152

Protein Accession #: NP_001430

Signal sequence: 1-38

Transmembrane domain: none found

Cellular Localization: plasma membrane

1 11 21 31 41 51
 HROCHICKLR GRNPQIRVLR LSLPVLVLA LVAGALTALL SVSEDKHML LRRISGSGK 60
 STMSPTLIM QYTNRLDLL KLANVQYAF NLRKIVVWV NIGRKAPDEL NWSLGRMP 120
 VIFKQZANR MNRLQVFFE LSTNALVMD DDLTISTPDL VFAPSVQQF PQIVGVFFR 180
 KRVTSSGIY SYGFETQAP QSDNQDYSV VLIAGSFNS KYLELFRQRP AAVALHIDT 240
 QNCIDIASPI IIAHNSDGT QYGVFVWME HLEKSTNGSY SGMWRARAR LDRSTCHML 300
 VNIVSPLA YKINISQFQ FFYANYKRT

DNA sequence 9

Gene name: Homo sapiens growth differentiation factor 1 (GDF1)

Unigene number: Rs.92614

Probeset Accession #: AL120193

Nucleic Acid Accession #: NM_021267

Coding sequence: 73-1125

70
 75
 80

1 11 21 31 41 51
 ACGCGGGGC CGCGGCTCCG TCGCTACCG CGCGCGGGCG CAGCGGACGC GCGCGCGGG 60
 CGAGCGGGCG GTATCGCGCG GCGCGCGGCC CGCGCGGGCG CGAGCGGCC CGAGCGCAT 120
 CGAGCTACG CCGACATCTG GCGCGCGCGC TCGCGCGCGC CCGTGGGCGT GCGCGCGCG 180
 TCGACAGCT CGCGCGGGGG GCGCGCGCGT CGCGCGCTGG CTGACGACGC GCGCGCGCG 240
 CGCGCGGCG TCGCTGTGCT GCGCTCTGCG CGCGTGGGCT GAGCGCGGCT CGCGCTCGCG 300
 CGCACTGCG CCGCTTTTGG CGCGCTGGGG AAGCGGTGCT GCGCTGCGCG CAGAGATGC 360
 CGCAAGTGC CGCGCGCGG TGTAAAGTCT CCGCTTCTAC TCGCGCGCGT GCGCGCGCG 420
 GCTACCTGCG TGTTTGGACG CGACTACCGC TCTTCCATG ACCCGACATC TGTCTCTAC 480
 GACTCGACGC CGCGCATGCG AGTGGCAAGG GACATTCGAG CCGCTTACT CCGCGCGCG 540
 AGCTCTTATG CGCACTCAT CTACGCTACG CTATCATGAT ACACCTGGCG CGAGCATGC 600
 GTGTGCTAC GTCACGCGC GTTAAAGTCT CCGCTTCTAC TCGTCTGCG CTGCGCGCG 660
 CGGTACACCA ATGTGGAGCT CTTGTGCTCT TCTTCCACG ATATCAAGTA CTGCGACTT 720

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GAGTTTACCA AGCTACACAT TTACTTCAGG TCCCGCGGGG GCTCTCTACCA TGGCTGTGAT 780
 GCTTCTGGGG GAGCTCTGAG CTGCTCTGAG TTGCGCTTCA GCTGGTCTCTG TCTCCCTCTG 840
 TACGCTGTCC GCTCTAGAGT CTTGTATAGC ACCATTCACAT GAGATCTAGG GACCTGTGCT 900
 GACTGCTGCT TCTATCTCTT CTTCAATGCG CTCTGCTGCT TACTCACCTT TATGAACCTC 960
 5 TACATGTTCG TTATACACTGT GGGCTTTGCA GCGAAAGTGT TCGTACAGGCA GCTCTGAGCG CAGCAAGAGC 1020
 CTGAAGAGAC TTGAGAGATA TGACACACCG AGAGCCACGA GCTCTGAGCG CAGCAAGAGC 1080
 GAGAGAGCAC TGAGAGACTG CTCTGTAGAG GACAGACCTG TCTGAGACCT TCGATCTTCC 1140
 CCGGCTGAGG CCGGCGCCAC CAGCAATAGC CGCGGCAAGC TCGCGCTGCT TGGCGGACCC 1200
 TCCACCGGCT CCAATCTGCT TCTCTTAGGG CCGCGCCACG CTCCCGCTGGG ACCCGGCCCC 1260
 10 CTCACTCTGG TGTCAATTTC GCGCTGAGCG CCGGAGAGCC CTTGCGCTCTG CCGGAGACAC 1320
 GCGCGCGGCT TGAGCGCTGG AGCTCTGAGG CCGCTGAGCG CCGTCTGAGCT CCGGAGAGCG 1380
 CCGCTGAGAG GAGATAGCCA CCGCGGAGAG AAGGTCCCTG GCGGACACAC CTCTCTCTCC 1440
 TCGCTGGGCT GCTGTGCGCC TCGTGTGCCC TGAOCGCGCG CCGGCTGCCC CCGAGGCGAG 1500
 15 CCGCGGCTCT GCTCTAGGCT CTAGAGATCG GCGATAGAGC CCGAGGTGCT CCGAGGCTCG 1560
 GCGCGCTGCT CTGCTGCTGT TCGCGCTGCT TCGAGCGGCG GACACGAGCT GACAGCGAGT 1620
 CTGGCTCGGG GCGAGAGTCC CAGAGGGTCA CCGTGCAGCC GTGCCAGGTG GAGAGAGTGG 1680
 GGGTGCCTGG AAGCATGTGT GCGCAATCTC GCGAGCGGCG TCGCGCCGCG CCGGCTCTGG 1740
 AGCTGTGTCT GCGCGCGGGG CATTGCTCTG AGTGAACAGT GTCTCTTGAG CTGTGTGAGCT 1800
 20 TGGAAACCCG TGAGCGCGCG AGCGCGGCGG GCGTGAAGCT GCGTTTGGG GCGAGCGGCG 1860
 CCGCAACCCC GAGAGCGCGC TGGAGACTTA GCGTGAAGCT AGCGGCGCG CCGAGCGGCG 1920
 GCGAGCCGCG GCGCTGTGCT CTCGCGAGT TGGTGCCTCG CTTGAGCGCG CAGTGTGCGG 1980
 GCGAGCTGCT GCGCGCGGCT TGGGCTCGCA AGCGCTCATG GCGCGCGAGC CTCCGCTCTG 2040
 CCGTGGGCTC AGCGCGCGCG GCGCTGCGCG CTTGAGCGAG CCGTGTGCTG GCGTGTGCTG 2100
 25 TGTGTGTGAG CTTGAGCGCG CCGCTGTGCG ACCGCTTCCG CCGGCGCGCG CCGAGCGGCG 2160
 AAGCGGTGTT GCGCGCGCGG CCGCGCGGCG CTTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220
 TCGCGGAGGT GCGCTGCGAC CCGTGGTCTA TCGCGCGCGG CGGCTTCTCT GCGCACTACT 2280
 GCGAGGTGTA GTGCGCGGCT GCGCTGCGCG TGTGCGGCTG CCGGCGGCGG CCGCGGCTCT 2340
 ACGACGCTGT GCGCTGCGCG GCGTGAAGCG CCGGCGCGCG GAGCTGCTCT GAGCTGCTCT 2400
 30 GCTGTGTCGC CCGCGCGGCT TCGCGCATCT CCGTGTCTCT CTTTGACAGC AGCGAGCAGG 2460
 TGTGTGCTCG CAGATATGAG GACATGTGTC TGGAGAGTGT TGGAGTGGCG TAAOCGCGGG

Protein sequence 9

Gene name: Homo sapiens growth differentiation factor 1 (GDF1)
 Unigene number: Hs.92614

Protein Accession #: NP_067090

Signal sequence: none found

Transmembrane domains: 106-128, 148-169, 184-206, 244-266, 285-307

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 40 MAAGAPGAPG TQPEIPKPSYA QLVORWQSGA LAAARCTDCC GWGLAKRGLA IHAHLAPPEL 60
 LLLALGALWG TALBSAATAR LFRPLAKRCC LQPEDANRPP BSAHFLFLYF GWSVSYAYLL 120
 PGTDFYFFPD PWSVFVDWTF GMAVPEIDIA AYLXGFSYTG HSIYATLWLD THRGSVWML 180
 45 LHRVYVILLI VSSATRIKIM VELLVLFPLD IBDVLEFTK IMIYFESRGG SHYKLARALAA 240
 DLCLSPSPGF HPWFLWYMP LKVLVATSHG SLFVFDPIPL VFFRMALLLI LITMLHWFLF 300
 YIVAFPAKVL TQVYHLLKDL RBYDTBAEQS LKPSKAERPL RMGLVDEKRF

DNA SEQUENCE 10

Gene name: epidermal growth factor receptor (avian erythroblastic leukemia

Unigene number: Hs.77432

Nucleic Acid Accession #: NM_005228

Coding sequence: 187-3819

1 11 21 31 41 51
 | | | | |
 55 GCGCGGCTCG GCGCGAGTCC GAGCTTAGCC CCGCGCGCGG CGCGCGCCAG ACCGAGAGAC 60
 AGCGACAGCT GCTGGGCTCC GCGCGAGTCC CGCGCTGCGC GCGAGACGCA CAGCACCGCG 120
 GCGCGCGCGC CTGACTGTCT CCGATPXTGT TCGCGAGAGC GCGAGCGAGC CTTCTGGGSA 180
 60 CCGAGCATCG GACCTTCGCG GAGCGCGGAG CCGAGCGCTC TGGCGCTGCT GCGTCTCGCT 240
 TCGCGCGGCG GCTCGGCTCT GAGGAGAAAG AAGATTTGCC AAGCGACAGG TAAACAGCTCG 300
 AGGACATGGG GCACTTTTGA AGATCATTTT CTGAGCTGCC AAGAGATGTT CAATAACTGT 360
 GAGGCGCTCC TGGATATTTT GAGAAATPAC TATGTGACGA GGAATATAGA CTCTTCTGAT 420
 65 TTAAGAAGCA TCGGAGAGGT GCTCTGTATG GTCTCATGTT CCGTCAACAC APTGAGAGCA 480
 ATTCTTTGG AAAAGCTGCA GATCATCGAG GAGAAATATG ACTAGGAAAT TCTCATGCGC 540
 TTAGCATGCT TATCTACTTA TGATGCAATG AAGACCGAGC TGAAGAGAGT GCGCATGAGA 600
 AATTTCAGAG AATTGCTGCA TCGCGGCTGT GCGCTGATGT AGCATGAGCT TTTTCACTGA CATTCGATG 660
 70 GTGAGAGAGC TCTCTGCTGT GCGCATGATG AGCATGAGCT TTTTCACTGA CATTCGATG 720
 GACTTCCAGA ACCACTCGGG GAGCTGCGAA AAGTGTGATC CAGCTGTGCC CAATGAGAGC 780
 TCGTGGGGTG CAGAGAGAGA GAGCTGCGAG AAGTGAACA AATCATCTGT TGCGCCAGCAG 840
 TCGTGGCGCG GCTGCGGCTG CAGTGCCTCC AGTGAAGTGT GCGACACAGA GTGTGTGCGA 900
 75 GCTCTCACTG GCTCTGCTGT GAGATATGAG CTCTGCTGCT GAGATATGAG GTGTGTGCGA 960
 AGCTGCGAGG ACACTGCTCC CCGCATCTGT CTTCAAGAAC CCGACCAOSTA CAGCATGGAT 1020
 TATGACCGCC AGGCGCAATA GAGATTTGGT CCGCATCTGT TGAAGAAGTG TCCCGGATAT 1080
 GTGTGTGTGA GAGATCTGCA CTTGCGCTGT GAGCTCTGTG GCGACAGAGG CTATGAGAGT 1140
 GAGAGAGAG CAGTCTTTTTT GAGTGAAGAG GTCTGCTGCT GTTCCGCGCA AGTCTGTGAC 1200
 80 GGAATAGGTA TTGCTGATTT TAAAGACTCA CTCTCATATA ATGCTAGGAA TATTAAACAC 1260
 TTCAAAATCT GACCTCTCAT CAGTGGCGAT CTCTCATATC TCGCGGTGCG ATTTAGGGGT 1320
 GAGCTCTTCA CAGATACTCT TCGTCTGATG CCGACGAGAG TGATATTTCT GAGAAACGTA 1380
 AAGGAAARCA CAGGCTTTTTT CAGTGTATGAG GCTGTGCTGT AAAACAGAGC GAGCTCTGAT 1440
 CAGTGTGAGA ACTTAGAGCT CAGTACGCGC AGCATGAGCT AAGATATCTA GTTATCTCT 1500
 GAGTGTGCTA GCGTGAACAT ACATCTCTTG GATTAAGCTC CCGTCAAGGA GATGATGAT 1560
 GAGATATGTA TAAATTCGAG AAAACAAATAT TTGTGCTATG CAATACATAT AAGTGTGAAA 1620
 AACTGTTTGG GAGTCTCTG TCGAGAAACC GAGATATATA GCGACAGAGC TGAAGAACAG 1680
 TGTCAAGGCA CCGCTGAGGT CTGCAATGCC TGTGTCTCTC CCGAGAGAGC GTTCTGAGAG 1740
 GAGCGCCAGG ACTGCTCTCT TTGCGGATAT TCTCAGCCAG CCGAGGATGT TCGAGACAGG 1800

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5 TCCAGCTTC TGGAGGGTGA GCCAAGGGA TTTGTGAGA ACTCTGAGTG CATACAGTGC 1860
 CACCCAGAGT GCTCTGCTCA GGCATGAAAC ATCACTCTGG CAGACAGGGG ACCAGAGAAC 1920
 TGTATCCAGT GTCCGACCTA CATGGAAGCC CCCCTCTGG TCGAGAGCTT CCGCTGAGA 1980
 GTCTGSGAG AACACACAG CTCAGTCTGG AAGTAGAGAG AGCCCGGCCA TGTGTGCCAC 2040
 CTGTGCGATC CAACCTGCA CTAAGGATGC ACTGGGCGAG GTCTTGAGGG CTCTCAAGG 2100
 AATGGGCTTA AGATCCCGTC CATCCGCAT GGGATGTTGG GAGCCCTCTT CTTCGCTGCT 2160
 GTGTGGGCC TGGGAGATGG CCTCTTCATG CGAAGCCGCC AACTGCTTCS GAAGCCAG 2220
 CTGGGAGGC TGTCCAGGA GATGGAGCTT GTGAGACCTC TTACACCCAG TGGAGAGCT 2280
 CCCCACAG CTCTCTTBAG GATCTTGAG GAACTGAAT TCAGAAAGAT CAAGTGTCT 2340
 GGCTCCGGTG CTTTCCGSCA GGTGTATAG GAGCTCTGCA TCCCAAGAG TGGAGAAATT 2400
 AAAATTCGG TCTCTATCA GGAATTAAGA GAGGACAACT CCGCAAGAGC CACAGAGGA 2460
 ATCTCTGAG AATCTCTGCA GATGGAGCTT GTGAGACCTC CATGCGCTT CCGCTCTG 2520
 GGCATCTGCC TACCTCTCAG COTGCAACTC ATCAAGCGAG CTATGCGCTT GCGTGGCT 2580
 CTGACATGT TCCGGGACCA CAAGACAAT ATTGGCTCCC AATACCTCT CACTGTGTT 2640
 GTGCAATGT CAAGAGGAGT GAGTACTGT GAGGACGCT CTGTGTGTA CCGGAGCT 2700
 GCGAGCTGC ACTACTGTT GAAACAGCG CAGCTCTG AGATGACGA TTTGDECT 2760
 GCGAACTGC TGGTTCGGA AGAGAAGAA TAACCTGCG AAGAGGCGCA AGTCCCTATC 2820
 AAGTGAATG CATTGGAATC AATTTTACAG AGAATCTATA CCGACAGAG TGAATCTG 2880
 ACTCAAGGG TGACCGTTT GAGATGTGAT ACCTTTGAT CCGAGCATA TGAAGGATC 2940
 GCTCCAGGG AGATCTCTCT CTCTCTGAG AAGAGGAGC GCTCTCTTA CCGACCGGTA 3000
 TCGACATGT ATCTCTCAT GATCAAGTGC AAGTCTGGA TGTATAGGC AGATAGTGC 3060
 CCAAGTTCG GTGAGTTGAT CATGGAATC TCCAAATGG CCGAGAGCC CAGCGCTAC 3120
 CTCTCTATT GAGGGGATGA AGAATGCAAT TGTCCAAATC CTACAGACT CAACTCTAC 3180
 CTTGCCCTGA TGAATGAGA AGACATGAGC GAGTGTGTGS ATGCCAGCA GTACCTCAT 3240
 CCGACGGGG GCTTCTTGA CAGCCCTCTC ACCTCAAGGA CTCCCTCTT GAGCTCTCT 3300
 AGTGCACCA CCAACATATC CAGCCTTGCT TGCATTGATA GAAATGGCT GCAAGCTGT 3360
 CCGATCAAG AGACAGCTCT CTTCAGGGA TACAGATCAG ACCCCAGAG GCGCTTGGC 3420
 GAGGACGA TAGAGACAG CCTTCCCGCA GTGCTTGAAT ACATAACCA GTCTCTCCC 3480
 AAAGGCCG CTGCTCTCT CCGAGTCTCT GTCTACACA ATCACTCTCT GAGCCCGGG 3540
 CCGAGCAG AGCCCACTA CAGAGCCGCC CACAGCACTC CAGTGGGCA CCGGAGTAT 3600
 CTCAACACTG TCAAGGCCAC CTGTGTCAAC AGCAATCTT CAGCGCCGCG CACTGTGCC 3660
 CAGAAAGCA CCGACCAAT TACGCTGAG AACCTGACT CAGAGCAGGA CCGTGTGCT 3720
 AAGAGACCA AGAATAAGT GAGAGAGAT GATCTCTTCC CTGAAATCC AGAATAGCTA 3780
 ATGGTCCGC CACAAAGCA TGAATTTAT GGAAGCTGAC CCGAGGAGT AGTATGAGC 3840
 CTAAATATCT AGACTCTTT GATACCCGAG ACCAAGAGCC AGCAAGTCTT CCAATCCAC 3900
 ACCAGTGGC GATTAAGCT TTGAGCCAGC AGCTGTGTTT TCGAAGCTTT ACAGCAGCA 3960
 GCGAGGAGT TGTGAGGAT GAGAGGAGT GATCTCTTCC GTCTCTGAG CTCTCTAAC 4020
 GTGAGGAT TTAGAGAAC GATCAAGCA AGAATATTGT CCGTTTGAG AGAATTTAT 4080
 CTTTCAAGA GGTATTATT AAAAANAANA AAAAGATATA TGTGAGGAT TTTATGAT 4140
 GGGATCTGT GAGTTTGTG TGTGCTGAT TGAATTTAG TGTATGAGC TTTTCCACA 4200
 AGAGAGAGC TTGCTGTGAG CACTGTGATA CTGAGTTGA TCGACGCCA CTCTCTGAG 4260
 AGAGACGA GGTCAACAT TCCAGAGGA TGCTTGATG GATCGTTGCT GCTTCAAGC 4320
 TTTCACTGA AATCAATAA GATCCAGAA GCGCTTCATG CGCCAGAGC GCGGATCGG 4380
 TAGCTATCA ATCATGCGA GTGACATGAG GATGAGCAC TCTGTCCCTT CCGAGGCAA 4440
 GAGAAAGG AGAGATGAA TTTCTCTTA GACTACTTT TGTAAATAT TCCCAAGT 4500
 ACTTACTCC CAGTAGGA CONGTGTT CCACTATGA GGTATAGCT GACTTTTGT 4560
 TCTTCCACT CATTTGTTT AAATCAGTA TGCCGCCCT GTCTCTGCT CATGAATCA 4620
 GCAAGAGAG ATGACATC AATATATAC TGGATTCOA GCCCACTG GATTCATAG 4680
 CATTTGACC ATAGGCCAC AGCTAGAAAT GTGATATCT TAGAGATAC ACCCTTTGT 4740
 TTCCGCGAA AAGATATCT CTATTTGAG CTTCAAGTA AATGATGAG GTCTTTGT 4800
 GCTATGATCA GAGACATCA AATATGAGC TGCTTGAAA TCTCCTTAG CATCAAGC 4860
 AACCOCODAA AATGATTTT TGTACTTAT GGAAGATAG TTCTCTCTT TACTTCACT 4920
 GAAAGCTTT TACTCAAG AGTATATGTT CCGTCAGGT CAGCTGCCCT CAACCCCTT 4980
 CCGTACGCT TGTCAAGA AAGATGCTT TGTCTGAT GACTATCA AGCTATCA 5040
 GCTCTGGCA CACAGCGCA TTTACAGT GCAATGACA ATAGATTAT GAGTAGTGT 5100
 AATTCAGTA GTAAATATGA AACTAGGTT TGAATTTGAT AATGCTTCA CACATTTCC 5160
 AGATGTTTA GAGGAAAAA AGTCTCTCC TAAATAATG TCTTACAT TGGAGATTG 5220
 GAGATATCA CTAGTTTGT TGTATGAT TCTGATGAT GATCTATG AGCTATCA 5280
 TCTTACAG CAGTCTTGT TAAACATGT TTTAACTCT CTATGCAAT ATCAAGCCA 5340
 TCCATTTAT CAAGAGAA AATGTTTCA AATATTTTC AGCTACAT TATGTGAGT 5400
 CACACACCA TACAAGAT TCTTTTGT TTTAAAGTAA TTTTGAAT CCGATGAT 5460
 CAGAGCCCT ACAGCATGT TAAGAAGTA TTGATTTT GTCTGAAG AATTAAGCT 5520
 ATATCAATT CC

Protein sequence 10

Gene name: epidermal growth factor receptor (avian erythroblastic leukemia

Unigene number: B1-77412

Protein Accession #: NP_005219

Signal sequence: 1-27

Fam domain: Recep_L_domain [57-190, 372-492]

Transmembrane domains: 1 546-658

1 11 21 31 41 51
 75 NPDSGTAGA LALLAALCP ASRALESKKV CXTSINKITQ LTFIDRPLS IQHSHNCEY 60
 VLRLEITYTHG LQFAGMLK TIFPAGATL LALNTYFIP LBNQIATN MYTFSTALA 120
 VLSNYDANKT GLKLEPMEL ORILGAGVET SNBPALCNVE STQNDRIYVS DFLSNENDF 180
 QHILSGCQRC DPSCPWGSLW GAGHBNQKL TFLCAQCS GRCRGRSPSD CCHNCCAAAC 240
 TQIPRESCLV CRKRFDEACT KDPCPLMLYV MPTTYGMQVW PEGKYSGEAT CVKRGPRNV 300
 TPTGSGCVLA CDAVDEER DQVWCKRCS GPKRWKMG ICSGFPGLS LKATVWIF 360
 80 NCTSLISLIL LUPVAFKRS PHTPPDLQV ELDLKTVKE ITGFLIQAW PEKTLDFAT 420
 ENLEILINRT KQIQPSLAV VELNLTSLG LSKLEISDQV VLISGNELIC YANTLNNKL 480
 LPTSGQIKYI LSNRGNBSK ATPOVJIALC SPBGCGPPEP RGCYSRWSV RGRGVDCKE 540
 LLGRKPEPEP EISCKIQCF ECLCPNHWIT CCGTDPSCV CSQKILNKH CACTPAGW 600
 GSNRTVREY ADAGVQVCL HNPCTDCTG PGLRCPFNG PKPISLATM VQALLLAV 660

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ALGIGLPMR RHIVREKTLR RLQERELVE PLTPGGRAPN QALLRLKET EPKKIKVLGS 720
GAPGVVKGIL NIPGGRKVKI PVATKELBA TEPANKREIL DEATVWASVD HPHVCLLGI 780
CLTSTVQIT QAPRQCLLO TVGRHKWIG SYLLAWKWD IARGRWYLED RLHVRELLA 840
RHVLVKTQPH VQITDFGLAK LLSAMEKYN ARQGVFVIM MALESILIRI YTHQSDWNSY 900
GVTVWELATP GSKPFDGIPA SEISSILEKH ERLFPFECT LDVYIMVVK UNIDADRPER 960
FRELLIIEPK MADPQRYVL IQCDREHSLP SPTDSHFYIA LMDREPMQDV VDADEYLIPO 1020
QGFPSRPSST RPLLESLDA TSMSTVACI DRKGLQCTF KEDPLGRYS SEPTCALCV 1080
STDTPLPVE EYINGSVPEK PAGESVNFYI HMOPLNAPS EEFHYDPIHS TAVCPFEYLN 1140
TVQPTCNST FDSAPRWAK GSHQISLQNP DYQDFFPER AKPHGIFKGS TALNAYELRV 1200
APQSSEITGA

DNA sequence 11

Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)

Unigene number: Hs.110903

Probeset Accession #: AW245805

Nucleic Acid Accession #: U00_003277

Coding sequence: 121-777

20	1	11	21	31	41	51	
	AGGGAGCTGG	GGCCAAAGAC	CGGGAGGCGG	GGCCCAAAGG	CACCAAGGCC	CGCCCAAGGC	60
	GGCCGCCAAG	ACGGCTCTGG	GGGTCTCTGG	GGCTTCGGGG	TGCCTCTCTC	GCTCTTAGCC	120
	ATGGGGTCCG	CAGCTTTGGA	GATCTTGCGC	CTGTCTCTCT	CTGTGTGTGG	CTGGGGGGGT	180
	CTATCTCTGG	CGTGGGAGCT	GGCATGACCG	CGCTCTCTGA	CGCAAGATCT		240
25	GTACCGCGCG	AGACCACTGG	GAAGGCGCTG	TGGATTCGCT	CGCTGTGTGA	GACCAACGCG	300
	CAGATCGAGT	GCAAAAGTGA	CGACTCGGTG	CTGGCTCTGA	GCACCGAGGT	CGAGCGGGGG	360
	CGAGCGCTCA	CGTGAACGCG	CGTGTGCTGT	CGCTTCGTGT	CGCTCTCTGT	GACCTCTGGG	420
	CGGCGAGAGT	GGACCACTGG	CGTGGCGCGG	GGCTCGGCGA	AGGCGGGGT	GGCTCTGAG	480
	GAAGGCGTGG	TCAACTCTGT	CGGCGCGCTG	CTGGCGCTCG	TGGCACTCTG	CTGTGTCGCC	540
30	AGCATTTGTG	TCCCGGAGTT	TTAGACCGCG	TCGTGTCCCG	TGTCCAGAGA	GTACGAGCTG	600
	GGCGAGCGCG	GTATCATGCG	CTGGGGGGCG	ACCGCGCTGC	TCATGTGTAG	CGGCTGCTCT	660
	TTGTCTCTAG	GGCTCTGGGT	CTACCAACCG	CGTCCGACCG	TGAGCTCTCG	CGTATGATCA	720
	TGAGCGCTCG	CGGCGGAC	CGACACCGCG	GGCTACGACG	AGAGAGACTA	CGTCTCGAGG	780
	CGCTGGCGAC	GGCGGGGGCG	CTCTGCCGAG	CCACGCGCTG	GAGGGTTGG	ATAAGCGTGC	840
	GGAGCGCGCG	GTGACCGCGG	CGCTCTCGCG	GGTAGGGCGG	CGCGCAAGCT	CTCTGGAGCG	900
	TCGGCTCTGT	CGTCCGACCG	CGGCTCTCGG	ATCGCTCTCT	CGCTGCGCGC	GGACATGAGC	960
35	TTCTCTCG	ATGAGCGCGG	CGCTGCTCTT	ACAGACGCGA	ATGAGCTCTT	CTTTCTCTGG	1020
	CGCGCGCTGT	TTTCCATAGG	CAGAGCGGGT	GTGACAGTGA	GGATTCTGCT	TCCCTCCCAA	1080
	GAGCTCTGGG	GTCTTGGCTG	GTGGCTTACT	TCCGACAGCG	TCTCTGCTAC	TTCCAGGGGG	1140
40	CGAGTACGAG	GGCGGGGGCG	CCGACCGGAG	GATGTGTAGA	GCTGTCTTTT	ATCTCATCTG	1200
	CGAGCGCGCG	CGGCGGCGCG	CTGCGGCGCG	CGGCTGCTCT	CGGCTGCTCT	TCCGAGTCTG	1260
	CTCCGACGCGA	GGCTTTGGGG	CAGCGGAGCT	TGAGAGAGGG	CGGAGCTGGG	AGGGCTAGGA	1320
	ATCTCTTAG						

Protein sequence 11

Gene name: claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)

Unigene number: Hs.110903

Protein Accession #: NP_003268

Signal sequence: none found

Pfam domain: PF022 Claudin [4-181]

Transmembrane domains: 5-27, 74-96, 123-145, 164-186

Cellular Localization: plasma membrane

55	1	11	21	31	41	51	
	MGSAALHILG	LVLCLVWGGG	LILACGLPMH	QVTFALDHBI	VTAQTFWKL	NMSGVVGSTG	60
	HMCKRVYDSV	LALSTEQAA	RAITVSAVLL	AFVPAFLVLA	GAQCTTCVAP	GPAKFAVALT	120
	GGVLYFLGCL	LALVFLGFA	NHIVREPYDF	SVFVSRYTEL	GAALYIGWAA	TALAWGGCL	180
	LCCAMVCTGS	RPLSFPVYK	SAPRRFATG	DYKGRVY			

DNA sequence 12

Gene name: vascular endothelial junction-associated molecule

Unigene number: Hs.54659

Probeset Accession #: AA410345

Nucleic Acid Accession #: AF255910

Coding sequence: 241-1137

65	1	11	21	31	41	51	
	TTACCATTTG	GTGGGCTGCG	GAGAGAGAGA	CAGAAAGGGG	ACCGGCTCTC	TGGCAGCCAG	60
	CTGACAAAGC	GGCCCGGGGA	GGGCGAAGCT	GACATCCGCT	CTGAGAGCGT	CGCTCTCTCT	120
70	CTCTCCCTCC	CGACTCTCTG	CGCTTTCTCC	CGCCGCGGAG	TTGAGGCCCG	CGCCGCTCTC	180
	TGCTCTCTCG	CGCCGCGGAG	CTTGAGCTCT	CTGACAGCGG	CGGCTCTGCG	CGCCGAGNAG	240
	ATGCGGAGGA	GGAGCGCGCG	CGCGCTCTCT	CTGCTGCTCT	TGCGCTACCT	GGTGTGCTCC	300
	CTGGGCTACT	ATAAGCGCTA	TGGGTTTTCT	CGCCCAAGAG	ACCAACAGGT	AGTCACAGCA	360
	GTAGAGTACC	AGAGTCTATT	TTTAGGCTGC	AAAGCCCGCA	AGAGAGCTCT	TTCTCTCGGA	420
	TTAGAGTCTA	AGAGTCTGAG	TGCGAGTCTT	TCTTTGCTCT	ACTATGATCT	GAGCTTTGGA	480
75	GGTATTTTAA	AAATCTGACG	TGAGATGATA	GATTTCAATA	TCCGAGTACA	AAATGTGACA	540
	AGAGGTGATG	CGGCGGAATA	TGCTTTGTGA	GTTAGTCCCC	CATCTGAGCA	AGGCCAAAGC	600
	CTGAGAGAGG	ATACAGTCTG	CTTGAGAGTA	TTATTTGGCT	CAGCTCTTCC	ATCATTTGAA	660
	GTAGCTCTCT	CTGCTCTGAG	TGACATCTGT	CTGAGAGCTG	GATTTCTAGA	CAGAGAGGGT	720
80	AATCCAGCTC	CTGACATACG	ATGCTTTAAG	GATGGCATCC	GTTTCTGAGA	AAATCCGAGA	780
	CTTGCTCCCC	AAAGCAGCGA	CAGCTCTATC	ACAATGARTA	CAAAAGCTCG	AACTCTGCAA	840
	TTTATATAGT	TTTCCAAACT	GGACATCTGA	GAATATCTCT	GTGAGACCGG	CAATCTCTGT	900
	GGATATCTCA	GTGATCTGAG	GAGAGAGTGG	ATCTACACTT	AGCTGAGTCT	AGCTGAGTCT	960
	ATACAGACCG	TAGTATGTTT	GGCTCTTAGT	ATTTCCCTTT	GTGCGCTTGG	TGATGTGCTT	1020

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5
GCTCAGAGGA AAGGCTACTT TTCAAAGAG ACCTCCCTCC AGAAGAGTAA TTCTTCATCT 1080
AAAGCCACGA CAATGAGTGA AATGATTTTC AAGCACACAA ATCTCTTAT ATTTATAGAA 1140
CTCTCACTTTA GAGATACACG AAGGCCACCG TTGTACACAA AGTATTATAA CTATTATAAA 1200
ATCTTCATTTA TCCGACATCT TCCAAAGAGG TACAGACAGA AATGAAATGT GTATTTCATT 1260
TTGATTTTCA TCACTACTAA CTGACTGAGA CTGCTACTT TAAAGAAATA GTTCGATGGA 1320
CACTAAATAT ATAACTCGCC TTCTGTGTGC TGGACTAAGT TAAAGGATTA AATATCACTT 1380
GTATGTCAA AAAAAA

Protein sequence 12

10
Gene name: vascular endothelial junction-associated molecule
Unigene number: Hs.54650
Protein Accession #: AAF81223
Signal sequence: 1-22
Igc2 domain: 41-115, 146-221
15
Transmembrane domains: 239-261
Cellular Localization: plasma membrane
1 11 21 31 41 51
20
MARSRRLRL LLLRLYLVA LGYHKAYGFS APKDDQVITA VEYORAILAC KTPKKTVSSR 60
LEENKLGREVS SFVTYQOTLG GDFENRADM DPHRIDQMT NDAAGKYRCE VSAPSEQQGN 120
LEEDVTYLEV LNAPAPVSCF VPSSALSGTV VELRQDQREG NPAPETWTFK DGRILLENPR 180
LGGSTGHSY TWKTGTGLG PTYVGLPLTG EYSCRAWNY GTRCKPRGM QVDLNLISGI 240
IAAVVVVALV ISVGLGLVCT AQRKYFSKEK TSFQKSNSSS KATMSKSDP RHTKSPFI

DNA sequence 13

25
Gene name: solute carrier family 11 (proton-coupled divalent metal ion
Unigene number: Hs.182611
Probeset Accession #: D50402
Nucleic Acid Accession #: NM_000578
30
Coding sequence: 1-1653
1 11 21 31 41 51
ATGACAGGTG CCAAGGGTCC CCAAAGGCTA AGCGGGTCCA GCTATGGTTC CATCTCCAGC 60
CGACAGCCGC CACACAGCCC AGGCCACAGG CAGGCACTCT CAGAGAGAAC CTACCTAGAT 120
GAGAGATCTG CACTCCCGCA CACAAACACG GCACACTCTA GCTATGGGAA GCTATGGGAC 180
TTACAGGGGC CTGGCTCTCT CATGAGCATT GCTTTCTCTG ACCDAGAAAT CATGAGATAT 240
GATCTTCAGC TGGHCCCHOT GGGGCGATTG AACTTCTCTG GGTGTCTGCT CTGGGCGACC 300
GATCTGGGCT TGTCTCTCCA CGGACTGGCT GCACATCTCG GGTGTGTGAC AGGCAAGAGC 360
TTGGGCGATC TGTCTCTCTA CTATGACTCT AGGPGGCCCG GACACTCTCT CTGGCTAGAC 420
ATCGAGCTAG CAGTTTGTGG CTCCGACATG CAGGAAATCA TGCGACAGCG CATGACTCTT 480
ATCTGACTCT CAGCTGGAGC AATCCCACTC TGGGGTGGCG TCTCATCTAC CATGTTGGAC 540
ACCTTCTCTT TCTCTCTCTG GATATATCAG GGGCTGGGGA AGCTGGAAGC TTTTCTTGGG 600
CTCTCTATGA CATTATGACT CTGACACTCT GCTGCTCTCG ATGTGTGGCG GGTCTCTGAG 660
CAGGAGAGGC TCTCTCGGCG CTTGTTCTCG CCTCTGTGCC GGGCTCTGCG CACCGCGGAG 720
CTGCTGCAGS GGTGTGGCAT TGTGGGCGCC ATCATCATCG CCGCAACAT CTACTGTGAC 780
TGGGCGCTGG TCAAGTCTCG AGAGATAGAC GGGGCGGCCG GAGTGCACAT CAGAGAAAGC 840
AGATGACTCT TCTGATATGA GGCACACACG GCGCTCTGCC TCTCTTTAT CATGACCTCT 900
TTTGTATGAG CTGACATTGG CAGAGCCTTC TACCAAGAAA CAGAGAGCG TGGTGTGAC 960
ATCTGTGCCA ACAGCAGCTC CCAAGACTAC GCTAAGATCT TCGCCATGGA CAAGCGCCAC 1020
GTGGCGGTGG ACATTATACA GGGGGGCGTG ATCTGTGGCT GCTGTGTGG CCGCGCGGCC 1080
CTTGATATCT GGGCATAGG TCTGCTGGG GCTGGCGAGA GCTCCACAT GAGGCGACAC 1140
TACGCGGAGC AATCTGCTAT GAGGCTCTG CTGAGCTGCG GTGTGTGAG CTGCGCCGT 1200
GTCTCTCTCA CCGCTCTCTG CGCCTATCTG CCGACGCTGC TGTGTGCTGT CTTCGCGGAC 1260
CTGCGGACT TGTGCGGCT CATGATCTCG CTGAACTGCG TCGAGAGCTC GCTGCTCCCG 1320
GTTGCGGCTC TCGCATCTCT GATCTCMC AGATATGCCA CCGCATGCG CCGGTTTTCG 1380
ATAGGCTGCG TCGCAAGCT GTGCACTCT TCGATCTGCG TCGATCTGCG CAGCTATGAG 1440
CTCTACTTGG TGGTCACTA CTGCGCCAGC CTGCGGCCCG CTGCTACTCT CGGCTGTGCA 1500
GCTTGTCTGG CGGACGCTTA CTTGGGCTCG AGCACTTACC TGGTCTGGAC CTGTTGCTCT 1560
CGGACGAGAG CCACTTTCT GGGCCACACG TCCCACTACC ATCTCTGTA TGGGCTCTCT 1620
GAGGCGACC ACAAGGGGA GACCTCTGCG TGG

Protein sequence 13

65
Gene name: solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1
Unigene number: Hs.182611
Protein Accession #: NP_000569
Signal sequence: none found
Pfam domain: Hraup [78-463]
Transmembrane domain: 58-69, 86-110, 159-181, 195-217, 284-306, 349-379, 394-416, 432-454, 468-490, 501-523
Cellular Localization: plasma membrane
70
1 11 21 31 41 51
MTGDKPQRL DSEYSGISS PSTSTPGFQ GMPRETYLE EKIPIDTRF GTRFLRKLWA 60
FTGPGFMISI ALPDGNISS DLQGFVAFK ELIAVLHANT VGLICILIA ARLOVTFKK 120
LGEYCHLPPY KVRPTVLMLT IEALIVGSM QEVGTATAP NLLSAGRIPL MCVGLITVD 180
TFFFLPLWNY GLKLEAFPG LUITTMALTY GSEYTVARPE GQALRKLGLF PSCGCGGHP 240
LLCAVGVGVA IIMRDIYILI SALVSKREID RAKRVDIIRA NMYPLISATI ALGVSPFIML 300
FYNAFSGAF YGTGQAAPN ICGMSLEHYR KTFPMNAT VADLYKGVG ILCLCPHFA 360
LYIAICILIA AGGSGTNTCT YAGGQVWRF LRKWSRPAR VALTRSCAL PTVLAVRFD 420
LRDLGLNLND LNVGLSLLPL VAVLPILTT EMTLMQFA NGLLNKVTTS SIMVLCTIN 480
LTFVSVSLFS LNPAPATGIA ALLAAATLGL STYLVWTCCL AGATATLARS SHIRFLYGLL 540
RUKNGCTGG

DNA sequence 14

Gene name: solute carrier family 7 (cationic amino acid transporter, y-

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[illegible]

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5
 10
 15
 20
 25

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COSTACGCC TCGGCTTGCT GAGGATAGGG CTCTAGGAGG CCGCCGAGCC CAAAGCTGCC 1440
TGACGAGCGA TGGTGTGGGA GCTCATGAC CCGAGACCGA ACCGREGTGT GCGCCCTCTC 1450
ACCATGACAG CTAGAGTGGG GAGGTGATC GACTTTTCCA AGCCTTTATG GACCTGGAGG 1460
ATCAGCATCC TCTACCGAGT GCACATGGGC CCGACGCGCT GACTATCTCT CTCTCTGGAC 1470
CCCTCTGCCC CTGCTGTGTG GCTCTTCATG GCTTTCGCTT ACCGTGGCTGT GAGCTGGGTC 1480
CTGTCTCTGG CTCCGAGGCT GAGCCGCTAT GAGTGGTATA ACCCACACCT ATGCGTGGG 1490
GCACGCGGCC AGCTCTGGA GAGACATGAC AGCTCTGGA AGACTCTGTG GTTTCGCGGG 1500
GGGCGCTTCA TGGACGAGGG CTGGAGATAT ATGCCCCGGG CCGTGTCCAC GCGCTGTGCT 1510
AGCGGAGTCT AGCGGCGCTT CACCTTGATC ATCATCTGCT CCTACACGCG CAACTGGGCC 1520
GCTGTCCTCA CCGTGGAGCG CARGAGAGTG CCTTGGAGTG GCGCTCATGA CTTGGCAGAT 1530
GACGACGAGA TCGAGTATCA GACTCATGCA GCGGCTCTCA GCTGTGCTT CTTCAGAGT 1540
TGACGTATCC AATCATGACA GCGCATGTGG AACTCATGCG ACTCGAAGCA GCGCAGCGTG 2100
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CTCGAGTCCA CAGTAAAGGA ATACACACGG GCGCTCAACT GAAACTTCAC CAGAGTGGG 2220
GACCTCTGCG ACACAAAGGG CTAAGGCAAT GCGCTGCCCG TGGCTCCCG GTTCCGGCAT 2280
GAGATGACAC TGGTATCTT GAGCTTCAG GAGACAACG GCGTGGAGAT CTTGAAAGCC 2340
AAGTGTGGGG AGGCGGCGCG GTGCCCCAAG GAGGAGGAGC ATGAGCTAA AGTTTTGGCG 2400
ATGAGAGACA TTGTGGCAT TTTTATGTTG CTCTATCTGT GCGCTCATCAT TCGTCTCTTC 2460
GTGCGGTCCA TGAATTCAT ATGTTCCACA CCGAGCTGAC CTGATGCCGA GGAAGTGTGT 2520
GTGTGCGGCA AGATCTCCA GCGACGCGCG GAGCGCTTT CTTCGCGCAA GAGCTCGGTT 2580
TCCCGCGCGC GCGGAGCGCC GGGCGCGCCG AGCGCGGCC TCGTCTCACT CCGCGCGCTC 2640
CGGAGATGCG GCTCTGACCA GCGCAAGCTC TACTCGCGCG GCGCGCGCGG GATGTCGCG 2700
AGCGGCGAGG GGGCGCGCGA GCGGCTCTGT GAGGACCGCG GCGCCCGGAG CGAACCGCG 2760
CGCGCGCGCC CGACCGCTGT CAGCGAGTGT CCGTCTGCG AGGAGTCCCG GCGCATACAG 2820
GCGCTCGCGG CCGTGGAGCG GCGCGCGCT CCGCTGGGCG TGGGCGTCC CCGCGAAGCC 2880
ACCAAGCGCG CCGCGCGCGG GCGTGGCGCG CCGCGCGCCC GGAGCTGCG GAGGACGAG 2940

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TGA

Protein sequence 15

Gene name: Glutamate receptor subunit

Unigene number: Hs.249141

Protein Accession #: A322591

Signal sequence: 1-27

Pfam domain: ANF Receptor [343-400];PBPe domain [416-785, 799-838]

Transmembrane domains: 297-319, 544-566, 624-646, 803-825

Cellular Localization: plasma membrane

30
 35
 40
 45
 50
 55

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      11      21      31      41      51
      |      |      |      |      |
NPAAELLLLI VAFAPSPQV LSSLNRMAIL DDQTVGRRG HAAALALARE INGIIEVPAK 60
ARVRVDIFEL QDSQSTETD THGILLKPGV VSLVGGSSP ASASTVSHIC GSEIIEPIKV 120
QFETVETGV LKPAFSLVP DHEVSLVLS RILKSPFYS ASLCAKAAEC LLEELSEIVG 180
FLIKSEITSLV RMDDSDRPT PLKIEIRDKR VSTIIIDNA SIHLLILEX SELMGTSIFY 240
EYLITMDFFP ILHLDIQVED SSNLIQSFNF NTHSPFFPEF VSLNMSHRE MCBASTITGP 300
ALEALAMPDA VHVVVAVRE LNRSGIIGK PLACTSANIM PHGTSNLYL RHVEITADLP 360
RVFVRSKRG TRITLILIK SQGSHREIV VYRSTPLAM ATTLDILHQ TLIAMTLMVT 420
TILENPVYVE RFPQOLSGN RFRDPCFDM LLEALLELF PYRELVVEDG LYGAPERNGS 480
WTGMVGLIN READLAAVA TITAREKVI DSKPFMTLG ISILYVRMG RKGYFSELD 540
PFSPAVLFLN LLAIVLSCV LLAIALRSPY DMNPHFICR APHILENVY TLGNSLAFPV 600
GPMQGSSEI RHPALSTRCV DQVWAPLI IISSTANLA ALTYQREYV PVSDADLAD 660
CTNLEDTIIR AGSTMTFFN RYVTVQRNI NYMOSQSPV FVSTSEBIA AVLMSRYALF 720
LESTMEYHRH ELNMLTQIG LGLDTGTVGI CMPLGSPFD EITLAILQLQ ENRLEILKR 780
NHWGDRCPCK EGRNRKGLG HENTGQIFIV LNCILIAVP VAMFPI MST RSASSESEVS 840
VQDGLQBLR HAVSCRSTR SKRRRPDPP SRALLSRAR IEMRLBNKL YGAGGARG 900
SRMDQRIIL DQDPPRGRH PAAFTPTCHV RVQGRERLQ ALASAGACAP PRGLGVPAEA 960
TSPFRPZPQ ACPELAERH

```

DNA sequence 16

Gene name: Adenosine A3 receptor

Unigene number: Hs.258

Probeset Accession #: NM_000677

Nucleic Acid Accession #: NM_000677

Coding sequence: 768-1724

60
 65
 70
 75
 80

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      11      21      31      41      51
      |      |      |      |      |
ATCTTTGGTG CAAAGGCTGG GTATCGGCTG TGTCTGGGAA AGCTTCNACT CTTCTCAGAA 60
CTTGCACGAG CTAGAGTGGG GAGCTGCCA CCGAGGCTAT CCAAACTGCT TTTTITGTT 120
CTCIGCTCTCT CGGCTTTGCC TCTTATCATC GAGACTTTIT TGTAAAGCTG GCAGAAAGAT 180
TGCATAGTCA GTGCTTCGAG CTCTGCTCCC ACGTATGCTT GCACTGTGCT CTGTCCTGT 240
AAGGAAATGA CTCTGTACG CAACTGTGCT TCGAGCTCTC TCTATGCCAC TCACTGGCTG 300
TCTCTCTGCG CTGCTGAGCA GAGTGTGCTA GCTTCTACTG CTCTGACTG CTCTGAGA 360
TCTTACTCTC TGAACAGCT CCGAAGAGG TGTCTTANCT TGTATGACAT CAAAAAGCCA 420
AAGAGCTGCA GCGCAGAGCG TGAGAGACAT CTGTTTGGGG AACTAGAGC AGCAGCACT 480
TCAGATTCAG TCAATATAGA CGTGKCCATC AGCTATCTGG AACTATGAG ATGTGGTGT 540
CATAAAGGGG CTGAAGATGA CCGCATGTGT AGACACCAT GAAATGAGC ATGTGGTGT 600
AGGKTCATCA CACACAGAA ASHTTGGCA TCGACAGTT GGAATTTTA GAGTGTACT 660
GCACATGACG CTTGCGGAGG AGCTCTGGCG AGAGCTGAGC CCACTGACC TACAGACAGA 720
TCTCTGTCGC TCACTGTGCC CTGTGAGGTT TCCCTGCGGA AGGCAGATG CCGACAGCA 780
GACAGCTGCT GTCAATGGC AATGTACTCT AGACACCAT GAAATTTTC ATTGACACT 840
GCGCACTAGT GGGACATGCT CTGTGACTT CTGTGCTGCA GCTGAACTC GCTGAGCA 900
CGACACACTT CAAATTCATT GTCTCTCTAG CCGTGGCTGA CATTGCTGTT GGGTCTGCTG 960
TCATGCGCTT GGCATGTGTT GTACGCGTGG GCATACAACT CAACTCTAC AGCTGCTTT 1020
TTATGACTGT GCACTGCTCT GTCTATTTACC AGACCTCAT CAGTCTCTTG CTGACACTG 1080
CTGTGAGCGT ATGAGAGGCG GTGACAGTCT CCGTGGATGA CAGAGAGGTC ACCACATCA 1140
GAAGATATAT GCTTGGCCGT GCGCTTTGCT GCGTGGTGTG ATTCTGCTGT GAAATGAGC 1200

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CCATCTTTGG CTGGAACATG AAACCTGACCT CAGAGTACCA CAGAAATGTC ACCTCTCTTT 1260
 CATGCCAATT TGTTTTCCTC ATGAGAGATG ACACACAGGT ATACTCTACG TCTCTACCT 1320
 GSHPTTTCAT GCTATGAGTT GTCATGTGCG GATCTATCTT TGCACCTTT TACCTATCTC 1380
 5 GGAACAAACT CAGTCTGAAC TTATCTAACT CCAAGAGACT AGTGTCATTT TATGACCGGG 1440
 AGTTCACAGC GCGTAAGTCC TTCTTTCTGG TTCTTTTCTT GTTTCCTCTG TCATGGCTCC 1500
 CTTATCTATC CATCACTGTC ATGACTTACT TTAAAGGTGA GGTACACAGA CTRTGCTGTT 1560
 ACTGTGGCAT CTCTGCTGTC CAGTCAACTC CAGTAGGAAA CCTCTATGTC TATGCTATTA 1620
 AATAAAGCA GTTACAGGAA ACCTAACCTT TGATCTCAA ACCCTCTGTG GTCTGCGACT 1680
 10 CCTCTGATTC TTGAGACATA AGCATTGAGA AGAATTTCTG GTAGTTATCC ATCAGAGATG 1740
 ACTCTGTCTC ATGAGACTTC AGMTTCCCA TCACACAACA CTTGAGGACC TGTATTCCTG 1800
 GCGCAAGGTA TTCTATCTC CTCTGATCTC CAGTAGGAAA TGTGAGACTC TCCATCTGCT 1860
 CCGAATATA TCTCCGCCAC TCACACTACT TCTTCCCTCA CTTCAATTTT CTTTGTGCTC 1920
 TTCTCTCTAA TTCAAGTGTT TGAAGGCTCG ACTTGGGGAC AACGTATTAT TGAATATTAT 1980
 15 TCTGTCTTTC CTCTCTCCCA ATGAGAAATC AAGCTATGGA GCTCTGAGGG TCCCTATGTC 2040
 ACTCTACAGC AAGAGAGGAT AGTTGGCTCG ACATAGGAAA TGTGATGAGC TCAATTTCTA 2100
 GGCATCTTGG AACTGAGGCG AGAAGCTGCT CTCGAGGAT GCTGAGAGA TTTTGGAGAC 2160
 AGAAGAAATA AACTGACTTT AGAGGGGACT TAAACTGCTG AATTCACCTG TGAATTTT 2220
 TGAATATA AAGCTATA G

Protein sequence 16

Gene name: adenosine A3 receptor

Unigene number: Hs.258

Protein Accession #: NP_006668

Signal sequence: none found

Pfam domain: 7tm_1 [29-282]

Transmembrane domains: 12-34, 50-72, 86-108, 120-150, 179-201, 229-251

Cellular Localization: plasma membrane

11 21 31 41 51
 | | | | |
 30 MPRNSIALSL ARVYITIMEI FGLCAIVRG VLVICVVRIN FSLQTTTFYF IVSLALADIA 60
 VGVVLMPAL VSLGIIITHEF TSLCPMLCL LFPTFRASIN LLAIADVRL NKLIVRYRIR 120
 VTRHRHIA LGLAGHVR NLSLSEYIN VPLAQVQIN FGLGHWYFV
 SFLTWIPI VLKCAIYLDI FYIIRNLSL NLSNKEFGA FYOREFKAK SFLVLFLFA 240
 LSLMLPLIIN CIIFYHGEVP QLVLYGMLL SHANSWPII FYVIEIKFK ETYLLILKAC 300
 35 VVCHPSDLD TSIEKISE

DNA sequence 17

Gene name: glypican 1

Unigene number: Hs.2699

Probeset Accession #: X54232

Nucleic Acid Accession #: NM_002081

Coding sequence: 222-1898

1 11 21 31 41 51
 | | | | |
 45 GACTGCGCGA GAGAGCTTC GAGACTGCGA CCGCGCGCGC CCGCGCGCGC CGCGCGCGCC 60
 GACTTTTGTI GTCTCCCGCT CCGCGCGCGC CCGCGCGCGC GAGACCGGAG CCGCGCGCGC 120
 CGGAGCTTGT GCTCTGCGCT TCGCGCGCGC GAGCTGCGCA GAGACCGGAG AGATCCGAG 180
 AGAGCGCGCG CCGCGTGGCC GCGCGCGCGC CCGCGCGCGC CAGTGGAGTC CGCGCGCGAG 240
 GCTGTGGCTC GCTATGTGCG CGCGCGCGCG TGGTGGCTGT CCGCGCGCGC GACCGCGCGA 300
 50 CAGAGAGCGC GAGCTGCGCG GAGTCTCGCG AGATCTAGCG AGCACAGGCG TCGAGCTGTA 360
 GCGAGCTGCC CAGCGCGAG ATCTCGCGGT AGCATCGTGG GATCTGTCCC CAGAGCTACA 420
 CCGTCTCGAC CAGCGAGATG GAGGAGAACG TGGCGCAACG CAGCATATCG CAGCTGAGGA 480
 CGCGCTCGCG GAGAGCGAG CCGCTCTGCG AGGCTATGCT TCGCACCGAG CTGCGAGACT 540
 55 TCGATACACA CTCTCCACAC CTCTCTAACG ACTCGAGGCG GAGCTCTGAG GCGCATCTCC 600
 CGCGCGCTT GAGAGAGCTG TACAGCGAGA ACGCGAGGCG CTTCCGCGAC CTGTACTCAG 660
 AGCTGCGCTT GTATACCGCG GGTGCGCAAC TCACACTGGA GAGAGACTCG CCGAGATCTT 720
 GAGCGCGCTT CAGAGAGCGC CTCTGAGAGC AGCTGCGAGC CAGCTCTGCT GCTGTATGAT 780
 ACTATGGA CTCTGCGCG GAGAGAGCGC AGGAGCTGCG CCGCTCTGCG GAGAGCGCGA 840
 60 GAGAGCTGCG CCGTGGCGCC ACCCGTGCTT TGGTGGCTGC TGCTCTCTTT GTGACGGGCC 900
 TGGGCGTGGC CAGGAGAGTG TCTCGGAGAG TGGCTCAGAT CCGCTCGGCG CCGAGATGCT 960
 GAGAGCTGCT GTGAGAGCTG GTCTATCTGT CTGACTGCTT GAGATCTCCC GAGCGAGGAG 1020
 CCGTCTGTA CTATGCGGA AATGTGCTCA AGGCTGCTCA TCGCACAGAG GCGAGCTCTT 1080
 65 ACGCGAGTGT GAGGAGACTC CTGAGCTCCA TGGTCTCTAT CAGGAGAGAG TCTTGGGTGA 1140
 CATCGCGTGT GAGAGATGTC ATCGCGAGCG TGCACAGTGT GCTGGGAGAG GCGATCAAGC 1200
 CCGTCTGCGA CAGCAGGAGC AGCTCTGCGG CAGAGGTCAT CAGAGGCTCG GGGAGACCGA 1260
 AGCTCTGAGC CAGCGCGCTG AATGTGCTCA AGGCTGCTCA TCGCACAGAG GCGAGCTCTT 1320
 GCGAGAGGCC AGCTTCTGAG AGCTCTGAGA AGCTGCTCTC TGAAGCGAGG GCGGAGCTCC 1380
 70 GCGAGTCCA GAGCTCTGAG ATGAGGCTCC CAGGAGACTC GTGAGTGAG AGATGCGGCC 1440
 TGGAGACTCG CAGTGTATAC CAGTGTGAGA AGCTGCTCTC TGAAGCGAGG GCGGAGCTCC 1500
 AGCTCTGAGC CAGCGCGCTG AATGTGCTCA AGGCTGCTCA TCGCACAGAG GCGAGCTCTT 1560
 75 CAGAGCGGGA CAGTACACTC CCGGAGAGAG CAGTGTCTAT GAGATCATGT ACCAACCGGC 1620
 TGGCGAGCGC CTAAGAGGCG AAGAGAGTGG ACTCTCAGGA GCGAGTGAAC GAGCGAGGCG 1680
 CCGTGGCGAG CCGTGTATGG TCTGTGATGT ACTCTGCGCG CCGAGAGTTC GCGAGAGAGA 1740
 GCTCTGCTCT TGGTGTGAGA CAGGAGGCGC CAGTGTCTAT GAGAGAGGAG CAGGAGAGAG 1800
 80 AGAGAGCTCT CAGTGTGAGC TGGTGTGAGA CCGTGTCTAT GAGATCATGT ACCAACCGGC 1860
 TCTGTGCGCT TACAGTAGCC AGGCGCGGCT GCGGTATACT GCGGAGAGG CCGAGAGAGA 1920
 GAGCGAGGAG ACTGACTGTT CCAAAATATC AAGCAGAGAG ATATTATATT CAGCTCAGCC 1980
 TGGAGAGGCT TGGTGTGAGA CAGGAGGCGC CAGTGTCTAT GAGAGAGGAG CAGGAGAGAG 2040
 GTGAGAGGCT CAGTGTGAGC TGGTGTGAGA CCGTGTCTAT GAGATCATGT ACCAACCGGC 2100
 CAGTGTGAGC CAGGAGGCGC GTGCGGAGAA GCGATGTATT TCGAGAGACT CAGGAGGAGC 2160
 TCGGCTGCTC TGGGCTGCTC CCGAGGCTCC TGCACCGCGC CAGAGAGAGC CCGTCTGAGG 2220
 CTACAGAGGA GAGTCTCAAG CAGGCGGCTG GAGCAGAGAG CAGAGCTGTT CAGCTCTGCT 2280
 CCGTGTCTC CAGGAGGCT CCGAGGCTGCT GAGTGTGCGC ATTCAGGCTG TGGTGTGAGC 2340
 CCGTGTGAGA AGCGCCGAC GCGCTTCTGT GAGTGTGCGC ATTCAGGCTG TGGTGTGAGC 2400

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5 TCTGAGTGA TGCATGATGC CTCTCCCTCA GCGCAGGCTG CAGAGCCGCG CCCCACTCC 2460
 CTGCGCCCTT GAGGGGCCCC AGGCTCTCCA GCGCTACCCG TGACAGACGA CAGCTCTCTGA 2520
 GAGGCTGAG GATGTCTCTC CTGAGAGACCT TCGAGTAGAG GCGCTCCATC GCGCGATGGA 2580
 GGGCGACCTG ACCCACTCTG GCTTCTCTCG GAGAGAGGGGA AGCTGGGCCG AAAGGCCGAG 2640
 GAGGAGCAGG TGAGCTCTGC CAATGTGCGC TGCCCTCCCG AGCAGAGGCT CACAGGGCAG 2700
 GCGTCTGCTG GGTCTAGGCG TTGTGAGAGA CCGCGAGGCC TGAGAGCAGC CCGAGACCCG 2760
 CCGTCTCCA TCTCAACCA GATCAGAAC CAGGCTCTCC CAGTCAACCG TGACACAGAT 2820
 CAGGCTCAGC AGTGAACCTC GCGCTGCACC TGCTCACAGG GATGCTGGTG GCTGTGTAGA 2880
 CCGCGATGCG CACAGCGGGA TGCCATGGTC CCTTCCCGAC CAGCCAGACT GCACCTCAGG 2940
 GCGCGGGAGC CTGAGTAGTT AGGCGCTTTT CCGAACATCG ATCAATTAC TGACACTGCT 3000
 TTCTCTTGTT CAGTAGAGAG TGTGCGTCTC TCCGAGATCG CTCTGAGATC CCGACAGGCC 3060
 CACTCTGAC CTGAGTAGCC TCTGCTCACT CACTGAGGCC ATCAGGGGCC TGCCCAAGGC 3120
 CTGAGGGGCG CCTCTCTCCG TCTGTGCCCG CAGCTGCCAG GTGGCCCTGG GAGGGGGTGG 3180
 TTGTGTGTTG GGAAGGGCTC CTGCGAGGGG AGGAGAGACT GAGAGGCTTG GGGGAGCAGT 3240
 TCTTGAAACG ACTGAGCTCG AGAGAGGCCG TTAGGCGCTG TTTCTCTTTG AGCAGCTTCT 3300
 CCGCAGTGGG ACCTGAGTCC GGGTGTGCTG GTCAGCTCCC GATGCTCTGT TCTCTGGAAC 3360
 CTGACTTAG ATGTTTGTGG ATCAGAGGCC CCGAACACAG GCAAGTCCAC CCATATATTA 3420
 CCGCGCAGT CCGAGGGTGG GCTGCGGACT CTGGACAGGT GATGCCGGCG CCGAGAGACG 3480
 CAGCACTCCG GCTGCACACA GAGTGCCTAG GAGTGCCTAG TGCTCAGGCG AGTGGCCAGC CCGCTGTGT 3540
 20 CTTCTTCCA CAGGCTCCCG CACGCGCTCA GTCTCACGCG GTGACGCTGT TTCTTTTAG 3600
 TCTTGTATG AATAAAGCG TGGAAACCTA AA 3660

Protein sequence 17

Gene name: glypican 1

Unigene number: Hs.2699

Protein Accession #: NP_002072

Signal sequence: none found

Pfam domain: Glypican protein [2-490]

Transmembrane domains: none found

Cellular Localization: plasma membrane

1 11 21 31 41 51
 MELIARGNWL LCRAALVAC ARQDPASKER SOSSEVRIYQ ANGFLSDVP QAEISGEHLR 60
 ICPGVGTCTT SEMENILANR SBAELETALR DSRVLAJALR ATULRSFLMR FQRLABSR 120
 TLQATPPQAF GELITORARA FRLYSIELRL YIRGARNHLS STLARPMELR LIRLFLQIR 180
 QLLPFLVDL CLGACAGGCA PSLAPSELEL LRATRAFVAE RSTVQGLQVA SVVRKVAQV 240
 PLGPECSRIV MELVYCAHCL GVPGARPCFD YCRHVLKGLC AMQADLDABR RHLLDSMVLI 300
 IDKFWGTSYR ESVIGSVETN LABAINALQD NRDLTAEVI QGCGPKVPIV QQIPSEKSR 360
 RGLAFRPRR PSETEKLKVS EAKQALRWQD FHTSLSPFLS CSDGVALSTA LKQVQVQ 420
 RNVLYFPMK DELANQHRFP EYRVDITRDP NRITRQIMQL KINTHRLBSA YWGVDDVDPD 480
 ASDGSGSGG

DNA sequence 18

Gene name: NT-BEN-24 antigen

Unigene number: Hs.128425

Nucleic Acid Accession #: AF155102

Coding sequence: 27-908

1 11 21 31 41 51
 GCGAGGGCGA GCGCGAGGCG GTGCTCATGG AGGAGGAGCT GATCCAGCAG AGCTCTGGAG 60
 ACTAGAGACG CGCGAGGTAC AGCCCGCGCG TCGCTACCGC GCGAGAGCTG CACTAGAGAG 120
 GCGACCTGCT GAGACCGGAT GAGGACCTCG AGCGCTGCTA GCTCTCGCGC CCGACGCTCC 180
 AGTCCAGCGG AGCGACCGAC GAGAGCGGCC AGGACATCTT CTCCCGCGCG CCGAGAGAGG 240
 GCGTGGCCCA GGAAGAGGCG CAGTTCAAGC TGAGAGATGCC ACTCACCGCG AGGCGCTTAC 300
 TTGTGGCGCA CAGATCAAGG CCGACGAGAG CCGCGCTTCT CAGCCCGGTG CAGACGAGCT 360
 TCGAGTGGGA CAGATCAAC CAGACCGCAT AGGACTTTCA CAGCCGACCG CCGAGAGTGC 420
 TGCGAGGATA CAGCTTCAAC ATCTTCTTAC CCGACTTCAT GAGCAGGCC TTCAAGCGCG 480
 AGTACTTCTT GAGGCGCTCG CCGCCACACA AGGATTTGCG ATCTCTGCGC TTCAAGCGGG 540
 GCGCGCTACG AGGACATGCG TTCTCAATCT GTCAACCGCG AGTGGAGATA CTGCGACCGC 600
 CAGCGCTTCC GCTGCGAGTT TGCCACCGCC ATCTTCCAGC GTGCTCTGCA CTCTAGAGG 660
 TACCGCTATC GCGCGCGAG GCGCTGAGGA AGCGAGAGCG AGAGAGGCGC AGGCGCACAC 720
 GCGTGGCCCA GCGGAGGTGG GATGTCGCCA CGCGCGAGCG TTGTTCTTCA CCAATCGCGC 780
 GGAACATCTC CAGCAGAGCG AAJAGGAGAA GTGCTTCCCG GACCCCGGAG GGGCGACCGA 840
 65 ACTATCAGG CAGCCAGGCC CAGAGCCAGC AGAGCGCCCT CAGACACACC GCGCTTCT 900
 GGAJATAGTT CGTGTGTGTT CTTCAAGAGG ACTGTAGAGT GGAJAGAAAA ATCTTTGTT 960
 CTAAGGAAT TTGCGTATTG GCGAGATGCG ATGTTTTTTT AATAAAGCTT GTATTTTAGA 1020
 AATAAAA

Protein sequence 19

Gene name: NT-BEN-24 antigen

Unigene number: Hs.128425

Protein Accession #: AAB42868

Signal sequence: none found

Transmembrane domains: none found

Cellular Localization: plasma membrane

1 11 21 31 41 51
 GGGGAVLWE EQLTQQLSDD YNGRYEPLR LTAHLEPLDA HVLKSPHEDLO RQLSROOLQ 60
 TGDASEAR DFFPRRAKES YGQGNQAFSV EMPLTGKAYL WADKYRPRKP RFFRHVHTGV 120
 RHKYQHTFY DFDNPPPKIV MCTDRIESTPE DLIDRSTPEE YLEACADNR DRAILRPTRG 180
 LRGRFPQDR QRVGLIAPP RLPLPVCQRR LPAVLSGLAL PLSNFTALGR GQVQGRAT 240
 80 PQRSEWPE RQACGASDGG NIDNSKSTGS ASRTPGDPFM LTRQGPQTH SPSQTRLIN 300

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DNA sequence 19

Gene name: tumor necrosis factor receptor superfamily, member 1A

Unigene number: Hs.159

Probeset Accession #: BE295782

Nucleic Acid Accession #: NM_001065

Coding sequence: 256-1623

	1	11	21	31	41	51	
10	CGGCCGATG	ATCTTGAACT	CGAAGGCCA	GAAGCTGGAC	CTACGTCAG	AGAACTCTGA	60
	GAATATAGG	CGAGAGAGT	CGCTGGGAC	AGAGCTGAT	CTCTATGGC		120
	GAGTCTCAAC	CTCTACAGT	CGACCCAGAG	CATTGGAGC	GTCTGTGACA	GACATGATCT	180
	CGGGAAGGCC	CAGCACTGCC	CTCTCCACAC	TGCTCTGAGC	CGAAATGGGG	GAGTGAGAGG	240
	CAATAGACGT	TGCGCATGAG	CTCTCCACAC	GTCTCTGAGC	TGCTGTGAGC	CTGCTGTGCT	300
15	CTGAGAGCT	TGCTGGAGAT	ATACCCCTCA	GGGTTATAT	GAGTGTCTCC	TACCTTAGGG	360
	GACACGGAGA	AGAGAGTAGT	TGCTGTCTCC	CAGGGAAGT	ATATCTCCCC	TCGAAATAT	420
	TGATTTGCT	GTACCAAGTG	CCACAAGGA	ACCTACTGT	ACATGACTG	TCCAGGCCCG	480
	GGGACAGATA	CGAGCTCAG	CGAGTGTGG	AGCGGCTCT	TACCCCTCT	AGAAAAACAC	540
	CTCAGACAT	GCTCCAGCT	CTCCAAATGC	CGAAGAGAA	TGAGTGGAT	GCGAATCTCT	600
20	TTCTTCAGC	TGACACGGG	CTCCCGTGT	GGCTCCAGA	AGAACCGTA	CCGCACTAT	660
	TGAGTGAAG	ACCTTTTCCA	GTCTCTCAT	TGCAAGCTCT	GCCCTAATGG	GACGCTGCAC	720
	CTCTCTGCC	AGGAGAACCA	GACACCGTG	TGCACTCTCC	ATCGAGGTT	CTTTCTAAGA	780
	GAAGACGAT	GTGTCTCTG	TAGTAACTGT	AGAGAAAGC	TGAGATGAC	GAGTGTGTG	840
	CTACCCGGA	TGAGAGATG	TAGGGGACT	GAGGCTCTG	GCAACACAT	GCTTTTGCC	900
	CTGGTCAATT	TCITTGHTCT	TGCTCTTTA	TCCTCTCTCT	TGATGTGTT	AATGTAATCC	960
	TGACCAAGT	GGAGGTCCAA	GCTCTACTCC	ATTGTTTTGT	GGAAATGAC	ACCTGAAGAA	1020
	GGGGGGGAGC	TGAGAGAAC	TAGTACTAG	CCCTCTGGCC	GAACCCAGG	ACTGATCTCC	1080
25	ACTCGAGCT	TGCTGGACT	CTCTGGCTTC	AGTCCCTGC	CGATGCTAC	CTTCAAGCTC	1140
	AGCTCCACT	ATACCCCGAG	TGACTTCTCC	AACTTTGGG	CTCCCGGAG	AGAGTGTGCA	1200
	CAACCCATAC	AGGGGGCTGA	CCCCATCTT	GGACAGGCC	TGGCTCCGA	CCCCATCCCC	1260
30	AAACCCCTTC	AGAGTGTGGA	GGAACGCCCC	CACAGCCAC	AGAGGCTAGA	CACATGATCG	1320
	CTCCGAGCC	TGTACCCCT	CGAGGACAG	GTCCGCCCT	TGGCTGTGA	GAATATCTGT	1380
	CGAGGCTAG	GGCTGAGCA	CGACACAGC	GATCCGCTG	AGCTGTGAA	GGGCTCTG	1440
	CTGCGGAGG	GGCAATACAG	CATGCTGGG	ACCTGAGGC	GGGCGACGCC	GGCGGGGAG	1500
	CGACGCTGG	AGCTGCTGGG	AGCGGCTCT	CGGACATGC	AGCTCTGGG	CTGCTCTGAG	1560
35	AGCATATGCT	AGGCGCTTG	GGGCTCTGG	GGCTCTGCG	GGGCGGCGC	CTCTCTCAGA	1620
	TGAGGCTCG	CCCTCTGGG	CAGCTCTAG	GAGCTCTCTG	AGGCTCTCTG	GGGCTCTCTG	1680
	ACTTTTTCT	GGAAAGAGG	GGTCTCTAG	GGGCTAGAG	CGGCTCTAGC	CGGCTCTACT	1740
	GGTCTTAAC	CCTCATGTA	CATAGCTTT	CTCAGCTCT	TGGCGCGCG	CGAGCATGAC	1800
40	CGGCTCTAG	CGGAGAGAG	GTCCGCTTG	GGCTCAGAG	CTGATGTGG	TGTTTGTGGA	1860
	GGATGAGGA	AGCTCTCT	CATGCTCTT	TGGCTCTG	TCAGCGGGA	GAGCTCTG	1920
	GGGCGGCTG	TGCTGCTCT	AGGCTTTTT	ACAGTGTGA	AGGATTTTT	TGTTTGTG	1980
	TTTGTGTT	TTTGTGTT	AATCAATCA	TGTTACACT	ATAGAACCT	GGCACTCTG	2040
	TGCTCTGCG	CTGACAGC	ACATACAGG	CTGAAGTTC	CTAGAGCAG	GGGCGAGCG	2100
45	GACCAATGG	GCTCTGAGT	GGAGCTGGG	ACTTTGTAC	ATAGCTAAA	ATCTGAAGT	2160
	T						

Protein sequence 19

Gene name: tumor necrosis factor receptor superfamily, member 1A

Unigene number: Hs.159

Protein Accession #: NP_001056

Signal sequence: 1-29

TMH domain: 41-61, 84-125, 127-166, 168-195

Transmembrane domains: 211-234

Cellular Localization: plasma membrane

	1	11	21	31	41	51	
55	MGSLTTPDLL	LEPLVLELLV	GIYPSOVLGL	VPHLGDRER	DSVCPQKRY	HPQANSICTD	60
	KCHGTLYLNI	DCPOPGDPTD	CRECESGFT	ASRNLKSL	CKSKRKBKG	QVSISSCTVD	120
	RDVVOGRH	QYRHWSEN	FQCPWCLCL	NGTVHLCQR	KQNTVCTGA	GFPLRMRVC	180
60	SCSKSKSLK	CTGLGLPTE	NRGTEDSGT	TVLLPLVIF	GLCLLLELFI	GLMYTGRMK	240
	GKLKSLVQKE	STPKRDELA	GTTLPLAPM	PEISPTPTG	PLGASPPPS	STTDSSTYT	300
	PGDCNFAAP	RREVAFFPG	ADPLATLATA	SDPIFWFLQK	WEDSNAKPS	LDTEPATLY	360
	AVYENVPFLR	NKRFVKRLG	SUEIDLELE	QNGRCLEBAQ	YSNLATMRG	TPREATLEL	420
65	LGRVLKDEL	LGCLDIREA	LGPALPPA	PSLLR			

DNA sequence 20

Gene name: prominin (mouse)-like 1

Unigene number: Hs.112360

Probeset Accession #: R04057

Nucleic Acid Accession #: NM_006017

Coding sequence: 38-2635

	1	11	21	31	41	51	
75	CCAGGTCTCA	CTCATGTTT	GGAGATCTT	GCTAGCTATG	CGCCTGTAC	TGCTCTCCCT	60
	GTCTCTCTG	GGGCTTGGG	GGAGCTCTT	TTGAGGAGG	CAGCCTTCAT	CCACAGATGC	120
	TCTTAAGCT	TGGATTTAT	AATGTGCTG	AACAAATAT	AGACCCAGC	ACTCCATAC	180
80	AGCTGAGAG	ATCTGCTTC	TCTTTAACT	AGTGCATATC	TTTCTCTAT	TGGHACAGC	240
	CTGTGATTC	CTGAGAGTA	CTTTAGAAA	ATTCTTACG	AGGCTAGAT	ATCTCAAT	300
	TGATTTAGC	AAAGCAAGAA	CTTAATATT	AGCTCTAAG	ATTGTCTACT	ATAGAGGCG	360
	GATTATTCTA	TCTGTGTGC	TGGGCTGCT	GTTTATTAT	CTGATGCTC	TGTTGGGTA	420
	TTTCTTTTG	ATGTTGCTT	GGTGAACAA	ATGTTGGGA	GAATGAGAC	AGGCAACAA	480
	GGAAATGGG	CTCTCTCTG	GGAAAGCTT	TGCATCTCT	CTTTTGGTA	TTGTATAT	540
	AATAGCAAT	GGCATCTCT	ATGTTTATT	GGCAATATC	CAGGTAGAA	CCGCAATCA	600
	AAGAGTCCG	AAATGTCAG	ATAGCAATT	CAAGCACTG	GAATCTCTT	TGATGTAAC	660

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	TCACAGACAA ATCAATATA TATTGGCCCA GTACCAACCT ACCAAGGACA AGGGGTTCAC	720
	AGATCTGAC AGTAAATAT GGTGCTGAG AGCGGCAAT CTGTAACGAC TGACACCAA	760
	GTACTCTCT GTTCTTGAG AGATTAGCT CAYGCGACCA GGGATCAAGG AGACCAAGA	840
5	GGCGTTGGAG AACATGACA GACACTTGGA AGCTTGGAC CAATCAAGTA AGCTGTTAG	900
	CAGCACTCT ACCAGGGTGA AAATAGCTG GGGGTCACT CTCAATGACC CTCGTGCTT	960
	GGTGACTCA TCAGGTGAAA CCTGCAACGC CATCAGATG TCTCTAGGC ACAGTAACT	1020
	CAACCTGAA CTGAGGAGCT TCCACCTCT GATGCGAAA CTGACAGAG TTAATAAGT	1080
	TCCTAGGACA GATTGTGAT GCGCTGCTCA ACAGGGCTAT CAATCCCTTA ATGATATACT	1140
	TGACGAGATA CAACGCCAAA CCAGGACTGT GCTAGCGGT ATCAAAAGGG TCTTGATCT	1200
10	GAATGGTTCA GATATGATCA ATTGTAACTA GGGTCTTCT ATTCAAGATA TACTCTCAG	1260
	TTCTCTGTT TATGATGTA AGCTGAGAG TTACATATC AGAAATTTAT CTACATCTGA	1320
	AGAGTATGAT TCATATGTTT GGGCTGGGTG CCGCTGATC TGCTCTCTGG TGACCTCAT	1380
	CGTGTATTT TACTACCTGG GCTTACTGTG TGGCGTGTG GGGTATGACA GGCATGCCAC	1440
	CGGAGCACCC GAGGGCTGTG TCTCTCAGAC CGGAGGATG TTCTCTATGG TGGAGTTTGG	1500
15	ATGAGTTTTC CTTTCTTCT GGAATATGAT GATCATGTG GTCTTACTT TTCTCTTGG	1560
	TCGCAATGTG GAAAGACTGA TCTGTGAACC TTACACGAG AAGGAATTAT TCGGGTTTTT	1620
	GGATACACCC TACTACTTAA ATGAGGACTG GGAATACTAT CTCTCTGGGA AGCTATTTTA	1680
	TAAATCAAAA ATGAGACTCA CTTTGTGACA GGTTTACAGT GACTCCGAAA AAATAGAGG	1740
	CATTCTAGGC ATCTCTCAGC TCGCGAGAGC GATGATATC ATGAGACAT TCACATTTAA	1800
20	TGCGATCTCT GGAAGCTAAA GCGATGAATT GGAAGCTGG AGGATTAAT TTAATATCT	1860
	TCGTGTTGGT GCGACAGGAA GAAAAAACC TCAGGATTTT GCTGCTGTTG GAATGACAG	1920
	AATGAATTAT GACAGACTCT TGCGTCAAGC TGGTAAATCC CCGCAGGAG TGATCTTTT	1980
	ATCATTTGCA TATGATCTAG AAGCAAAAGC AACCGTTTGT CCCCAGGGA ATTGAGGAA	2040
	CTCCGTGAAA AGAAGAGGAC AACTATTATA AACATTTTGT CAGCAAGAG TCGTCTCAT	2100
25	AGAACATCA CTGAGCACTC TATACCAAG GTCGAGATA CTTCAAGCA CAGGAAGATG	2160
	ATTGTTGGAG AGGATTAATA GGAATCTAG TTCTCTGAG TTTCGTCAGA ACTTCATCAC	2220
	AAACATACTT TCTCTGTTA TTATTAAGGA AACTAAGAG TATGAGGAAA CATGATAGG	2280
	ATATTTTGA CATATCTGC AGTGAATGA GTTCTCTAC AGTGAAGAG TGCACTCTG	2340
	CNAACCTGTG GCCAACGCTC TAGATATGCT TGTTGAATCT TTCTGTGTA GCTACATAT	2400
	CGAACCTGTG AATTGTTTTT GTTGTGGCAT AGGAAGATCT ACTGTATTTT TACTTCGCG	2460
30	TCTATATTTT GCGGTAAAC TGCGTAAATA CTATGTGGA ATGAGTATCG AGACATGTA	2520
	CGATGATGTA CATATCTGC AGTGAATGA GTTCTCTAC AGTGAAGAG TGCACTCTG	2580
	AGATCATGTA TATGTTATTC ACATATCTGT TATGACAGC CCATCAGAAC ATTGATAGT	2640
	GATGTTGAAA CTGCTTGAGC ATCAGGATAC TCAGAAATGA AAGGATCACA GATTTTGGT	2700
	AGTTTCTGGG CTCACAGGAA GTTCCATAC CAGAGGAAA CGCCAGTGGC AAGCATAGTA	2760
	CTCAGAGGAA CAGCATCTGC TATGTCGAT TATTCAGTA AGATATGAC TGGTCAAG	2820
	ACAAATCAAGT TATATGCGT CTGCAACAT TATTCAGGAA TGACTCTCTC CTTTCTGTC	2880
	TATTTTGT TTATGACTTT TTACACTGAG TTCTATTTA GACATACACA CAZATGGGGT	2940
	GTTTTGTCCC ATTGATGCA TTTCATGCA AACTCTATCA AATGTAGAG CTAGATTTCTA	3000
40	ACAAATGCC ATGGGTGGAG GTTCTGAGC ATGAGCAAGT TTACAGAAA GATGATTTT	3060
	GTGACAGCA AAGCATGAT ATCTCTGTT TTACACAGCA GTTTTITAAA CAATAGATA	3120
	TTATAGACTT TCTCTTAAA TGAGCTAAAT AAGTCAACAT TGACTCTGT GTGCTGTTGA	3180
	AAATATCCCA TTTCAGTAA AAGTGTGTGA AACTCAGAG ATATTTCTCA CCAGAGATAT	3240
	TTCTATATAT ATACTTTATC AAGATTTGCG CTTGTTCCAC TTGSAAGTG CATGCAAG	3300
45	CGATCATG CAACACTGG TACTCTCTC TGCAATCT AAAGAGAGG AGGATCTTT	3360
	GGAGGAGAAA TGCTGTTGTT TCAGAAATGG ACTGTTATTA ACAGATGCCA ATTAGCGTGT	3420
	ACAGTTTAA ACAGTTTCTT GTTGCAATG GATAAAATAT AATTGGAGTG GAGCTAACAT	3480
	GGATCATC AGATAGATAT CAGGTGTTCT AAATGAATAT ATGAAAGAT CTGTTACAA	3540
	TTCTGATAT TGTTGTGAG CATGAGTAA ACTGTTGAT TTGTTGCTTA AATTGATG	3600
50	AAAGCACAG GTAATATCT ATTGCTTCA GGAATGTTCA GTTGATGTCG TCAATTACAA	3660
	AAGTGATGAG CAATGAAGAA CTGGTGGAC AAAATTTAAC GTTGATGTTA TGAATTTCA	3720
	GATGTAGACA TCCGCCGAG GTCTTTTAT GTGCAAGTTG CAGTCTGAT TCAATTGAT	3780
	AAAAGGAGAC TTGGC	

55	Protein sequence 20	
	Gene name: prominin (mouse)-like 1	
	Unigene Number: Hs.112460	
	Protein Accession #: NP_066008	
	Signal sequence: 1-21	
	Transmembrane domains: 105-127, 157-179, 438-460, 482-504, 784-806	
	Cellular Localization: plasma membrane	
	1 11 21 31 41 51	
65	NALVLGSLLL LGLCNSFSG QQPSTDAFK AMVVELPATN YTGQDSEKAG PIGILFLVH	60
	IFLYVQFROD PVDLTKRFL QYAFSEKIDH DEFEYVLGL KIVYFNGHJ LCVGLKFT	120
	LIHFVWVDF CWKCTCRQD GSGHSDQDWH GFLKELPA SILVCTIIS IGFYFVAM	180
	HOVETRIKRS KKLADENFDQ LHTLLNTEPE QIKYILAQYN TTQKAFTHL INSNVLOGG	240
	ILDRLENRII PVLDEIKSMA TAIKRTKRL EBNSTLKLK HQOSTLSSS LTSVKSLSL	300
	SLNDPLCLVR PSSTCHSIR LIGLSLNSNP ELNOLPPVDA ELDMNVNVLK TDLGLSGTG	360
70	YQSLIDNDFR VQVSLGVPIA GIVTGLVHGF FQIQLGLAF VYNNVYVH	420
	HNHLPTLEY ISVHSLGGLV ICSLLTLIVI FFYLLGLLCV QYDSHATPT TGGVSNFTG	480
	VFLMVGVGLGS FLPCQILMI I VVLTVFPGAN VEKLICEPT SKELFVRLDT FYLLNDWEX	540
	VFLGKLNKNS KMKLTEDVY SCKCKNGYH GTULQNSPW ISRHLLNDR TQSISSLEGS	600
	LDVNLNPLF GAKSEKFLF GIVTGLVHGF SPQNLNGLF AYLKLEKNS	660
75	LPQNLNLSL KEDATYIKI HOORVLPIFO SLSTLYOSVK ILQRTGNILL SRVTEILASL	720
	DFQNFITIN TSIVSIRKTK KYRGTIIQGF EHYLVNIRFS ISKVSACPK VATALDTAD	780
	VFLCSYIIDP DLNLFPGIIG ATVPLLPALI FAVELAKYTR HNSDESVYDD VETIPMRNG	840
	NKNGYKEDH VYGHNPVNT SPSSH	

80	DNA sequence 21	
	Gene name: G protein-coupled receptor 39	
	Unigene number: Hs.85339	
	Nucleic Acid Accession #: NM_001508	
	Coding sequence: 1-1362	

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	1	11	21	31	41	51	
	ATGGCTTCAC	CCAGCTGCC	GSGAGTGAC	TGCTGCCAAA	TCATTGATCA	CAGTCAATGC	60
	CCGAGTTTG	AGGTGGCCAC	CTGATGAAA	ATCACCTTA	TTCTCGTGA	CTGTGATCAT	120
5	TTCTGATGG	GGCTCTGGG	GACAGGGCC	ACACTTCGG	TACCCAGGT	CTGACGAGG	180
	AAAGTAACT	CTGAGACGA	GCTGACAGC	CACTGATGA	CTTTGGCTT	CTGACGATC	240
	TTGTGTGTC	TCATCGCAT	GCCACAGAG	TTCTACAGA	TGATCTGAA	TCCTCTGAC	300
	ACGTCAGCT	ACAACCTGT	CTGAGCTG	CACACTTCC	TTCTGAGGC	CTGCACTAC	360
	GCTACGCTG	CCCTAGTGT	GACACTGAG	TTTGAAGCT	ACATGTCAT	CTGTGACCC	420
10	TTCTGATCA	AGGCTGTGC	GGAAGCTGC	CAGTGAAGC	TGCTGATGG	CTTGTCTGG	480
	CTCACTCGC	CCCTGATGC	ACAGCGCTG	CTGTGTGCA	TGGGTACTA	GTAACCCCTG	540
	GTGAAGCTG	CCAGCAACG	GATCTCTCT	TGCAACGCT	CCAGCACCC	CCACACGAG	600
	CAGCGGAGA	CCTGCATAT	GTGCACTGT	ACCAACTCT	CCAGCGCTG	GACGTGTTC	660
	CAGTCAAGA	TTCTGATGC	CTGCGTGC	TACTGCGG	TCTCTCTCT	CGAGACTTC	720
15	ATGCTGGA	ACATGATGA	GAGCTCAT	AAAGACAGA	GGGCTGCT	GACCGGCGC	780
	ACGCGGCTC	CCAGCTGAG	GAGTCCGAG	AGGAAAGGA	CAGGAGCCG	CAGGAGCGG	840
	ACCATCATC	TCTGAGCT	GATTGTGTT	ACATTGCGC	TATGCTGAT	GCACCAACG	900
	ATTGAGAGA	TGATGACTC	GCTCAAAAC	AAGCAAGCT	GACAGAGCT	CTACTCCGG	960
	GCTGACAGA	TCTCTCTC	CTTCTCGAG	ACCTTTTCT	ACTCAGCTC	GATCAACAC	1020
20	CGCTCTGCT	ACAGCGTGC	CTGCGAGAG	TTTGGCGGG	TGTTCTGTCA	GATCTGTGC	1080
	TGCGCGCTG	CGCTGACGA	GGCAACAC	GAGAGCGCC	TGCGGTACA	TGCGACTCC	1140
	ACCAACGGA	GGGCGGCTT	TGTGACGCG	CGTGTGCTT	TGCGGTCCG	GCGCGACTC	1200
	TCTGACAGA	GAGCTGAGA	GATTCTCTA	AGCATTTTC	AGAGGAGGC	CGAGCGGAG	1260
	TCTAAGTCC	AGTCATTAG	TCTGAGTCA	CTAGAGCCA	ACTGAGGCG	GAAACAGCC	1320
25	AATTCCTGC	CAGAGATGG	TTTTCAGAG	CATGAAGTT	CA		

Protein sequence 21

Gene name: G protein-coupled receptor 39

Unigene number: Hs.65339

Protein Accession #: NM_001508, NP_001409

Signal sequence: none found

Pfam domains: 7tm_1 [72-172, 224-344]

Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342

Cellular Localization: plasma membrane

	1	11	21	31	41	51	
35	MASPSLPSD	CSQIIDHSRV	PEFEVATWIK	LTILVYLII	FVWGLGNSA	TIRVTQVLQK	60
	KYVLQKRVLD	HMSVLACSDI	LVFLIOMPMR	FVSIINPLT	TSYTLCKLK	HTFLFEAGSY	120
40	ALLGLAVLFL	FERTIAICHP	FETKAVSGCC	GVLLLIQPN	VTSALVAFLL	LFAMKEITPL	180
	TVYVSHRGLT	CRSRLPSTG	QPTENRNIC	GLSDLSWYF	QESIPUNYV	YLVLLSLVAF	240
	MCNNYQVLV	KSQGSLAAG	TEPPQLRKE	BEBSRTAKSQ	TIIFLRLIVV	TLAVQVMPNQ	300
	IRIVIAAAXP	IGDHTFRSY	ATMILLPFE	TFYFLSVIN	PLLTVSSQG	PRVLPVQVLC	360
	CRSLQAHAK	EKLRLVHMS	TDSARPVQR	PLLPASRRQS	SARKTRKPL	STPQSRAPQ	420
45	SISGLSELES	LEPNSGALPA	HGAANQPS	HEV			

TABLE 8A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 8A lists about 1260 genes up-regulated in glioblastoma tissues. These were selected from 59680 probesets on the Affymetrix/Exon-Hu30 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Key: Unigene: Unique Exon/ProbeSet Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 RT: Ratio of 75th percentile tumor to 85th percentile normal body tissue

	Key	ExAccn	UnigeneID	Unigene Title	RT
60	431917	D16181	Hs.2888	peripheral myelin protein 2	75.2
	423343	A168044	Hs.17877	protein kinase C binding protein 2	74.6
	45801	A369080	Hs.816	SRY (sex determining region Y)-box 2	74.2
	428321	A169994	Hs.2668	peripheral myelin protein 2	71.6
	412719	AW016610	Hs.129811	ESTs	70.7
65	444904	AW237014	Hs.15359	Homo sapiens cDNA FLJ23075 fs, clone L	66.3
	415517	U85867	Hs.7887	protein tyrosine phosphatase, receptor-L	64.3
	413472	BE242870	Hs.75319	solute carrier family 1 (glial high affinity)	60.1
	456759	BE29150	Hs.127792	delta (Drosophila)-like 3	52.3
70	432147	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp751C172 (f	46.7
	425842	A1681490	Hs.19823	NK-2 (Drosophila) homolog B	46.3
	412733	AA984472	Hs.74554	KIA0000 protein	39.0
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	38.7
	453392	U23752	Hs.32094	SRY (sex determining region Y)-box 11	37.2
	422849	AL1157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp781J1324 (f	36.8
75	413333	M14028	Hs.75297	fibroblast growth factor 1 (peptide)	32.6
	416829	AB013805	Hs.60220	catenin (cadherin-associated protein), d	31.6
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	31.8
	438676	BE485204	Hs.47148	ESTs	31.4
	426325	D26114	Hs.163009	myelin-associated oligodendrocyte basic	30.9
80	425057	AA82634	Hs.1619	achilles-seal complex (Drosophila) homolog	30.4
	446711	AF163692	Hs.12450	protocadherin 9	30.2
	439415	F65538	Hs.12825	ESTs	26.3
	430838	N46604	Hs.163095	hypothetical protein FLJ12015	25.9

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	429466	ME5035	Ha.12827	ESTs	25.9
	447004	AW296968	Ha.157539	ESTs	25.3
	424581	ME2062	Ha.150917	catenin (cadherin-associated protein), a	24.8
	452744	A297652	Ha.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (r	24.3
5	411285	NM_002374	Ha.167	microtubule-associated protein 2	24.3
	453642	AK70936	Ha.34074	oleuropein-lipidase VI	24.3
	424140	Z48051	Ha.141308	myelin oligodendrocyte glycoprotein	24.2
	450133	AW697979	Ha.105201	ESTs	24.2
	408662	AK56223	Ha.31141	Homo sapiens mRNA for KIAA1568 protein,	23.3
10	449672	AW65111	Ha.225106	ESTs	22.7
	436708	AI362940	Ha.75199	ESTs	22.0
	407034	UB4540		ghv-human dystrobrein isoform DTN-3 (DTN	21.9
	401198	R45175	Ha.117183	ESTs	21.7
	431019	NM_005249	Ha.2714	Arifadest box G10	21.5
15	409049	AK23132	Ha.146343	ESTs	21.4
	433896	AW294729	Ha.274461	ESTs	21.1
	445041	TC4193	Ha.282382	solute carrier	21.0
	418738	AW386533	Ha.5682	solute carrier family 7, (cationic amino	20.4
	444378	RA1339	Ha.12689	ESTs	20.0
20	411305	BE241596	Ha.69547	myelin basic protein	19.9
	437414	AW694071	Ha.48448	hypothetical protein DKFZp547C175	19.8
	441016	AW138653	Ha.25845	ESTs	19.6
	440455	ALJ42201	Ha.21273	transcription factor NYD-spt10	18.5
25	438209	AL120699	Ha.61111	aryl hydrocarbon receptor nuclear trans	18.4
	452461	N78223	Ha.108106	transcription factor	18.1
	405395	U46745	Ha.54435	dystrobrein, alpha	18.1
	417163	RS2269	Ha.172717	ESTs	18.1
	407838	AW460420	Ha.21535	ESTs	18.0
	428392	H10233	Ha.2285	secretory granule, neuroendocrine protel	18.0
30	449611	AI870394	Ha.197075	ESTs	17.0
	446932	Z44514	Ha.195929	Homo sapiens mRNA for KIAA1763 protein,	16.9
	429288	AA493272	Ha.105395	hypothetical protein FLJ12015	16.9
	444471	AB020694	Ha.11217	KIAA0877 protein	16.8
35	421659	NM_014459	Ha.106511	protocadherin 17	16.7
	431725	X05724	Ha.2839	Hemle disease (pseudoglossia)	16.6
	422276	AF269085	Ha.109812	G-protein-coupled receptor 51	16.6
	419922	L24489	Ha.80409	growth arrest and DNA-damage-inducible,	16.5
	441440	AB079891	Ha.50495	ESTs	15.7
40	449433	AB720996	Ha.9012	ESTs, Weakly similar to S2650 DNA-bind	15.7
	421284	AL109123	Ha.103542	microtubule-associated protein 18	15.5
	419810	U20350	Ha.78913	chemokine (C-X-C) receptor 1	15.1
	413597	AW302865	Ha.117183	ESTs	15.1
	424845	AJ221919	Ha.173438	hypothetical protein FLJ10582	14.9
45	441614	DB2343	Ha.19361	neuroblastoma (nerve tissue) protein	14.9
	422299	H15302	Ha.159350	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	14.8
	416857	AA188775	Ha.229453	ESTs	14.7
	419721	NM_001650	Ha.238650	aquaporin 4	14.6
	411078	AJ222020	Ha.192364	CocosaCrip	14.4
50	451924	RA4936	Ha.24686	ESTs	14.4
	403699	AB007979	Ha.301284	Homo sapiens mRNA, chromosome 1 specific	14.3
	430130	AL137311	Ha.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (14.1
	410909	AW898161	Ha.53112	ESTs, Moderately similar to ALU8_HUMAN A	14.0
	412266	N58006	Ha.26133	ESTs	14.0
55	412286	X81120	Ha.75119	corneal endothelial receptor 1 (brain)	14.0
	424790	AL119344	Ha.13326	ESTs, Weakly similar to 2004399A chromos	14.0
	439229	AO31540	Ha.235331	ESTs	14.0
	441459	R31064	Ha.23172	ESTs	14.0
	445495	BE522641	Ha.38469	ESTs, Weakly similar to 130222 hypotheli	14.0
60	414245	BE148072	Ha.75580	WAS protein family, member 1	13.7
	429900	AA460421	Ha.30875	ESTs	13.6
	448595	AB014544	Ha.21672	KIAA0644 gene product	13.6
	448605	AW138591	Ha.139416	ESTs	13.6
	452265	Y93637	Ha.280740	hypothetical protein MG23040	13.6
65	426547	AF155140	Ha.58738	gonadotropin-regulated testicular RNA ho	13.3
	441350	AB020690	Ha.7792	peranemoplastic antigen MA2	13.3
	424077	AW912260	Ha.87767	ESTs	13.2
	424120	T80576	Ha.299292	ESTs	13.2
	450965	AW131888	Ha.172792	ESTs, Weakly similar to hypothetical pro	13.2
	423361	AW170055	Ha.47628	ESTs	13.1
70	429409	AW117207	Ha.98523	ESTs	12.9
	417160	NT6497	Ha.1787	proteolipid protein 1 (Pellegrini-Merzba	12.6
	451621	AB79248	Ha.26770	folly acid binding protein 7, brain	12.5
	411379	AI816344	Ha.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
75	438954	AA740151	Ha.130425	ESTs	12.4
	430691	CI1487	Ha.103538	ESTs	12.4
	433531	AB865444	Ha.124560	protocadherin 9	12.4
	422544	AB018259	Ha.118140	KIAA0716 gene product	12.2
	427540	R12014	Ha.20976	ESTs	12.1
80	435024	AF218942	Ha.24889	formin 2	12.1
	418449	P23329	Ha.6826	ESTs	12.1
	428945	AL157579	Ha.153610	KIAA0751 gene product	11.9
	424671	A005968	Ha.134779	EST	11.9
	444396	T65213	Ha.4257	ESTs	11.8

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5	457752	AW044058	Hs.33578	KIAA0650 protein	11.8
	425523	AB007948	Hs.158244	KIAA0479 protein	11.8
	416072	AL110370	Hs.79000	growth associated protein 43	11.7
	440184	AB002257	Hs.7022	deficator of cyto-kinesis 3	11.7
	428618	AL373234	Hs.194965	ras homolog gene family, member 1	11.6
	447483	AK001468	Hs.62180	actin (Drosophila Scargel homolog), act	11.6
	448255	AA457044	Hs.20887	hypothetical protein FLJ10352	11.6
	414214	D45558	Hs.75919	glycoprotein MGA	11.5
10	426862	NM_005097	Hs.194704	leucine-rich, glycosylated 1	11.4
	402338				11.4
	420382	U75734	Hs.87206	huntingtin interacting protein 1	11.4
	422580	N46569	Hs.76722	CDAT/enhancer binding protein (CEBP),	11.4
	424518	R13582	Hs.105903	myelin-associated oligodendrocyte basic	11.4
	434777	X77748	Hs.5788	glutamate receptor, metabotropic 3	11.4
15	451952	AL120173	Hs.301663	ESTs	11.3
	408829	NM_006042	Hs.48384	heparan sulfate (glycosamin) 3-O-sulfot	11.3
	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	11.3
	425418	AC381028	Hs.118765	ESTs	11.3
	429818	AW073586	Hs.115583	ESTs	11.3
20	443912	R37257	Hs.164780	ESTs	11.3
	448743	AB032962	Hs.21866	KIAA1136 protein	11.3
	420562	AA814043	Hs.88045	ESTs	11.2
	408461	AAW41597	Hs.167408	ESTs	11.2
25	411642	NM_014932	Hs.71132	neurotrophin 1	10.9
	415170	RA4386	Hs.164578	ESTs	10.8
	428520	W47595	Hs.169300	transforming growth factor, beta 2	10.8
	459568	AL050708	Hs.25159	Homo sapiens cDNA FLJ10784 fl., clone NT	10.8
	425799	T08133	Hs.182908	Homo sapiens mRNA for KIAA1872 protein,	10.8
30	423853	AB011537	Hs.133456	sit (Drosophila) homolog 1	10.7
	400293	N51002	Hs.306480	Homo sapiens mRNA; cDNA DKFZp761E2112 (I	10.7
	447773	AA233830	Hs.30759	ESTs, Weakly similar to putative p150 (H	10.7
	448321	NM_005683	Hs.20912	adenomatous polyposis coli like	10.5
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
35	440684	AZ53123	Hs.127356	ESTs, Highly similar to S21424 neslin (H	10.3
	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	10.3
	433380	T05430	Hs.5194	cholesterol sulfate proteoglycan SHAB/B	10.2
	440471	AA085146	Hs.307944	ESTs	10.2
	413083	AL035737	Hs.75164	chitinase 3-like 1 (cartilage glycoprote	10.1
40	439578	B139460	Hs.124673	Homo sapiens cDNA FLJ11477 fl., clone HE	10.1
	448802	Z45918	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76116192 (I	10.1
	424932	R14070	Hs.315369	Homo sapiens cDNA; FLJ23075 fl., clone L	9.9
	431721	AB032996	Hs.268044	KIAA1170 protein	9.9
	419088	AJ538323	Hs.52820	integrin, beta 8	9.8
45	420602	AF065877	Hs.99236	regulator of G-protein signalling 20	9.8
	436511	A4721252	Hs.291502	ESTs	9.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	9.7
	449539	W08363	Hs.58446	ESTs	9.7
	412559	D87458	Hs.75090	KIAA0282 protein	9.6
	412811	H05382	Hs.21400	ESTs	9.6
50	445930	AI659669	Hs.227185	ESTs	9.6
	428344	H41821	Hs.322469	transcriptional activator of the c-fos g	9.5
	419271	N34901	Hs.238632	ESTs	9.5
	415078	M83119	Hs.89584	insulinoma-associated 1	9.4
55	451518	AB00515	Hs.12024	ESTs	9.4
	422655	AJ870435	Hs.1569	LIM homeobox protein 2	9.3
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	9.3
	414175	AJ338876	Hs.103848	hypothetical protein DKFZp761D112	9.3
	415278	F04337	Hs.1447	glial fibrillary acidic protein	9.3
60	428784	Y12851	Hs.193470	purinergic receptor P2X ₂ , ligand-gated io	9.2
	425903	AL134197	Hs.83597	cyclic-nucleotide kinase 5, regulatory su	9.2
	424641	AB001108	Hs.151413	glia maturation factor, beta	9.1
	417435	NM_005181	Hs.82129	carbonic anhydrase II, muscle specific	9.1
	449448	D60730	Hs.57471	ESTs	9.1
65	408508	AI806109	Hs.135738	KIAA1580 protein	9.0
	452785	AL365942	Hs.296434	erythroid differentiation and demucosif	9.0
	448686	H47169	Hs.18653	hypothetical protein FLJ14627	8.9
	447072	D61594	Hs.17276	tyrosine-protein sulfotransferase 1	8.9
	433900	AI034361	Hs.135150	lung type I cell membrane-associated gly	8.9
70	408926	AF217625	Hs.49002	Down syndrome cell adhesion molecule	8.8
	445626	NM_014263	Hs.23756	otzf (odd Ozten-m, Drosophila) homolog 1	8.8
	400352	AA250737	Hs.72472	ESTs	8.7
	417404	NM_007350	Hs.82101	precalsin homology-like domain, family	8.7
	420345	AW256230	Hs.25231	ESTs	8.7
75	425627	NM_001115	Hs.2522	aromatase cytochrome b (brain)	8.7
	437528	N55546	Hs.169745	crinoid (Drosophila) homolog 1	8.7
	440152	AB002376	Hs.7005	KIAA0378 protein	8.7
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	8.6
	400780				8.6
80	434991	AA814305	Hs.125653	ESTs	8.6
	449277	AA001064	Hs.172876	ESTs	8.6
	451709	AA645850	Hs.278550	ESTs	8.5
	439547	AB006827	Hs.5788	alpha-tubulin	8.5
	447197	R36875	Hs.19355	glycylglycyl-11 Soames placenta h22HP Homo	8.5

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	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fic, clone HE	8.4
	416370	N90470	Hs.203697	ESTs, Weakly similar to B3022 hypothel	8.4
	457766	P81382	Hs.165642	ESTs, Weakly similar to T0552 hypothel	8.4
	415796	P07548	Hs.78854	ATPase, Na/K+ transporting, beta 2 poly	8.3
5	426271	AF026547	Hs.169047	chondroin sulfate proteoglycan 3 (near	8.3
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKF2p654N1662 (f	8.3
	416863	AW52691	Hs.93485	Homo sapiens mRNA; cDNA DKF2p761D191 (fr	8.3
	433447	U29195	Hs.3261	neuronal pentonin II	8.3
10	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKF2p43ME052 (f	8.3
	409327	L41162	Hs.53363	collagen, type IX, alpha 3	8.3
	414300	AC04670	Hs.186860	ESTs	8.2
	407728	AW071502	Hs.175931	ESTs	8.2
	422798	P92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
15	429007	D30542		gltcHUM092E093 Human fetal brain (TFijawa	8.1
	442710	AD15531	Hs.23210	ESTs	8.1
	425046	H05458	Hs.164502	ESTs	8.1
	429145	AW193360	Hs.197962	ESTs, Weakly similar to B3022 hypothel	8.0
	445740	T76281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	8.0
20	416771	AA077881	Hs.25329	ESTs	7.9
	422728	AW527826	Hs.103062	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.9
	425984	AW536277	Hs.165636	hypothetical protein DKF2p761C07121	7.9
	448408	AA322865	Hs.21107	neuroigin	7.9
25	455354	H72176	Hs.4273	hypothetical protein FLJ13159	7.9
	446119	ALJ076543	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.9
	435501	AW051819	Hs.120908	KIA00501 protein	7.8
	423600	AB335559	Hs.310359	ESTs	7.8
	450525	AW970107	Hs.5422	gltcEST382188 MAGE resequences, MAGK Homo	7.8
30	415314	B38802	Hs.52722	glycoprotein M50	7.7
	420035	R03036	Hs.1570	Homo sapiens mRNA; cDNA DKF2p56G1823 (f	7.7
	427587	AW003857	Hs.1570	histamine receptor H1	7.7
	449328	A962453	Hs.107647	ESTs	7.7
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	7.7
	407895	U07935	Hs.41154	Zc family member 1 (odd-skipped Drosophi	7.7
35	419103	Z40229	Hs.95423	hypothetical protein FLJ22035	7.5
	438779	NM_003787	Hs.5414	nucleolin protein 4	7.6
	433552	AW575367		gltcEST387475 MAGE resequences, MAGN Homo	7.5
	448555	A155597	Hs.159653	ESTs	7.5
	439652	R06352	Hs.269390	ESTs	7.5
40	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKF2p56P1124 (f	7.5
	410099	AA081630	Hs.159387	KIAA0036 gene product	7.5
	431552	R69016	Hs.213194	hypothetical protein MGC10895	7.4
	409731	AA125585	Hs.55145	lysinin, beta, identified in neuroblast	7.4
	405819				7.4
45	407885	AW959588	Hs.100826	ESTs	7.4
	437416	AL359005	Hs.283851	Homo sapiens mRNA; cDNA DKF2p547G036 (fr	7.4
	437898	R51837	Hs.7990	ESTs, Moderately similar to J94505 cald	7.4
	408204	D51468	Hs.21925	ESTs	7.4
50	418505	AA084248	Hs.85330	G protein-coupled receptor 36	7.3
	474499	AW252580	Hs.147674	protocadherin beta 16	7.3
	454035	AA374756	Hs.83550	Homo sapiens mRNA for KIAA1771 protein,	7.3
	409745	NM_004734	Hs.55294	RAS35A, member RAS oncogene family	7.2
	410037	AB020725	Hs.58009	KIAA0918 protein	7.2
55	419318	AW089742	Hs.291005	ESTs	7.2
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKF2p38G1922 (f	7.2
	440206	AD43749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2
	448243	AW369771	Hs.52520	integrin, beta 8	7.2
	436281	AW411154	Hs.85155	myeloid leukemia factor 1	7.2
60	426429	X73114	Hs.159849	myosin-binding protein C, slow-type	7.2
	407162	AA312551	Hs.230157	ESTs	7.1
	415293	R04642	Hs.105541	ESTs	7.1
	422764	AD767727	Hs.47522	ESTs	7.1
	451892	AB05415	Hs.213897	ESTs	7.1
65	429469	MA4590	Hs.27	glycine dehydrogenase (oxocarboxylate);	7.0
	415734	NM_014747	Hs.16748	KIAA0237 gene product	7.0
	434149	Z43629	Hs.15574	hypothetical protein MGC5469	7.0
	436725	AA324975	Hs.128993	ESTs, Weakly similar to T00079 hypothel	7.0
	417632	R03655	Hs.5422	glycoprotein ME3	7.0
70	424421	AA325138	Hs.23659	hypothetical protein FLJ22672	6.9
	432627	NZ3791	Hs.110114	ESTs	6.9
	437117	AL049256	Hs.122993	ESTs	6.9
	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	6.9
	445900	AF070520	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.8
	445745	AW007324	Hs.13245	KIAA0455 gene product	6.9
75	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.9
	426586	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	6.8
	421723	AA020400	Hs.300717	sodium channel, voltage-gated, type III,	6.8
	447342	A199265	Hs.183322	Homo sapiens, Similar to RIKEN cDNA 2010	6.7
	443297	AL049664	Hs.133029	ESTs	6.7
80	443992	AW022226	Hs.322922	ESTs	6.7
	453096	AW24631	Hs.11325	ESTs	6.7
	453657	AL060235	Hs.35861	DKF2P589E1621 protein	6.7
	443761	A1525743	Hs.350903	ESTs	6.6

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	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	6.6
	430356	AW023357	Hs.5422	glycoprotein M6B	6.5
	433331	AF094754	Hs.32973	glycine receptor, beta	6.5
	444190	AB878918	Hs.10526	cysteine and glycine-rich protein 2	6.5
5	418110	R43523	l.s.217754	hypothetical protein FLJ22202	6.5
	413988	M61983	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	6.4
	420805	L10333	Hs.59947	elafasin 1	6.4
	429125	AA468554	Hs.271004	ESTs, Weakly similar to 138022 hypothetical	6.4
	432256	AF193766	Hs.13872	cytokine-like protein C17	6.4
10	407866	AW088232	Hs.85956	paired box gene 6 (aniridia, keratitis)	6.3
	440700	AW552281	Hs.226184	guanine nucleotide binding protein (G pr	6.3
	427701	AA411101	Hs.24386	nuclear autoantigenic sperm protein (Nu	6.3
	422949	AA319435	Hs.21657	Adrenal gland tumor Homo sap	6.2
	445102	AW204610	Hs.22270	ESTs	6.2
15	452401	RM_007115	Hs.25362	tumor necrosis factor, alpha-induced pro	6.2
	433533	AB011540	Hs.4590	low density lipoprotein receptor-related	6.2
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fls, clone HE	6.2
	416871	H98716	Hs.13808.s1	Soares melanocyte 2NDHM Ho	6.1
	416702	AA186428	Hs.85591	ESTs	6.1
20	413847	C15644	Hs.30005	superior cervical ganglia, neurast apicil	6.1
	424587	AL138167	Hs.56920	ESTs	6.1
	436690	U95740	Hs.6349	Homo sapiens, clone IMAGE301055, mRNA,	6.1
	453649	Y07454	Hs.34114	ATPase, Na+K+ transporting, alpha 2 (-)	6.1
	416444	AW818436	Hs.23590	soluble carrier family 16 (monocarboxylic	6.1
25	414117	W85559	Hs.1737	proteolipid protein 1 (Pellicaeus-Merzbac	6.0
	425517	AF121179	Hs.12179	glc:AF121179 Homo sapiens liver (Chang L-	6.0
	427457	AW779105	Hs.164682	ESTs	6.0
	437034	AA742643	Hs.976101.s1	NCL_CGAP_GCB1 Homo sapiens	6.0
	444170	AA581879	Hs.102408	ESTs	6.0
30	457183	H91382	Hs.118569	Ov-binding protein IDAX (inhibition of	6.0
	448599	AF179274	Hs.22791	transmembrane protein with EGF-like and	6.0
	450408	H05626	Hs.6521	ESTs	6.0
	439772	AL385406	Hs.10268	Homo sapiens mRNA full length insert cDN	5.9
	446044	AB014605	Hs.72599	aripin-1: Interacting protein 1, activ	5.9
35	410011	AB020641	Hs.57856	*PFAIRE protein kinase 1	5.9
	415486	H12214	Hs.13284	ESTs, Weakly similar to 210920A B cell	5.9
	438993	AA828955	Hs.27668.s1	NCL_CGAP_Ov2 Homo sapiens	5.9
	447350	AF135752	Hs.172634	ESTs	5.9
	451793	R42554	Hs.210862	T-box, brain, 1	5.9
40	447101	N72185	Hs.44189	ESTs	5.9
	440482	R39127	Hs.21433	hypothetical protein DKFZp547J036	5.9
	440274	R24595	Hs.7122	serpine responsive protein 1	5.9
	438461	AW075485	Hs.28049	phosphoenolpyruvate carboxylase	5.9
	418064	BE387287	Hs.83334	S100 calcium-binding protein, beta (neur	5.7
45	437036	AS171514	Hs.133022	ESTs	5.7
	412225	AW802942	Hs.169375	gk:CV0-NN1022-170400-193-c02 NN1022 Homo	5.7
	428342	AF058419	Hs.163973	multiple PCZ domain protein	5.7
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	5.7
	445828	F05802	Hs.81907	ESTs	5.7
50	447198	D61528	Hs.253438	ESTs	5.7
	427397	NL_017413	Hs.303904	apocin: peptide ligand for APJ receptor	5.7
	446499	BE513280	Hs.77550	hypothetical protein MGC1780	5.7
	443672	AA323362	Hs.35957	butyrobetaine (gamma), 2-oxoglutarate di	5.6
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	5.6
55	435718	R06369	Hs.263534	ESTs	5.6
	449340	AW023576	Hs.193359	hypothetical protein MGC10954	5.6
	424481	R19453	Hs.1737	proteolipid protein 1 (Pellicaeus-Merzbac	5.6
	451996	AW514021	Hs.245510	ESTs	5.6
	422411	AW748443	Hs.22511	ESTs	5.6
60	438328	A962281	Hs.32440	ESTs	5.6
	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
	435191	R15912	Hs.4817	Homo sapiens clone 24451 mRNA sequence	5.5
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5
65	400859				5.5
	413625	AW451103	Hs.71371	ESTs	5.5
	421863	AB62677	Hs.108872	Homo sapiens mRNA; cDNA DKFZp434P228 (r	5.5
	434933	R91095	Hs.4276	KIAA1701 protein	5.5
	438702	AB170054	Hs.54518	ESTs	5.5
	432055	AS77431	Hs.141653	hypothetical protein MGC10858	5.5
70	430979	AA79755	Hs.129010	ESTs	5.5
	412709	AL022327	Hs.74518	KIAA0027 protein	5.5
	429920	H05430	Hs.288433	neurotrophin	5.5
	424343	AW056260	Hs.4748	adenylylate cyclase activating polypeptide	5.4
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	5.4
	419235	AW470411	Hs.288433	neurotrophin	5.4
	418030	BE207573	Hs.83321	neurexomedin B	5.4
	410330	AW026230	Hs.46785	ESTs	5.4
	410781	AS78672	Hs.165026	ESTs	5.4
80	420658	AW65215	Hs.336655	ESTs	5.4
	421308	AA887322	Hs.192843	leucine zipper protein FKSG14	5.4
	443740	R55434	Hs.21062	ESTs	5.4
	426457	AW846667	Hs.169895	chimerin (chlauserin)	5.4
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	5.4

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412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4
426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.4
424432	AJ037821	Hs.146358	protocadherin 10	5.4
429250	H65835	Hs.198038	tyrosophan rich basic protein	5.4
443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
426282	RS1913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	5.4
404584				5.3
430281	AB029568	Hs.230023	KIAA1132 protein	5.3
438945	AL355743	Hs.55663	Homo sapiens EST from clone 41214, full	5.3
424001	W67883	Hs.134746	paternally expressed 10	5.3
425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitter	5.3
426625	T76300	Hs.300642	serologically defined colon cancer antigen	5.3
438197	AA421732	Hs.170989	ESTs	5.3
426795	AA431765		glucz603d3.1 Soames_testis_NHT Homo sap	5.3
438176	AW138870	Hs.122113	ESTs	5.3
440138	AB043023	Hs.318127	hypothetical protein FLJ102671	5.3
451018	AW65589	Hs.247324	mitochondrial ribosomal protein S14	5.3
418340	N31772	Hs.79202	fasciculation and elongation protein zeta	5.3
432544	N77221	Hs.187824	ESTs	5.3
446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	5.3
424624	AB029247	Hs.151301	Ca2+-dependent activator protein for onc	5.3
427748	ALD79403	Hs.381705	KIAA0506 protein; SCN Cardiac Oscillator	5.3
430437	A768801	Hs.105943	Homo sapiens cDNA FLJ13569 fa, clone PL	5.3
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	5.2
453941	U38617	Hs.36620	Bloom syndrome	5.2
424988	U58515	Hs.154136	chitinase 3-like 2	5.2
423419	R55336	Hs.23539	ESTs	5.2
424922	BE386547	Hs.217112	hypothetical protein MGCT0825	5.2
447359	NM_012093	Hs.18258	adenylate kinase 5	5.2
430206	AF041853	Hs.43670	kinasin family member 3A	5.2
421013	M62397	Hs.1345	mutated in colorectal cancers	5.2
429443	AB028957	Hs.202687	potassium voltage-gated channel, Shal-re	5.2
434367	AB020700	Hs.3830	KIAA0893 protein	5.2
444861	RAG789	Hs.76118	oligomeric carboxyl-terminal esterase L1	5.2
446142	A794693	Hs.145958	ESTs	5.2
448816	AB033052	Hs.22151	KIAA1226 protein	5.2
451050	AW637420	Hs.69902	ESTs	5.2
451106	BE382701	Hs.25950	v-myc avian myelocytomatosis viral relist	5.2
432835	AL133916	Hs.172872	hypothetical protein FLJ20393	5.2
416737	AF154335	Hs.79591	LIM domain protein	5.2
424800	ALC35588	Hs.153203	MyoD family inhibitor	5.2
434695	AW204099	Hs.337720	ESTs, Weakly similar to AF126780 1 retin	5.1
416257	FC03616	Hs.27513	ESTs	5.1
433929	A375489	Hs.27079	ESTs	5.1
415651	A207162	Hs.3615	statmin-like o-protein RB3	5.1
451027	AW516204	Hs.40008	ESTs	5.1
426172	Z95339	Hs.118145	ESTs	5.1
423343	AA324643	Hs.246106	ESTs	5.1
429172	AA447417	Hs.285491	ESTs	5.1
437268	A754847	Hs.227571	regulator of G-protein signalling 4	5.1
451270	AW341392	Hs.235795	ESTs	5.1
452854	AL157891	Hs.30367	Homo sapiens mRNA; cDNA DKFZp434E026 (l	5.1
420560	AW207748	Hs.59115	ESTs	5.1
418097	R45137	Hs.21868	ESTs	5.1
442610	AJ365130	Hs.11307	ESTs, Weakly similar to T193261 hypothetical	5.1
431494	AW292755	Hs.6053	ESTs	5.1
413554	AA315146	Hs.75426	acrogelarginin II (chromogranin C)	5.1
414217	AJ309298	Hs.279898	Homo sapiens cDNA; FLJ23105 fa, clone L	5.1
412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	5.0
413627	BE182082	Hs.246073	ESTs	5.0
418651	NM_001949	Hs.1182	EST, transcription factor 3	5.0
422438	AA445925	Hs.720896	ESTs, Moderately similar to Z195_HUMAN Z	5.0
423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.0
431431	AL096711	Hs.252953	Human DNA sequence from clone RP3-403A15	5.0
435087	AW912411	Hs.23567	ESTs	5.0
452097	AB022364	Hs.27916	a-disintegrin-like and metalloprotease (5.0
410434	AF051152	Hs.63668	int-like receptor 2	4.9
408692	AL040127	Hs.34074	dipeptidyl/peptidase VI	4.9
407808	AA603569	Hs.279789	histone deacetylase 3	4.9
418540	H17739	Hs.388513	Human DNA sequence from clone RP5-899C14	4.9
425977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.9
426814	AF036943	Hs.172619	myelin transcription factor 1-like	4.9
447112	H17800	Hs.7154	ESTs	4.9
448574	F05040	Hs.175373	ESTs	4.9
453892	AW009640	Hs.26366	ESTs, Moderately similar to S65657 alpha	4.9
423869	BE409301	Hs.134012	C1q-related factor	4.9
413248	T64856	Hs.21433	hypothetical protein DKFZp547J036	4.9
448176	AK533545	Hs.139072	ESTs	4.9
444151	AW015994		gsh-H2B0p-ahb-g-06-9-Uts1 NCL_CGAP_S	4.8
402604				4.8
436039	AW023323	Hs.121070	ESTs	4.8
448769	N60037	Hs.38173	ESTs	4.8
423678	AW963357	Hs.7847	ESTs	4.8

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5	430451	AF066279	Hs.278554	heterochromatin-like protein 1	4.8
	425870	R13406	Hs.26782	ESTs	4.8
	435777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
	413409	AA635416	Hs.76580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.8
	413623	AA825721	Hs.246973	ESTs	4.8
10	417246	AF60098	Hs.21411	ESTs	4.8
	423930	AD045333	Hs.44209	ESTs	4.8
	421153	AA451737	Hs.141485	MAGE-like 2	4.8
	443539	AF076182	Hs.134074	ESTs, Moderately similar to ALU5_HUMAN A	4.8
	448750	U85020	Hs.21903	calcium channel, voltage-dependent, beta	4.8
15	454030	AW021429	Hs.231980	ESTs	4.8
	44456	M23273	Hs.1780	myelin associated glycoprotein	4.8
	444119	R41231	Hs.164261	ESTs, Weakly similar to T26865 hypotheli	4.7
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.7
	431482	AW553672	Hs.256311	grainin-like neuroendocrine peptide procu	4.7
20	431103	M57389	Hs.44	pleiotrophin (heparin binding growth fac	4.7
	428956	AF374851	Hs.22542	ESTs	4.7
	435060	AA422719	Hs.233349	ESTs, Weakly similar to fork head like p	4.7
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22126 fs, clone H	4.7
	443475	BE913134	Hs.247474	hypothetical protein FLJ21032	4.7
25	422222	AB959372	Hs.195247	hypothetical protein DKFZ434A171	4.7
	431733	AW298410	Hs.21475	ESTs	4.7
	449363	AA001220	Hs.271369	ESTs	4.7
	452022	AW072330	Hs.283675	ESTs	4.7
	454269	AG961093	Hs.129906	KIA0599 ⁺ protein	4.7
30	405441				4.7
	426189	AA424030	Hs.46627	ESTs	4.7
	409125	R17265	Hs.259673	axonal transport of synaptic vesicles	4.7
	454545	AA18718	Hs.144121	ESTs, Weakly similar to T48216 hypotheli	4.6
	425745	AA4090	Hs.14427	Homo sapiens cDNA: FLJ21600 fs, clone H	4.6
35	413492	D67470	Hs.75400	KIA0260 protein	4.6
	419629	AB020695	Hs.91962	KIA0688 protein	4.6
	407636	AAJ04672	Hs.334403	hypothetical protein FLJ23571	4.6
	436140	WB7255	Hs.289537	ESTs	4.6
	439169	AB121222	Hs.41095	ESTs	4.6
40	443150	AA034467	Hs.34650	ESTs	4.6
	451073	AT758095	Hs.206063	ESTs	4.6
	451659	BE379761	Hs.14246	ESTs	4.6
	452106	AA141331	Hs.21342	ESTs	4.6
	451407	AA181376	Hs.326401	fibroblast growth factor 12b	4.6
45	446765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (r	4.6
	430147	BE07704	Hs.234434	haly/enhancer-of-split related with YRP	4.6
	437204	AL110216	Hs.12385	ESTs, Weakly similar to BS214 salivary	4.6
	431117	AF003522	Hs.220500	della (Drosophila)-like 1	4.5
	422175	N78685	Hs.6382	ESTs, Highly similar to T00391 hypotheli	4.5
50	407889	R34556	Hs.30800	ESTs, Weakly similar to S65657 alpha-1C	4.5
	419343	AA456245	Hs.65603	down-regulated by Clonin, a	4.5
	421780	AW069201	Hs.22654	sodium channel, voltage-gated, type I, a	4.5
	429399	AA452244	Hs.16727	ESTs	4.5
	450149	AW989761	Hs.132663	Zic family member 2 (odd-paired Drosophi	4.5
55	453118	AW195449	Hs.252757	ESTs	4.5
	443465	AB011025	Hs.9348	synuclein receptor 3	4.4
	442613	AB044092	Hs.130522	Kv channel-interacting protein 1	4.4
	429643	AA455689	Hs.167279	FYVE-finger-containing Rab5 effector pro	4.4
	416269	AA226776	Hs.78078	MAD2 [mitotic arrest deficient, yeast, 1	4.4
60	418845	AA552685	Hs.19422	chromos. homolog 5 (Drosophila) Ap1	4.4
	435202	AB713713	Hs.170204	KIA09551 protein	4.4
	437496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZp547J125 (r	4.4
	451254	AI571916	Hs.172967	ESTs	4.4
	439338	AI558707	Hs.46713	ESTs	4.4
65	459279	AW500291	Hs.8623	hypothetical protein FLJ110430	4.4
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.4
	424983	AT742434	Hs.169911	ESTs	4.4
	410611	AW954134	Hs.20324	KIAA1628 protein	4.4
	420606				4.4
70	409248	AB033335	Hs.51965	KIAA1209 protein	4.4
	442222	AI081301	Hs.164773	ESTs	4.4
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.4
	454293	H45738	Hs.134069	ESTs, Moderately similar to HKG1_HUMAN H	4.4
	442632	AW206560	Hs.255569	ESTs	4.4
75	407304	AA566832		ghn32m3.s1 NCL_GCAP_AAI Homo sapiens	4.3
	423279	AW959661	Hs.290043	ESTs	4.3
	427194	AA390918	Hs.250835	ESTs	4.3
	419723	AL112015	Hs.52614	longevity assurance (LAG1, S. cerevisiae	4.3
	445610	AW265700	Hs.155660	ESTs	4.3
80	409734	BE161654	Hs.98155	hypothetical protein	4.3
	410389	AW950419	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	4.3
	411571	AA122283	Hs.106111	hypothetical protein FLJ25515	4.3
	433024	AA573847	Hs.26549	KIAA1708 protein	4.3
	453202	AW065781	Hs.26270	hypothetical protein FLJ11588	4.3
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	4.3
	416427	BE244050	Hs.79307	Rac2/Cdc42 guanine exchange factor (GEF)	4.3
	431789	H19530	Hs.269222	mitogen-activated protein kinase 4	4.3

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	444620	R41398	Hs.6996	ESTs	4.3
	454042	H22570	Hs.17572	hypothetical protein FLJ20093	4.3
	441889	A372568	Hs.8022	TUS-1 protein	4.3
	425256	BE257611	Hs.156382	collagen response modulator protein 1	4.3
5	410356	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	4.2
	430291	AV660345	Hs.236126	DGL-49 protein	4.2
	433597	AA706205	Hs.100343	ESTs	4.2
	441127	HE3620	Hs.13061	ESTs	4.2
10	446507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZ666N1047 (f	4.2
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF157833.1 noncl	4.2
	408577	H60572	Hs.19515	ESTs, Highly similar to NR63_HUMAN PRO-AN	4.2
	457119	AT65160	Hs.106681	Homo sapiens brain tumor associated prot	4.2
	426836	A143139	Hs.22288	vesilin-like 1	4.2
15	429116	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
	432665	AT733709	Hs.152494	ESTs, Weakly similar to 380222 hypotheti	4.2
	447136	AA439112	Hs.93828	ESTs, Weakly similar to 2199260A.9 cont	4.2
	425646	AT03366	Hs.26766	ESTs	4.2
	451459	AT797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMAN A	4.2
20	421666	AB011156	Hs.106794	KIA00594 protein	4.2
	432776	AA194940	Hs.13522	ESTs, Weakly similar to 380222 hypotheti	4.2
	436421	AT576031	Hs.122613	ESTs, Weakly similar to ZM22_HUMAN ZM2C	4.2
	423658	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZp434B0650 (f	4.2
	434001	AW880505	Hs.3697	serine (or cysteine) proteinase inhibito	4.2
25	437360	AL339577	Hs.112196	Homo sapiens mRNA; cDNA DKFZp547M073 (fr	4.1
	432326	AW572739	Hs.115471	6-phospho-2-oxo-2-kinase/thiolase-2,5-M	4.1
	439007	BE446566	Hs.159460	ESTs	4.1
	424026	AF055064	Hs.153692	Homo sapiens cDNA FLJ14354 fs, clone Y7	4.1
	446936	H10207	Hs.47314	ESTs	4.1
30	424240	AB023185	Hs.148335	calcium/calmodulin-dependent protein kin	4.1
	412446	AT68015	Hs.52127	ESTs	4.1
	409653	AA332277	Hs.57691	cathepsin 18, type 2	4.1
	416220	N49778	Hs.170594	hypothetical protein MGC10946	4.1
	419463	AA246857	Hs.46784	ESTs	4.1
	429071	AW135857	Hs.153805	ESTs	4.1
	426743	AL080050	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	4.1
	432609	AA565509	Hs.131703	ESTs	4.1
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	4.1
	452039	A1922968	Hs.172610	ESTs	4.1
40	425905	AB023269	Hs.316584	novel CHC4 type Zinc finger (ring finger)	4.1
	457561	AA331517	Hs.286055	chimerin (chimerin) 2	4.1
	429036	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	4.1
	433832	AW354599	Hs.169330	neuronal protein	4.1
	436637	AT63629	Hs.76766	ESTs	4.1
45	430231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N479 (fr	4.1
	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
	407661	AW072903	Hs.40968	hepican sulfate (heparan sulfate) 3-O-sulfat	4.1
	410465	AW255094	Hs.69233	zinc finger protein	4.0
	413816	N48813	Hs.75515	apolipoprotein C-II	4.0
50	436703	AB03373	Hs.31599	ESTs	4.0
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fs, clone HE	4.0
	435771				4.0
	416841	NM_002332	Hs.69137	low density lipoprotein-related protein	4.0
	421764	AB615135	Hs.148135	serine/threonine kinase 33	4.0
55	424716	AL137273	Hs.142307	hypothetical protein	4.0
	425773	H21278	Hs.337149	ESTs	4.0
	427304	AA761626	Hs.163663	ESTs	4.0
	428882	AA438915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	4.0
	452834	AA636827	Hs.106635	KIA1668 protein	4.0
	453745	AA552969	Hs.53906	hypothetical protein MGC14726	4.0
	452232	U85281	Hs.11986	oxidative 3 alpha hydroxysteroid dehydro	4.0
	413901	M82246	Hs.35406	ESTs, Highly similar to unnamed protein	4.0
	429696	AB65066	Hs.26339	ESTs, Highly similar to S21348 probable	4.0
65	435824	AJ276120	Hs.4959	putative ankyrin-repeat containing prote	4.0
	439199	RA6373	Hs.26292	ESTs	4.0
	439450	RS1613	Hs.125304	ESTs	4.0
	446782	AB63048	Hs.144006	ESTs	4.0
	419687	AB63866	Hs.227699	ESTs, Weakly similar to T203_HUMAN TRANS	3.5
	420408				3.5
70	453382	H14966	Hs.107375	ESTs	3.5
	414219	W20010	Hs.75823	ALL-1 fused gene from chromosome 1q	3.9
	420576	AA613546	Hs.99034	GTP-binding protein Rho7	3.9
	425010	T18637	Hs.4241	ESTs	3.5
	414230	HE5537	Hs.146057	ESTs	3.9
75	441736	AW292779	Hs.108795	ESTs	3.9
	418951	F07609	Hs.69506	paired box gene 6 (peritidin, keratins)	3.9
	406311				3.9
	406460	AA064726	Hs.265574	ESTs	3.9
	410658	AW105231	Hs.192035	ESTs	3.9
80	414699	AB185523	Hs.76930	synuclein, alpha (non-A4 component of am	3.9
	419349	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.9
	429477	AJ275514	Hs.6656	ESTs	3.9
	433766	AA699224	Hs.112669	ESTs	3.9

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	436190	AK001059	glt.Homo sapiens cDNA FLJ10197 fs, clone	3.9	
	417991	RA1754	Hs.6496	ESTs	3.9
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	3.9
	404283				3.9
5	453919	AW699912	Hs.7076	KIAA1705 protein	3.9
	429656	XD5608	Hs.211584	neurofilament, light polypeptide (58kD)	3.9
	412754	AW160375	Hs.74565	anyfold beta (AF) precursor-like protein	3.9
	453314	AB099143	Hs.45489	Homo sapiens cDNA: FLJ21517 fs, clone C	3.9
	435052	NS3288	Hs.334370	uncharacterized hypothetical protein HBE	3.9
10	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.9
	438054	AA776626	Hs.62183	ESTs	3.9
	435420	AA443966	Hs.31595	ESTs	3.9
	445133	AW157646	Hs.153506	ESTs	3.9
	432590	A1609273	Hs.110733	ESTs	3.9
15	453331	A1240665	Hs.8895	ESTs	3.9
	410227	AB005284	Hs.61152	carboxinase (multiple)-like 2	3.9
	424635	AA425887	Hs.115458	Homo sapiens cDNA: FLJ14259 fs, clone PL	3.9
	451489	NM_005503	Hs.26468	emylfold beta (A4) precursor protein-bind	3.9
	447247	AW369351	Hs.287855	Homo sapiens cDNA FLJ13090 fs, clone NT	3.9
20	448302	AI480208	Hs.182906	Homo sapiens mRNA for KIAA1812 protein,	3.9
	415689	NM_005525	Hs.78306	serine (or cysteine) proteinase inhibitor	3.9
	417355	D13168	Hs.82002	endothelin receptor type B	3.9
	449727	AD011096	Hs.10032	KIAA0523 protein	3.9
	424340	AA339036	Hs.7033	ESTs	3.9
25	425346	AD267677	Hs.127416	synaptotagmin 1	3.9
	412788	AA120990	Hs.164416	ESTs	3.9
	404593				3.9
	416856	N27833	Hs.263028	ESTs, Weakly similar to I38022 hypot	3.9
	429986	AA480357	Hs.224223	ESTs, Moderately similar to I38022 hypot	3.9
30	439619	AW875986	Hs.58955	ESTs, Weakly similar to I38022 hypot	3.9
	439034	W79377	Hs.167	microtubule-associated protein 2	3.9
	404322	AA879430	Hs.91008	glt.Hs.91008.s1 Soares_NFL_T_GBC_S1 Homo s	3.9
	447761	AF361573	Hs.19492	protocadherin 5	3.9
	452453	AB025119	Hs.10009	glt.CD1006-101198-051 BT009 Homo sapien	3.9
35	439671	AW162840	Hs.6641	kinesin family member 5C	3.9
	447937	AL109716	Hs.20034	Homo sapiens mRNA full length insert cDN	3.9
	459276	AW294609	Hs.34054	Homo sapiens cDNA: FLJ22458 fs, clone H	3.9
	447028	AB73128	Hs.167257	brain filin protein-1	3.9
	449458	AB05578	Hs.208261	ESTs	3.9
40	445938	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.9
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypot	3.9
	428841	AA184350	Hs.104935	ESTs	3.9
	433645	AB070005	Hs.287435	MEGF3 protein	3.9
	422263	AA307639	Hs.129908	KIAA0591 protein	3.9
45	451625	RS6793	Hs.108576	alanine-glyoxylate aminotransferase 2-lf	3.9
	435236	BE100952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN1	3.9
	441928	AA370188	Hs.211468	ESTs	3.9
	441787	AB389633	Hs.214635	ESTs	3.9
	414822	CO0723	Hs.77631	glycine cleavage system protein H (amino	3.9
50	425588	F07396	Hs.46751	ESTs	3.9
	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypot	3.9
	435793	AC037734	Hs.4393	KIAA1313 protein	3.9
	443682	AB383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	3.9
55	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.9
	440080	AA051587	Hs.143707	ESTs	3.9
	453088	AA814467	Hs.18752	ESTs	3.9
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	3.9
	409234	AB879419	Hs.27206	ESTs	3.9
60	420489	AA15008	Hs.133513	ESTs	3.9
	428890	AA355167	Hs.41291	ESTs	3.9
	433349	W22948	Hs.10762	ESTs	3.9
	441869	NM_009847	Hs.8004	huntingtin-associated protein interact	3.9
	448796	AA147821	Hs.391431	endothelial zinc finger protein fold	3.9
65	453319	NM_000038	Hs.11821	glt.Homo sapiens adenomatous polyposis c	3.9
	459518	AA937419	Hs.294069	Homo sapiens cDNA FLJ13384 fs, clone PL	3.9
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	3.9
	421183	AL135740	Hs.102447	TSC-22-like	3.9
	410555	U02648	Hs.64311	a disintegrin and metalloproteinase doma	3.9
70	421837	AF058290	Hs.106300	Homo sapiens clone 23556 mRNA sequence	3.9
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fs, clone H	3.9
	420007	AA280627	Hs.57846	ESTs	3.9
	449961	AA265834	Hs.133100	ESTs	3.9
	422634	NM_016110	Hs.118121	CCG-42 protein	3.9
75	421030	AW161357	Hs.101174	microtubule-associated protein tau	3.9
	427099	AB032953	Hs.173560	odd O/ten-a homolog 2 (Drosophila, mos	3.9
	452355	NS4926	Hs.25002	G protein-coupled receptor 34	3.9
	440493	AZ00036	Hs.150286	ESTs	3.9
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.9
80	423756	AA828125	Hs.1009.s1 NCL_CGAP_Ov2 Homo sapiens	3.9	
	426187	AW014486	Hs.22509	ESTs	3.9
	434869	BE255890	Hs.299316	collagen response mediator protein-5, C	3.9
	413199	MS2843	Hs.73236	ELAV (embryonic lethal, abnormal vision,	3.9

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	415725	H21066	Ha.13223	Homo sapiens mRNA full length insert cDN	3.6
	416120	H46739	Ha.45209	glyco14h22.1 Soares adult brain N26GH5	3.6
	426239	AA048419	Ha.85209	ESTs	3.6
	419066	NM_000216	Ha.85991	Kallmann syndrome 1 sequence	3.6
5	446659	AI335361	Ha.226376	ESTs	3.6
	426757	AW205640	Ha.158206	ESTs	3.6
	418619	AA326776	Ha.191721	ESTs	3.6
	488332	AI000341	Ha.220451	ESTs	3.6
10	408626	AF216077	Ha.46376	Homo sapiens clone HD-2 mRNA sequence	3.6
	410343	AA084273	Ha.76561	ESTs, Weakly similar to S47072 finger pr	3.6
	410507	AA355268	Ha.40834	translational epithelia response protein	3.6
	422977	AA511498	gln295300.1 NCI, CCAP, Thy1 Homo sapiens	3.6	
	425305	AA363025	Ha.155572	human clone Z8001 mRNA sequence	3.6
	426002	AA418703	gln295300.1 Soares, NIH/NIH, S1 Homo sapi	3.6	
15	426505	AL035461	Ha.2261	chromogranin B (secretogranin 1)	3.6
	433530	AA408670	Ha.47650	ESTs	3.6
	436426	AB111446	Ha.318725	CSG-72 protein	3.6
	438078	AI016377	Ha.131693	ESTs	3.6
20	442927	AI024347	Ha.131519	ESTs	3.6
	446242	N66336	Ha.7360	ESTs	3.6
	446631	AL080123	Ha.22182	zinc finger protein 23 (CX16)	3.6
	450474	AW872644	Ha.201919	ESTs	3.6
	452196	AI057560	Ha.61210	ESTs, Weakly similar to t33022 hypophat	3.6
25	453800	R22479	Ha.167073	Homo sapiens cDNA FLJ13047, lit, clone NT	3.6
	435443	AW138211	Ha.128746	ESTs	3.6
	426514	BE511663	Ha.170195	bone morphogenetic protein 7 (osteogenic	3.6
	456038	AA203285	Ha.254141	ESTs, Weakly similar to alternatively sp	3.6
	408902	AW014869	Ha.5510	ESTs	3.6
	442950	AI500417	Ha.467564	ESTs	3.6
30	423905	AW579860	Ha.135150	lung type-I cell membrane-associated gly	3.6
	425478	AB007953	Ha.268840	ESTs	3.6
	453884	AA355925	Ha.36232	KIAA0186 gene product	3.6
	404721				3.6
35	408453	AI356838	Ha.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	440553	AA089416	Ha.295362	Homo sapiens cDNA FLJ14459, lit, clone HE	3.6
	446372	AB020644	Ha.14945	long fatty acyl-CoA synthetase 2 gene	3.6
	413599	N46124	Ha.34480	ESTs	3.6
	421456	NM_003564	Ha.104576	carboxylate (N-acetyl sulfate Gal-6) sul	3.6
40	425017	AL119306	Ha.288405	ESTs	3.6
	435968	H98180	Ha.117975	ESTs	3.6
	415101	RA5531	Ha.144534	ESTs	3.6
	451320	AIY118072	Ha.63991	diacylglycerol kinase, zeta (1040d)	3.6
	452090	AT341110	Ha.136355	ESTs	3.6
	416836	DI4745	Ha.80247	cholesterolin	3.6
45	414821	M63835	Ha.77424	Fc fragment of IgG, high affinity Ia, re	3.6
	415412	AW161058	Ha.39267	syncytin, beta	3.6
	437860	AA330063	Ha.273998	Homo sapiens cDNA: FLJ23165, lit, clone L	3.6
	452689	F33688	Ha.284176	transferrin	3.6
	416661	AA634543	Ha.79440	IGF-II mRNA-binding protein 3	3.6
	427491	RA3279	Ha.22574	ESTs, Weakly similar to t38022 hypophat	3.6
	428037	N47474	Ha.89230	potassium intermediate/small conductance	3.6
	444084	AI169422	Ha.44155	gln295300.1 Soares, NSF, F8_9W_OT_PA_P_5	3.6
	408296	AL117452	Ha.44155	DKFZP586G1517 protein	3.6
	453775	NM_002216	Ha.35120	replication factor C (activator 1) 4 (37	3.6
55	412659	AW573865	Ha.74376	oligodendrocyte related ER localized prot	3.6
	429077	AB020965	Ha.2352	adenylyl cyclase 2 (beta)	3.6
	436887	AW953157	Ha.193236	hypothetical protein DKFZ47D155	3.6
	450784	AW246803	Ha.47289	ESTs	3.6
	448627	AW461243	Ha.157069	ESTs	3.6
60	435434	AA50465	Ha.33927	putative 47 kDa protein	3.6
	412777	AI335773	Ha.270123	ESTs	3.6
	436476	AA326106	Ha.33829	bHLH protein DEC2	3.6
	406601	U47928	Ha.86122	protein A	3.6
	429401	AW296102	Ha.26272	ESTs, Weakly similar to S32567 A4 prot	3.6
65	448426	AA003359	Ha.23401	ESTs	3.6
	416727	AA227609	Ha.94634	ESTs	3.6
	451729	AW150725	Ha.312469	ESTs	3.6
	435910	AI084152	Ha.21782	ESTs, Weakly similar to ALU2_HUMAN ALU S	3.6
	434677	IC7316	Ha.170769	Homo sapiens cDNA: FLJ22467, lit, clone H	3.6
70	414598	AI084221	Ha.135150	lung type-I cell membrane-associated gly	3.6
	439627	BE621702	Ha.29076	hypothetical protein FLJ21841	3.6
	413293	AL047463	Ha.302498	GTP-binding protein homologous to Saccha	3.6
	423952	AW658292	Ha.137206	Homo sapiens mRNA, cDNA DKFZps4H1663 (p	3.6
	420249	F03422	Ha.166352	nucleoside-RNA protein 1	3.6
75	426968	U07616	Ha.173034	amphiphysin (SHE-Mann syndrome with b	3.6
	430388	AA356823	Ha.240770	nuclear cap binding protein subunit 2, 2	3.6
	435061	AI051474	Ha.153944	ESTs	3.6
	452251	AF015092	Ha.28653	CLKF (cell division cycle 7, S. cerevisi	3.6
	449714	AB033015	Ha.23941	KIAA1169 protein	3.6
80	443392	AI055621	Ha.283420	ESTs	3.6
	410082	AA081894	Ha.195311	Musashi (Drosophila) homolog 1	3.6
	445337	NM_015280	Ha.12523	Ribonucleic leucine-rich transmembrane p	3.6
	408493	BE206554	Ha.46039	phenylglyoxylate mutase 2 (muscle)	3.6

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5	432731	R31178	Hs.287820	fluticasone 1	3.4
	446758	AD016311	Hs.21917	KIAA0766 protein	3.4
	432813	AWB11898	Hs.30712	KIAA0202 protein	3.4
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.4
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.4
	410108	AA081859	Hs.319775	OSG1-related protein 6	3.4
	406815	AA033930	Hs.258036	RNA isopentenylpyrophosphate transferase	3.4
	402855				3.3
10	422170	A0791949	Hs.112432	anti-Müllerian hormone	3.3
	445034	AW293376	Hs.143659	ESTs	3.3
	424378	W26020	Hs.167586	nasal cell adhesion molecule 1	3.3
	423811	AB011163	Hs.123908	KIAA0591 protein	3.3
	435293	R88872	Hs.4964	DKFZP564J624 protein	3.3
	404819				3.3
15	436907	AW661783	Hs.211061	ESTs	3.3
	427315	AA179949	Hs.175563	Homo sapiens mRNA: cDNA DKFZp564N0763 (f	3.3
	452893	T79153	Hs.48589	zinc finger protein 228	3.3
	454996	AW650130		gbl3L3-CT0219-271099-022-C09 CT0219 Homo	3.3
	406827	M28460		gblHomo sapiens (clone 104) retrovirus	3.3
20	409145	AA435062	Hs.59094	Homo sapiens mRNA: cDNA DKFZp43M00515 (f	3.3
	415238	R37780	Hs.21422	ESTs	3.3
	417845	AL117461	Hs.822719	Homo sapiens mRNA: cDNA DKFZp566F1822 (f	3.3
	421192	AA833718	Hs.204529	KIAA1806 protein	3.3
	426895	AW118191	Hs.112729	ESTs	3.3
25	430895	A086529	Hs.184867	ESTs	3.3
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
	452703	RA2764	Hs.339854	ESTs, Weakly similar to 138022 hypothal	3.3
	433690	AF150278	Hs.33578	KIAA0620 protein	3.3
30	433616	NM_003482	Hs.33345	dysm, axonemal, light intermediate pol	3.3
	457285	AB038858	Hs.130522	Kv channel-interacting protein 1	3.3
	436045	AB037723	Hs.5028	DKFZP564O0423 protein	3.3
	431470	AL390147	Hs.134742	hypothetical protein DKFZp564/D065	3.3
	448520	AB020367	Hs.213365	doublecortin and Cdk5 kinase-like 1	3.3
	434440	A1771945	Hs.27468	putative acid-sensing ion channel 3	3.3
35	432658	NM_000246	Hs.3076	MHC class II transactivator	3.3
	434888	AW604295	Hs.9950	Sec61 gamma	3.3
	423582	BE010831	Hs.28357	Homo sapiens cDNA FLJ11812 f6, clone HE	3.3
	446553	AA12775	Hs.145710	ESTs	3.3
	427940	AA417812	Hs.38775	ESTs	3.3
40	414683	S78296	Hs.76888	hypothetical protein MGC12702	3.3
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.3
	426545	A080584	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.3
	419488	AL038591	Hs.20837	hypothetical protein FLJ19392	3.3
	457579	A0300816	Hs.36781	HRAS-like suppressor	3.3
45	436556	A0364987	Hs.7572	ESTs	3.2
	424369	R87622	Hs.26714	KIAA1631 protein	3.2
	457055	AA76318	Hs.124480	ESTs	3.2
	440210	AW574562	Hs.125296	ESTs	3.2
50	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
	434363	AA630863	Hs.131375	ESTs, Moderately similar to ALUS_HUMAN1	3.2
	414430	A046201	Hs.76116	ubiquitin carboxyl-terminal esterase L1	3.2
	439924	A0565897	Hs.125283	ESTs	3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2
	423175	W27585	Hs.18653	hypothetical protein FLJ14627	3.2
55	415115	AA214228	Hs.127751	hypothetical protein	3.2
	407874	D57458	Hs.40888	acutely-regulated cytoskeleton-associated	3.2
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.2
	437762	T78028	Hs.154679	synaptotagmin I	3.2
60	438844	AA302517	Hs.52732	KIAA1444 protein	3.2
	450313	A033669	Hs.330333	Brucella-Bred syndrome 2	3.2
	409459	D06407	Hs.54481	low density lipoprotein receptor-related	3.2
	410953	AW611766	Hs.334658	hypothetical protein MGC12260	3.2
	416527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 f5, clone H	3.2
	420081	AW510776	Hs.349558	tubulin tyrosine ligase-like 1	3.2
65	429485	AA453900	Hs.192793	ESTs	3.2
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	3.2
	434928	AW915695	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	3.2
	435632	AW291498	Hs.171305	Homo sapiens, clone IMAGE:3552908, mRNA	3.2
	435306	AW18266	Hs.15345	ESTs	3.2
70	439274	AF086092	Hs.48372	ESTs	3.2
	404847	AA907511	Hs.130178	ESTs	3.2
	447750	AA22234	Hs.143434	corinacin 1	3.2
	452550	AW901809		gblC010 NH620-170400-195-h02 NH1020 Homo	3.2
75	430890	XS4232	Hs.2699	glypican 1	3.2
	420563	F09247	Hs.247735	protocadherin alpha 10	3.2
	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	3.2
	427450	AB014558	Hs.173127	KIAA0626 gene product	3.2
	430456	AA314998	Hs.241933	hypothetical protein	3.2
	430181	AF065314	Hs.234785	cyclic nucleotide-gated channel alpha 3	3.2
80	419512	AW489874	Hs.89981	disacylglycerol kinase, zeta (10404)	3.2
	419912	AF249745	Hs.60086	Rho guanine nucleotide exchange factor (3.2
	450689	AB06976	Hs.243000	Homo sapiens cDNA: FLJ14445 f5, clone HE	3.2
	424989	AL119387	Hs.119362	ESTs	3.2

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	436277	R88520	Hs.120817	ESTs	3.2
	451455	A932727	Hs.8821	hepelin antimicrobial peptide	3.2
	449078	A1869975	Hs.4775	jundophilin 3	3.2
5	447746	AW015920	Hs.161359	ESTs	3.2
	435458	F11872	Hs.4892	Homo sapiens clone 24841 mRNA sequence	3.2
	427729	AB033100	Hs.300946	HsUA protein (similar to mouse pols1)	3.2
	417417	F05745	Hs.89512	ATPase, Ca++-transporting, plasma membra	3.1
	439310	AW897046	Hs.6421	hypothetical protein DKFZp76 IN05121	3.1
10	435870	T79925	Hs.289165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	435257	AF095028	Hs.102754	ESTs	3.1
	416801	X93854	Hs.79971	cell (Discothelium)-like 2	3.1
	421988	AW450481	Hs.161333	ESTs	3.1
	428509	M31186	Hs.2050	pentactin-related gene, rapidly induced b	3.1
15	408788	AA773167	Hs.294027	ESTs	3.1
	433484	AB023398	Hs.3363	beta-1,3-glucosyltransferase 1 (glucos	3.1
	412723	AA648459	Hs.335951	hypothetical protein AF301222	3.1
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	3.1
	439458	A0752409	Hs.109314	hypothetical protein FLJ20980	3.1
20	428532	AA578225	Hs.324239	ESTs, Moderately similar to ZNF1_L_HUMAN Z	3.1
	452780	BE171598	Hs.13522	ESTs, Weakly similar to 138022 hypofth	3.1
	438192	AB859085	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.1
	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.1
	403053	FS8624	Hs.2196	eukaryotic translation elongation factor	3.1
	404299				3.1
25	407864	AF069291	Hs.40539	chromosome 3 open reading frame 1	3.1
	410181	A1468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	3.1
	418862	BE537537	Hs.272324	hypothetical protein FLJ20069	3.1
	440101	AA205847	Hs.230116	G-protein-coupled receptor	3.1
30	453240	A1969564	Hs.168254	hypothetical protein DKFZp568133	3.1
	440486	BE243513	Hs.7212	hypothetical protein PP1044	3.1
	408906	BE250162	Hs.83765	dihydrofolate reductase	3.1
	439884	A1720078	Hs.291597	ESTs, Weakly similar to A47502 B-cell gr	3.1
	414708	AW340125	Hs.78989	Hs-4A057 gene product	3.1
35	436315	BE390513	Hs.27935	hypothetical protein MGC0437	3.1
	428855	AL117427	Hs.127278	Homo sapiens mRNA; cDNA DKFZp666P013 (fr	3.1
	425683	AB037913	Hs.155200	hypothetical protein DKFZp762h222	3.1
40	410126	BE169274	Hs.165387	Hs-A4036 gene product	3.1
	435312	A243306	Hs.4965	voltage-gated sodium channel beta-3 subu	3.1
	425491	AA883316	Hs.255221	ESTs	3.1
	456273	AF154948	Hs.1148	zinc finger protein	3.1
45	412140	AA215981	Hs.73525	RbB5 interacting, kinase-like (rablins	3.1
	445255	NM_014841	Hs.12477	synaptonemal-associated protein, 91 kDa	3.1
	432154	A0701523	Hs.112577	ESTs	3.1
	451328	AW028516	Hs.31791	acylphosphatase 2, muscle type	3.1
50	433458	AW875186		gR-E1387294 IMAGE missense, MAGN Homo	3.1
	449616	AF703521	Hs.21511	kinasin family member 3C	3.0
	429281	AA330856	Hs.29908	Homo sapiens cDNA: FLJ2122 fls, clone C	3.0
	443906	AA348031	Hs.7913	ESTs	3.0
	417318	AW963937	Hs.12861	ESTs	3.0
55	428819	AW298597	Hs.61894	Homo sapiens, clone IMAGE:429802; mRNA,	3.0
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3.0
	408790	AW580227	Hs.47380	neurotrophic tyrosine kinase, receptor,	3.0
	426327	W03242	Hs.44488	Homo sapiens clone TC0CTA00151 mRNA seq	3.0
	451483	AW630398	Hs.232863	ESTs, Moderately similar to 138022 hypot	3.0
	422753	AF152329	Hs.284180	prothelastin gamma subfamily C, 3	3.0
	421633	AF121860	Hs.106290	sorting nexin 10	3.0
	428361	NM_015005	Hs.193858	transcriptional intermediary factor 1	3.0
	419332	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (refseq)	3.0
60	416965	F13271	Hs.79981	Human clone 23548 mRNA sequence	3.0
	419618	U79289	Hs.90798	Human clone 23595 mRNA sequence	3.0
	422709	AA315331	Hs.153485	ESTs	3.0
	421335	N87655	Hs.28411	ESTs	3.0
	424901	Z11932	Hs.132055	POU domain, class 3, transcription facto	3.0
65	426617	W58006	Hs.286255	endoruclease G-like 1	3.0
	427386	AW836261	Hs.337717	ESTs	3.0
	428689	NM_007050	Hs.229592	protein tyrosine phosphatase, receptor I	3.0
	430071	D86883	Hs.35495	ESTs	3.0
	435002	AL137310	Hs.4746	Homo sapiens mRNA; cDNA DKFZp761E13121 (3.0
70	436211	AK001581	Hs.334828	hypothetical protein FLJ10718; KIAA1794	3.0
	440936	AL134451	Hs.197478	ESTs	3.0
	445655	BE247129	Hs.145669	ESTs	3.0
	452294	AB71325	Hs.117056	ESTs, Moderately similar to A47562 B-cell	3.0
	439890	AA137162	Hs.286045	phosphoserine aminotransferase	3.0
75	430228	AW960939	Hs.6382	ESTs, Highly similar to T00391 hypofth	3.0
	451026	AA013218	Hs.157492	cer-4 (mouse) homolog	3.0
	435332	NM_001262	Hs.4834	cyclin-dependent kinase inhibitor 2C (p1	3.0
	435666	AF686387		qf-Homo sapiens full length insert cDNA	3.0
	425762	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.0
	416598	D44643	Hs.14144	secreted modular calcium-binding protein	3.0
80	416874	H96752	Hs.42698	ESTs	3.0
	410386	W68167	Hs.3327	Homo sapiens cDNA: FLJ22219 fls, clone H	3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	424066	Z99346	Hs.112461	ESTs, Weakly similar to 138022 hypofth	3.0

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404048	A4884766	Hs.40368	gluam20a10.a1 Scores_MFL_T_GBC, S1 Homo s	3.0
429163	BE410100	Hs.40368	adipocyte-related protein complex 1, sigma	3.0
481117	A7745649	Hs.26549	KIAA1708 protein	3.0
434131	A888275	Hs.143659	ESTs	3.0
441255	R08550	Hs.171635	ESTs	3.0
453300	AW033382	Hs.228414	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
453905	NM_002314	Hs.36566	LIM domain kinase 1	2.9
416602	NM_006159	Hs.79389	nal (chicken)-like 2	2.9
431173	AW971198	Hs.294068	ESTs	2.9
425209	AW306745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
434401	A037658	Hs.70088	ESTs	2.9
422660	AW890487	Hs.63994	cathepsin 13, H-cathepsin (heart)	2.9
415558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.9
412490	AW803564	Hs.28850	Homo sapiens cDNA: FLJ22528 fs, clone H	2.9
433149	BE257572	Hs.42949	hypothetical protein HE35	2.9
434811	AW971205	Hs.114280	ESTs	2.9
425897	AA535315	Hs.49955	Homo sapiens cDNA: FLJ21693 fs, clone C	2.9
452092	BE244574	Hs.27842	hypothetical protein FLJ11210	2.9
453496	AA442103	Hs.20394	solute carrier family 2 (facilitated glu	2.9
411124	AW199337	Hs.33929	ESTs, Weakly similar to ALU1_HUMAN III	2.9
419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.9
427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fs, clone MA	2.9
441707	RA2537	Hs.21963	hypothetical protein DKFZp76160514	2.9
437241	A206068	Hs.113029	ESTs	2.9
437273	AL137451	Hs.120873	ESTs, Highly similar to T46266 hypothetical	2.9
422939	AW394055	Hs.98427	ESTs, Weakly similar to L380222 hypothetical	2.9
439376	AA836321	Hs.222054	ESTs	2.9
439335	S75155	Hs.301976	phosphate receptor, inositol, kalirin	2.9
437267	AW511443	Hs.258110	ESTs	2.9
453740	AL120296	Hs.311809	ESTs, Moderately similar to PC4259 keri	2.9
400250				2.9
400492				2.9
408914	N62499	Hs.178227	hypothetical protein FLJ11155	2.9
411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	2.9
414853	UJ1116	Hs.77501	serocyclophilin, beta (3kD cyclophilin-assoc	2.9
423751	AW235633	Hs.46525	ESTs	2.9
428910	AA170223	Hs.190289	ESTs, Moderately similar to ALU1_HUMAN A	2.9
450203	AF097994	Hs.301520	L-lysine:serine:alpha-aminoisobutyrate aminoha	2.9
459311	RA0192	Hs.21527	Human DNA sequence from clone GSI-115M3	2.9
425204	AA463844	Hs.91339	fibroblast growth factor 11	2.9
426500	AB15395	Hs.154641	fatty acid desaturase 2	2.9
421641	AJ538184	Hs.106334	Homo sapiens clone Z3C36 mRNA sequence	2.9
421141	AW117261	Hs.129914	ESTs	2.9
407870	AD032990	Hs.40719	hypothetical protein KIAA1164	2.9
456723	Z43922	Hs.4748	adenylate cyclase activating polypeptide	2.9
438456	AW292877	Hs.249422	G-protein coupled receptor 24	2.9
421483	NM_003368	Hs.104717	hypothetical protein MGCI1333	2.9
412190	R16180	Hs.274461	ESTs	2.9
446131	NM_003929	Hs.290	phospholipase A2, group V	2.9
441668	AB11973	Hs.127625	ESTs	2.9
437387	AT198874	Hs.28847	AC026 protein	2.9
422420	AJ571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp7611224 (f	2.9
427958	AA418000	Hs.98280	potassium intermediate/small conductance	2.9
429084	AJ501443	Hs.1193614	gating factor 3b, subunit 3, 130kD	2.9
447067	RA2098	Hs.21964	ESTs	2.9
430687	N68601	Hs.260287	KIAA1641 protein	2.9
441824	AB007871	Hs.7977	KIAA0411 gene product	2.9
424126	AA335535	Hs.96917	ESTs	2.9
400739	WD156	Hs.248797	ESTs, Moderately similar to L380222 hypot	2.9
447422	BE618703	Hs.98258	orthopedia (Drosophila) homolog	2.9
435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-8k	2.9
446997	AA383439	Hs.16758	Sgk-1 protein	2.9
433573	AF242687	Hs.57832	cathepsin, EGF-LAG seven-pass G-type rece	2.9
408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fs, clone PL	2.9
419586	AJ039485	Hs.144759	ESTs, Weakly similar to L380222 hypothetical	2.8
417022	NM_014737	Hs.80905	Ras association (RasGAP/RAF-) domain fam	2.8
406432	AW195262	Hs.63667	glucocorticoid x1 NCL CGAP_CML1 Homo sapiens	2.8
420520	AB002951	Hs.95533	KIAA1353 protein	2.8
425241	AA324524	Hs.155247	aldolase C, fructose-bisphosphate	2.8
428670	AA431682	Hs.134832	ESTs	2.8
424415	NM_00101975	Hs.146580	enolase 2, (gamma, neuronal)	2.8
420185	AW961601	Hs.252908	hypothetical protein FLJ12295 similar to	2.8
411555	AF113537	Hs.70669	HMP19 protein	2.8
426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	2.8
458809	AW872512	Hs.20385	sin3-associated polypeptide, 30kD	2.8
420071	AB228985	Hs.54806	ATP-binding cassette, sub-family A (ABC1	2.8
426572	N119650	Hs.150741	2',3'-cyclic nucleotide 3'-phosphodiester	2.8
444670	H58733	Hs.332938	hypothetical protein MG25370	2.8
411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PTSLRE pr	2.8
415111	AA333813	Hs.79018	chromatin assembly factor 1, subunit A (2.8
440337	AW501115	Hs.7209	Homo sapiens clone Z3T41 mRNA sequence	2.8
408554	AA336381	Hs.151111	nuclear receptor co-repressor/NCOA3 comp	2.8

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[illegible]

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	445568	H00818	Hs.288744	KIAA1796 protein	2.7
	433315	R09754	Hs.239706	GRB2-associated binding protein 1	2.7
	428862	NM_000346	Hs.2516	SRV (tax determining region V) box 9 (p)	2.7
	447959	AI452784	Hs.270270	ESTs, Weakly similar to 2109259A B cell	2.7
5	426420	BE383808	Hs.322430	NDRG family, member 4	2.7
	436999	AA764852	Hs.291567	ESTs	2.7
	444100	AA363343	Hs.22116	CDC14 (cell division cycle 14, S. cerevisiae)	2.7
	436501	AW043782	Hs.293816	ESTs	2.7
	449892	U91641	Hs.22985	alpha2,8-sialyltransferase	2.7
10	427311	AB020872	Hs.175411	KIAA0955 protein	2.7
	453513	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	404629				2.7
	416289	Y026333	Hs.337438	ESTs	2.7
15	439108	AW163034	Hs.6467	synaptogyrin 3	2.6
	418746	A185209	Hs.300759	ribosomal protein L36	2.6
	412046	Y07847	Hs.73088	RAS-related on chromosome 22	2.6
	433040	A1852350	Hs.152935	ESTs	2.6
	453083	U87223	Hs.31622	contactin associated protein 1	2.6
20	428167	AA770021	Hs.16332	ESTs	2.6
	420028	AB014880	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	2.6
	437115	A1853187	Hs.3700	cyclin E1	2.6
	421247	BE391727	Hs.102910	general transcription factor IIf, polype	2.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.6
	415058	AB004862	Hs.77887	adenosine A1 receptor	2.6
25	415687	AW448774	Hs.205380	POM (POM121 rat homing) and ZP3 fusion	2.6
	433701	AW445023	Hs.15155	ESTs	2.6
	457358	AW479755	Hs.129010	ESTs	2.6
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.6
30	418527	AB537807	Hs.52353	hypothetical protein	2.6
	440491	F35252	Hs.24844	ESTs, Weakly similar to 2109260A B cell	2.6
	425171	AW732240	Hs.16385	ESTs	2.6
	458335	AW298545	Hs.250728	EST	2.6
	425402	AQ215881	Hs.24970	ESTs, Weakly similar to E343523 GTP-bind	2.6
35	451789	AB437815	Hs.32156	KIAA1194 protein	2.6
	436347	AA803367	Hs.222234	ESTs	2.6
	450414	A1807735	Hs.21446	KIAA1716 protein	2.6
	446233	A1282028	Hs.25205	ESTs	2.6
	415448	F08898	Hs.60075	ESTs	2.6
	445873	AA235870	Hs.251948	poly(A)-binding protein, cytoplasmic 14	2.6
40	413612	D83777	Hs.75137	KIAA0193 gene product	2.6
	428871	BE297851	Hs.189482	zinc finger protein 179	2.6
	427158	AA935603	Hs.166231	ESTs	2.6
	426888	AI119344	Hs.49478	Homo sapiens clone TUNA8 C6-de-ctet regl	2.6
	458516	A1049882	Hs.248558	EST	2.6
45	402693				2.6
	408039	AA131424	Hs.50340	ESTs	2.6
	422688	A1861489	Hs.154118	ESTs	2.6
	423130	AW087586	Hs.21213	ESTs	2.6
	438796	W67821	Hs.105860	genehonin 1	2.6
50	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.6
	440192	AA872282	Hs.190598	ESTs	2.6
	418708	AK000753	Hs.52274	hypothetical protein	2.6
	448438	AA880329	Hs.279307	hypothetical protein DKFZ434217	2.6
	436870	AW204219	Hs.155560	catechin	2.6
55	448424	AW009892	Hs.31924	ESTs	2.6
	401324				2.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	433943	AA92805	Hs.44885	lymphoid enhancer-binding factor 1	2.6
60	420001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	2.6
	429139	F08092	Hs.66067	ESTs	2.6
	423733	BE262822	Hs.123189	MAD (mothers against decapentaplegic, Dr	2.6
	445996	AW372914	Hs.86149	phosphoinositid 3-phosphate-binding prot	2.6
	444001	A1080587	Hs.152799	ESTs, Moderately similar to S65657 alpha	2.6
65	412049	N53437	Hs.18268	adenylylase kinase 5	2.6
	441783	BE313412	Hs.7961	Homo sapiens clone 25012 mRNA sequence	2.6
	425287	R881249	Hs.155524	peanut (Dioscorea)-like 2	2.6
	432148	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.6
	452234	AW084176	Hs.222396	ESTs, Weakly similar to R08022 hypotheti	2.6
70	453475	AF108386	Hs.33621	neuro-ectodermal ventral antigen 2	2.6
	418952	AF714635	Hs.271653	ESTs	2.6
	418858	AW951605	Hs.21145	hypothetical protein RG083M05.2	2.6
	443257	A1334040	Hs.11614	HSPC065 protein	2.6
	428748	AW993206	Hs.98785	Ksp37 protein	2.6
	444984	H15474	Hs.132888	fatty acid desaturase 1	2.6
75	433404	T32982	Hs.102720	ESTs	2.6
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.6
	402582	BE047878	Hs.39993	Homo sapiens chromosome 19, contig R2837	2.6
	452656	AF134789	Hs.30281	protein tyrosine phosphatase, receptor 1	2.6
	436440	AA747862	Hs.196008	Homo sapiens cDNA FL117223 fs, clone HE	2.6
80	438527	A1988251	Hs.115325	RAB7, member RAS oncogene family-like 1	2.6
	433216	AF217412	Hs.47320	neurodin 3	2.6
	435380	AA676001	Hs.192221	ESTs	2.6
	428866	AF359214	Hs.194687	cholesterol 25-hydroxylase	2.6

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	439653	AW021103	Hs.5631	hypothetical protein FLJ20373	2.6
	419304	AZ71326	Hs.146101	ESTs, Weakly similar to T45070 protein h	2.6
	422891	U110340	Hs.49862	Homo sapiens cDNA: FLJ16551 like clone C	2.6
5	448548	U13209	Hs.21413	solute carrier family 12, (potassium-ch)	2.6
	435370	A1964074	Hs.225938	ESTs	2.6
	408875	NM_015434	Hs.48604	DKGZP434E168 protein	2.5
	457005	AJ097471	Hs.172257	sal (Drosophila-like 3	2.5
	430154	AW533268	Hs.224726	sedlin (or cyclin) peptidase inhibitor	2.5
10	438549	BE336601	Hs.21855	truncuslike repeat containing 3	2.5
	427951	A1826125	Hs.43546	ESTs	2.5
	411800	U13942	Hs.103042	microtubule-associated protein 1B	2.5
	457893	A1821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451422	AF002336	Hs.26395	erythrocyte membrane protein band 4.1-i	2.5
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.5
15	428826	AL048942	Hs.194019	altrecin	2.5
	429963	AW332582	Hs.252068	Homo sapiens, clone MGC-15606, mRNA, com	2.5
	428141	D59402	Hs.162611	solute carrier family 11 (proton-coupled	2.5
	429550	AW293055	Hs.119357	ESTs	2.5
	438662	AA223599	Hs.6351	cleavage end polyadenylation specific fa	2.5
20	435760	AF231592	Hs.215304	chromosome 21 open reading frame 62	2.5
	427213	AL476316	Hs.192490	ESTs	2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	2.5
	417123	BE226221	Hs.159450	ESTs	2.5
25	439899	AF068534	Hs.167861	ESTs, Moderately similar to ALU1_HUMAN A	2.5
	412980	A1815750	Hs.20977	hypothetical protein MGC3129 similar to	2.5
	427208	H06509	Hs.92423	KIAA1566 protein	2.5
	424327	AA431707	Hs.31209	ESTs	2.5
	438340	R42246	Hs.21626	ESTs	2.5
30	450550	T65617	Hs.101257	hypothetical protein MGC3296	2.5
	436444	A277652	Hs.45478	ESTs, Weakly similar to 138022 hypotheti	2.5
	400777	AF049460	Hs.8574	deformed epidermal autoregulatory factor	2.5
	459407	NM_000510	Hs.24989	gamma-aminobutyric acid (GABA) A recepto	2.5
35	450385	A1831024	Hs.24048	synuclein, alpha intercalating protein (sy	2.5
	432558	R97268	Hs.177289	ESTs	2.5
	400860	BE391804	Hs.62061	guanylate binding protein 1, interferon-	2.5
	410351	BE047699	Hs.93454	ESTs	2.5
40	416963	NM_002543	Hs.77729	oxidized low density lipoprotein (oxldn	2.5
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	2.5
	417791	AW955539	Hs.114471	ESTs	2.5
	418079	R40564	Hs.8911	ESTs	2.5
	408495	W68796	Hs.237731	ESTs	2.5
45	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.5
	437370	AL359567	Hs.161962	Homo sapiens mRNA: cDNA DHFZp547D023 (r	2.5
	429803	V181489	Hs.223025	RAB21, member RAS-oncogene family	2.5
	424959	NM_006791	Hs.153537	activated p21cdc42Hs kinase	2.5
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.5
50	408955	BE316170	Hs.8087	NAG-5 protein	2.5
	415261	T49926	Hs.8346	ESTs	2.5
	415716	N52924	Hs.179862	nucleosome assembly protein 1-like 1	2.5
	417873	BE266859	Hs.293058	Homo sapiens, similar to RIKEN cDNA A430	2.5
	418388	R72332	Hs.29258	Homo sapiens cDNA FLJ11364 fs, clone HE	2.5
55	421002	AF116630	Hs.100532	transcription factor 17	2.5
	423244	AL033279	Hs.209692	ESTs, Weakly similar to ubiquitously TPR m	2.5
	423653	AA405635	Hs.96554	ESTs, Weakly similar to DYLL_HUMAN CYTO	2.5
	427961	AW293165	Hs.143134	ESTs	2.5
	428301	AW628666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	2.5
60	428308	BE252383	Hs.184968	SEB331 protein	2.5
	428359	AA438760	Hs.96554	gpcz67011.1 Secretes_solid_foliar_Nb2HFR	2.5
	428943	AW068180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein	2.5
	432427	AL037630	Hs.9638	Homo sapiens cDNA FLJ11602 fs, clone HE	2.5
	435347	AW041683	Hs.118963	ESTs	2.5
65	437949	U71819	Hs.41654	ESTs, Weakly similar to A46010 X-linked	2.5
	438208	AL041224	Hs.65379	ESTs	2.5
	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	2.5
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALU7_HUMAN III	2.5
	441665	AA285138	Hs.301814	neuronal specific transcription factor 3	2.5
70	442337	AC371029	Hs.129257	ESTs, Weakly similar to TC17_HUMAN TRANS	2.5
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.5
	445566	A1910241	Hs.12887	actin-related protein 3-beta	2.5
	449096	A1628257	Hs.208037	ESTs	2.5
75	459593	A1907673	Hs.101257	gtrL-BT152-080399-004 BT152 Homo sapien	2.5

TABLE 8B:

Play:	Unique Exon probe set identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

80	Play	CAT Number	Accession
	429432	1058867_1	AW195262 R27968 AWB11262
	412225	1284108_1	AW902642 N77591

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	412436	129439_1	AA655089 AA135130 AA494059 AA102419 AW677765
	416120	1571266_1	H46739 H51513 H57879
	416871	1620761_1	H59716 H60752 H24293
5	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749964 BE162498 BE161005 AA190445 AW513465 BE161006 BE162499
	422864	222336_1	AA318323 H11145 R15289 AA461845 AA476960 AA436954 Z43802 F11763 T65491 D81821
	422949	223104_1	AA319435 H56456 AA319377 AW961532 T49452 AA894424
	422977	223410_1	AA311498 AW11011 AA451211 AA761823 AA74555 AA768099 AA808286 AB34065 AA570223 AA574438 AA582438 AA745336 AW964510 AA319642
			AW853759 H56414
10	423756	231725_1	AA828125 AA834883 AA330655
	425168	247552_1	R96366 AL133926 AA351636 H78818 AA477084 Z28957 H80194
	425517	252729_1	AF121179 BE162736 AA353827
	428415	266650_1	AA378223 AW954494 AW22888
	428002	266602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	428679	294049_1	AA431765 AA432015
15	428858	296453_1	AA436790 AW237453 BE327855 H47347 H56967
	429207	293321_1	D08642 AA45145 AL115015 AW904593
	429163	301543_1	AA884786 AW974271 AA592975 AA447312
	433532	368950_1	AW975367 AA598607 AA747235
	436190	41555_1	AK001058 AA833595
20	437034	431715_1	AA742645 AA808575 AW979568
	438458	437637_1	AW575188 AA507697 D29548
	438993	467851_1	AA828955 AA034679 AS26361
	439566	47387_1	AF086387 W77884 W72711
	440222	49186_1	AA879430 BE070062 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400
25	444584	81466_1	A1618422 D81113 D80074
	447197	711623_1	R36075 A368546 R06167
	448451	764068_1	AW015994 R38898 AW000978 AS96202 AS21706
	450625	60302_1	AW970107 AA513951 AA010406
	454553	918320_1	AS252518 AW22519 AW252516
30	454988	124840_1	AW850180 AW850326
	455350	1283853_1	AW901808 AW901787 AW901735 AW901792 AW901744 AW901753 AW901807 AW901759

TABLE 8C:

Play: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "Human DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

40	Play	Ref	Strand	NL_position
	400777	8131663	Plus	70745-71121
	400780	8151663	Minus	116372-116819
	400859	9757499	Minus	91888-92018,98131-98294,99474-99670
	400860	9757499	Minus	151830-152104,152649-152744
45	400992	8096828	Plus	140390-140922
	401124	9863791	Plus	234057-234174
	402108	9798929	Minus	110326-110491
	402694	9909420	Plus	20393-20767
	402805	9909420	Minus	47680-47973
50	402819	8569863	Plus	82358-82515
	402835	9892353	Minus	58763-58909
	404029	7671292	Plus	108718-111112
	404048	3688074	Minus	54421-56808
	404049	3688074	Minus	75705-78155
55	404083	2276311	Minus	99460-99564
	404299	5784682	Minus	3820-4025
	404541	8318559	Plus	103456-103664
	404584	9857511	Plus	138651-139153
	404593	9844086	Minus	74822-75768
60	404721	9856648	Minus	173763-174264
	404819	4678240	Plus	16223-16319,16427-16513,16736-16855,16941-17075,17170-17287,17399-17528,18261-18357,19443-18578
	405238	7249119	Minus	51728-51836
	405771	7018349	Plus	91181-91254,91510-91589
	405819	407857	Plus	2630-2967
65	406311	9211559	Minus	137114-139033

TABLE 9A: ABOUT 1200 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)

Table 9A lists about 1200 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix Eos HUG GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average" glioblastoma level was set to be the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to be the 95th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Play: Unique Eos probe set identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenetID: Unigen number
 Unigen Title: Unigen gene title
 RT: Ratio of 75th percentile tumor to 95th percentile normal adult nervous system tissue

80	Play	ExAccn	UnigenetID	Unigen Title	RT
	452461	H07223	Hs.108108	transcription factor	26.1
	438195	AF037335	Hs.5339	carbonic anhydrase XII	15.2
	453941	U39817	Hs.38620	Bloom syndrome	14.2

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443247	BE614387	Ha.333893	c-Myc target JPO1	12.4
428330	L22524	Ha.2295	matrix metalloproteinase 7 (matrilysin)	12.9
447242	A199268	Ha.118372	Homo sapiens. Similar to RIKEN cDNA 2010	11.7
422163	AF027208	Ha.112360	proinin (mouse)-like 1	11.4
439451	AF085270	Ha.278554	heterochromatin-like protein 1	11.2
424900	AL035588	Ha.153303	MyoD family inhibitor	10.2
416111	AA338113	Ha.75018	chromatin assembly factor 1, subunit A (10.0
444190	AB39518	Ha.10525	cysteine and glycine-rich protein 2	9.9
412140	AA219691	Ha.73625	RAB6 interacting, kinesin-like (gabins)	9.9
446340	AW235796	Ha.155359	hypothetical protein MG010954	9.8
409731	AA125965	Ha.56145	thymic, beta, identified in neuroblast	9.4
439978	BE136440	Ha.124673	Homo sapiens cDNA FLJ11477.1s, clone HE	8.9
411411	AA345241	Ha.55950	ESTs. Weakly similar to KIAA1330 protein	8.9
456516	BE127704	Ha.222746	KIAA1610 protein	8.2
420092	AA014043	Ha.89045	ESTs	7.9
422631	BE126191	Ha.118793	hypothetical protein FLJ10698	7.9
453392	UZ3752	Ha.32964	SRY (sex determining region Y)-box 11	7.9
438527	A969251	Ha.115325	RAB7, member RAS oncogene family-like 1	7.9
427551	NM_014788	Ha.179703	KIAA0129 gene product	7.8
418661	NM_001949	Ha.1169	E2F transcription factor 3	7.8
440684	AZ53123	Ha.127356	ESTs. Highly similar to S21424 nestin [H	7.8
429643	AA456869	Ha.167279	PYVE-finger-containing Rab5 effector pro	7.7
409638	AW450420	Ha.21335	ESTs	7.5
444665	BE613126	Ha.47763	B aggressive lymphoma gene	7.5
456759	BE291550	Ha.127792	della (Drosophila)-like 3	7.5
412777	A135773	Ha.270123	ESTs	7.4
436607	AW681793	Ha.211061	ESTs	7.3
432058	AW989996	Ha.130729	ESTs. Weakly similar to ALU1_HUMAN ALU S	7.3
417061	A967594	Ha.158911	Homo sapiens cDNA FLJ12035.1s, clone HE	7.2
406876	AL037824	Ha.194955	ras homolog gene family, member 1	7.2
432244	AB040843	Ha.271285	KIAA1510 protein	7.1
436726	AA324975	Ha.128993	ESTs. Weakly similar to T00079 hypothet	7.1
408432	AW155262	Ha.143135	gbox67b05.x1 NCL_CGAP_CM1.1 Homo sapiens	7.1
434164	AW207019	Ha.145135	serine/threonine kinase 33	7.1
446873	AA250670	Ha.251946	poly(A)-binding protein, cytoplasmic t-1	7.0
439726	AW443953	Ha.253707	ESTs. Weakly similar to 138556 zinc fin	7.0
432656	NM_002466	Ha.3076	MHC class II transactivator	6.8
431117	AF003522	Ha.255050	della (Drosophila)-like 1	6.8
453387	A1990741	Ha.252805	ESTs	6.8
418821	AA436002	Ha.183161	ESTs	6.6
437034	AA42643	Ha.65320	gbox51c01.s1 NCL_CGAP_CCB1 Homo sapiens	6.6
411252	AB018569	Ha.151738	MD-2 protein	6.5
424637	JG5076	Ha.151738	matrix metalloproteinase 9 (gelatinase B	6.4
452553	A1932894	Ha.271741	ESTs. Weakly similar to A48010 X-linked	6.3
433532	AW575367	Ha.33207	gboxEST38745 MAGS resequences, MAGN Homo	6.3
420311	AW445044	Ha.21868	Human DNA sequence from clone RP4-5301.5	6.3
418957	RA51127	Ha.13372	ESTs	6.2
407304	AA555832	Ha.13372	gbox32b03.s1 NCL_CGAP_AA1 Homo sapiens	6.2
435266	AF193766	Ha.57471	cyclin-like protein C17	6.1
449448	D60730	Ha.57471	ESTs	6.1
403790				6.0
425517	AF121179	Ha.1327	gboxAF121179 Homo sapiens liver (Chang L-	6.0
420674	NM_000055	Ha.286533	butyrylcholinesterase	6.0
435542	AA887376	Ha.286533	ESTs	5.9
418216	AA062240	Ha.283099	AF15q14 protein	5.8
435086	AF062447	Ha.42233	gboxHomo sapiens full length insert cDNA	5.8
408037	AW271720	Ha.42233	hypothetical protein FLJ10300	5.7
412225	AW902042	Ha.132780	gboxOVO-NN1022-170400-153-c02 NN1022 Homo	5.7
436109	AA322153	Ha.132780	hypothetical protein MG015729	5.7
435555	AB9743	Ha.390894	nucleotide repeat containing 12	5.7
429149	AW193360	Ha.197952	ESTs. Weakly similar to 380222 hypothet	5.7
418113	AL272141	Ha.83484	SRY (sex determining region Y)-box 4	5.6
405558				5.6
442422	BE033699	Ha.381878	hypothetical protein FLJ23688	5.6
442547	AA306997	Ha.217494	ESTs. Weakly similar to ALU1_HUMAN ALU S	5.6
413063	AL035737	Ha.75184	chitinase 3-like 1 (chitinase glycoprotein	5.5
420560	AW207748	Ha.59115	ESTs	5.5
408096	BE292162	Ha.83765	dihydrofolate reductase	5.5
443539	AW76182	Ha.134974	ESTs. Moderately similar to ALU1_HUMAN A	5.4
426318	AA375125	Ha.147112	Homo sapiens cDNA: FLJ23232.1s, clone H	5.4
429115	AA446728	Ha.289020	Homo sapiens cDNA FLJ14086.1s, clone MA	5.3
453900	AW003582	Ha.226414	ESTs. Weakly similar to ALU1_HUMAN ALU S	5.3
444168	AW379879	Ha.226414	gboxC1-HT0256-081155-011-011 HT0256 Homo	5.3
432789	D63661	Ha.3104	KOJ4042 gene product	5.3
437036	A1571514	Ha.133022	ESTs	5.2
412147	BE391727	Ha.102510	general transcription factor IIF, polype	5.2
421523	AW514263	Ha.301771	ESTs. Weakly similar to ALU1_HUMAN III	5.2
431106	BE382701	Ha.252960	v-neg when myeloblastoma virus is not	5.1
457211	AW972565	Ha.32399	ESTs. Weakly similar to S51797 v-susflat	5.1
454157	AW162906	Ha.312481	ESTs. Weakly similar to S08666 hydrogen	5.1
423343	AA324643	Ha.248106	ESTs	5.1
432592	NM_055824	Ha.155545	37 kDa leucine-rich repeat (LRR) protein	5.1
406679	AA070786	Ha.155545	gboxm6907.1 Sitagliptin neuroepithelium	5.1

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442671	AD05668	Hs.134779	EST	5.1
433001	AF217513	Hs.279605	clone HQ0310 PRO0310p1	5.0
418819	AA228776	Hs.191721	ESTs	5.0
432946	U60899	Hs.279854	mannosidase, alpha, class B2, member 1	4.9
420730	NM_002891	Hs.95890	polymerase (DNA directed), delta 1, cat	4.9
441217	A0922183	Hs.213246	ESTs	4.9
453385	AW295101	Hs.253405	ESTs	4.8
418203	X54942	Hs.830758	CDC28 protein kinase 2	4.7
450813	AF393625	Hs.203376	ESTs	4.7
444006	BE350605	Hs.10086	type 1 transmembrane protein Fn14	4.7
412530	AA765628	Hs.206271	hypothetical protein FLJ13245	4.7
431070	AW406154	Hs.245194	transcription factor 19 (SC1)	4.7
429786	AL080232	Hs.220656	Homo sapiens mRNA; cDNA DKF2p568A061 p	4.7
405771				4.6
457055	AA75318	Hs.192460	ESTs	4.6
436190	AK001059		g0Homo sapiens cDNA FLJ10197 fa, clone	4.6
400859				4.6
435287	N23797	Hs.110114	ESTs	4.6
443454	AF057484	Hs.133421	ESTs	4.6
452811	AA337079	Hs.110803	hypothetical protein FLJ12150	4.5
437257	AW511443	Hs.258110	ESTs	4.5
435020	AW505075	Hs.301855	DiGeorge syndrome critical region gene B	4.5
454289	AB61060	Hs.122950	KIA0261 protein	4.5
422108	D84235	Hs.111732	Fe fragment of IgG binding protein	4.5
422755	AW406701	Hs.1576	bacterial W9 repeat-containing 5 (par	4.5
455534	X31195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	4.5
423755	AA028125		g0cd71a09.1 NCL_CGAP_Ov2 Homo sapiens	4.5
417308	H50720	Hs.81852	KIA0101 gene product	4.5
422170	AF791349	Hs.112432	anti-Müllerian hormone	4.4
429500	X75595	Hs.285114	harabachion (tenascin C, cyclotactin)	4.4
405568	AF060606	Hs.115590	cathepsin F	4.4
426812	AF105365	Hs.172613	solute carrier family 12 (potassium/chlo	4.4
402515				4.4
432865	AF53709	Hs.152404	ESTs, Weakly similar to 133022 hypotheti	4.4
413625	AW451103	Hs.71371	ESTs	4.4
436036	R20597	Hs.5739	glyoxal-3-phosphate dehydrogenase 1 (so	4.4
413333	W52113		g0zth45d01.1 Soares_kela_liver_spleen_	4.4
418933	BE581850	Hs.80505	small nuclear ribonucleoprotein polypep	4.4
438192	AB589055	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	4.3
457374	AA483662		g0mh05d12s1 NCL_CGAP_Thyl1 Homo sapiens	4.3
431359	AB035698	Hs.150587	kinesin-like protein 2	4.3
444038	BE055183		g0bCr1-BT0314-020000-012-c04 BT0314 Homo	4.3
453202	AF005731	Hs.26270	hypothetical protein FLJ11536	4.3
441020	W79283	Hs.35392	ESTs	4.3
414733	BE514335	Hs.77171	mitochondrion maintenance deficient (S	4.3
407902	AL117474	Hs.41193	Homo sapiens mRNA; cDNA DKF2p727C181 (tr	4.3
405701				4.3
451559	BE379781	Hs.14248	ESTs	4.3
418945	AA952995	Hs.592322	chromobox homolog 5 (Drosophila HP1 alp	4.2
433323	AA005132	Hs.30701	ESTs	4.2
439811	AA135332	Hs.71993	ESTs	4.2
415406	T25510		g0AB282FBR Infant brain, L1/N1, array of	4.2
435282	RS1913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.1
441289	AW015206	Hs.176734	ESTs	4.1
413727	AA227609	Hs.94034	ESTs	4.1
433005	BE242758	Hs.190223	ESTs, Moderately similar to T25295 hypot	4.1
436480	AJ271543	Hs.97469	putative acid-sensing ion channel1	4.1
430766	AA456144	Hs.31293	ESTs	4.1
445372	N36417	Hs.144928	ESTs	4.1
410555	U92849	Hs.64311	a-disintegrin and metalloproteinase doma	4.0
457455	AW301344	Hs.122906	DNA replication factor	4.0
422094	AF129535	Hs.272027	F-box only protein 5	4.0
440229	AW556698	Hs.14455	neural precursor cell expressed, develop	4.0
459321	AW044477	Hs.299536	ESTs	4.0
421308	AA087322	Hs.152843	leucine zipper protein FKSG14	4.0
420667	AW000812	Hs.98874	similar to prolactin-like protein 48	4.0
447004	AW296958	Hs.157539	ESTs	4.0
442255	AA381911	Hs.334859	NAB1814 protein	3.9
439599	AF086534	Hs.187551	ESTs, Moderately similar to ALU1_HUMAN A	3.9
440704	M5241	Hs.162	Insulin-like growth factor binding prote	3.9
453096	AW294631	Hs.11325	ESTs	3.9
457025	AA397620	Hs.48932	ESTs	3.9
404642				3.9
450375	AA009647	Hs.8850	a-disintegrin and metalloproteinase doma	3.9
430132	AA204586	Hs.234149	hypothetical protein FLJ20647	3.9
437718	AF922788	Hs.196779	ESTs	3.9
438490	AW453272	Hs.301259	ESTs	3.9
429919	AA450592	Hs.278945	hypothetical protein FLJ23024	3.9
413604	RS1767		g0yrg73g1s1 Soares infant brain 11NB H	3.9
423599	AW336745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
449796	AA147829	Hs.331431	antibacterial zinc finger protein induced	3.9
445300	AB585659	Hs.272165	ESTs	3.8
452203	X57522	Hs.158164	transporter 1, ATP-binding cassette, sub	3.8

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	425765	U72513	Hs.155486	Human RPL13.2 pseudogene mRNA, complete	3.8
	404295				3.8
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.8
	428728	NM_016625	Hs.191381	hypothetical protein	3.8
5	409142	AL136877	Hs.50750	SMCA (structural maintenance of chromoso	3.8
	430172	AA668591	Hs.161889	ESTs	3.8
	147499	AW262580	Hs.147674	proteasome beta 16	3.8
	408984				3.8
10	437236	AW137817	Hs.244353	ESTs	3.7
	418883	BE367036	Hs.1211	acid phosphatase 5, tartrate resistant	3.7
	444143	AW747996	Hs.160599	ESTs, Moderately similar to A56194 throm	3.7
	425529	NM_014656	Hs.158292	KIAA0400 gene product	3.7
	425502	R98895	Hs.128323	ESTs	3.7
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.7
15	402424				3.7
	429463	M54590	Hs.27	glycine dehydrogenase (decarboxylating;	3.7
	457072	H70854	Hs.263059	Homo sapiens PR01082 mRNA, complete cds	3.7
	414672	U82010	Hs.77513	COX10 (yeast) homolog, cytochrome c oxid	3.7
20	426071	AW138057	Hs.163635	ESTs	3.7
	419078	M31119	Hs.83594	neutrophin-associated 1	3.7
	425037	W17474	Hs.85230	potassium intermediate/small conductance	3.7
	416547	H62914	Hs.269946	ESTs, Weakly similar to PC4259 keratin	3.7
	436999	AA764852	Hs.291567	ESTs	3.6
25	436722	AW975977		gbcST1389086 MAGE resequences, MAGN Homo	3.6
	440552	A216751	Hs.143977	ESTs	3.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	3.6
	452103	R42764	Hs.339654	ESTs, Weakly similar to 138022 hypothei	3.6
	409048	H59990		ESTs	3.6
30	439546	AF038056		gbcHomo sapiens full length insert cDNA	3.6
	443544	A078315	Hs.16359	ESTs	3.6
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.6
	435899	A1249107	Hs.229901	ESTs	3.6
	420301	AA787526	Hs.22303	paired box gene 5 (B-cell lineage specifi	3.6
	436078	A015377	Hs.131953	ESTs	3.6
35	406420	NM_005915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	3.6
	416871	H98716		gbcX133008.1 Soares melanocyte 2NBHM Ho	3.5
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.5
	446291	BE597753	Hs.14623	Interferon, gamma-inducible protein 30	3.5
	432261	A0001239	Hs.274253	hypothetical protein FLJ10377	3.5
40	439123	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	3.5
	411256	AW834039		gbcCNO T10010-08199-063-469 T10010 Homo	3.5
	413929	AA468163	Hs.184599	Homo sapiens cDNA: FLJ20411, clone C	3.5
	435065	BE064391		gbcRC4-BT0310-110300-015-045 BT0310 Homo	3.5
	435532	AW251439	Hs.117305	Homo sapiens, clone IMAGE368230, mRNA	3.5
45	447101	N72185	Hs.44189	ESTs	3.5
	410530	M26809	Hs.64173	ATPase, H ⁺ -transporting, lysosomal (vacu	3.5
	422156	H54524		gbcY55610.1 Soares, multiple sclerosis, _	3.5
	458116	NM_003462	Hs.333846	dymin, axonemal, light intermediate pol	3.5
	439743	AL389956	Hs.283858	Homo sapiens mRNA full length insert cDN	3.5
50	453884	AA355925	Hs.26232	KIAA0186 gene product	3.5
	426954	NM_002548	Hs.15465	tumor protein p53 (Li-Fraumeni syndrome)	3.5
	420721	A4627802	Hs.169471	ZAP3 protein	3.5
	428784	AA732524	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN III	3.4
	420849	A089994	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.4
55	448531	AL030123	Hs.22182	zinc finger protein 23 (K0X 16)	3.4
	444371	BE540274	Hs.239	forkhead box M1	3.4
	402694				3.4
	442407	AW466584	Hs.32353	mitogen-activated protein kinase kinase	3.4
	414300	A1048470	Hs.166880	ESTs	3.4
60	444670	H58373	Hs.332938	hypothetical protein MGC5370	3.4
	414550	BE37808		gbc601159567T1 NH_MGC_53 Homo sapiens c	3.4
	452211	A985513	Hs.233420	ESTs	3.4
	414416	AW409885	Hs.76094	hypothetical protein MGC2721	3.4
65	445361	AW265634	Hs.133100	ESTs	3.4
	413257	BE176035		gbcTMs-BT0642-268000.002 g05 BT0564 Homo	3.4
	453857	AL060235	Hs.35661	DKFZP586E1621 protein	3.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.4
	422846	BE133634	Hs.1083	myotubular cytosolic factor 1 (MYT), chr	3.4
	446189	H63284	Hs.214013	ESTs	3.4
70	437385	AA757055	Hs.164600	ESTs	3.4
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	3.4
	406298	A1745326	Hs.271923	Homo sapiens cDNA: FLJ22785, clone K	3.4
	455778	BE089746		gbcCAR-BT0693-210300-125-d09 BT0693 Homo	3.3
	417546	HE5669	Hs.18845	ESTs	3.3
75	412471	M63193	Hs.73946	endothelial cell growth factor 1 (pleiot	3.3
	454631	AW811324		gbcIL3-BT0141-131099-017-A02 ST0141 Homo	3.3
	442924	AB000734	Hs.52640	JAK binding protein	3.3
	457131	AC002510	Hs.300463	Human Chromosome 16 BAC clone C17B78K.A	3.3
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035, clone HE	3.3
80	449676	AW380579	Hs.209567	ESTs	3.3
	436211	A0001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.3
	453746	AL126111		gbcCMT2p/WH119_17181 (synonym: homy2)	3.3
	452799	A3948629	Hs.213786	ESTs	3.3

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5	434008	AA740878	Hs.112882	ESTs	3.0
	432268	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	3.0
	414239	A1288330	Hs.182330	ESTs	3.0
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.0
	424636	AA420987	Hs.115455	Homo sapiens cDNA FLJ14259 fs, clone PL	3.0
10	410276	A154545	Hs.18301	ESTs	3.0
	433865	N26862	Hs.44104	ESTs	3.0
	406028				3.0
	401626				3.0
	415949	H10552	Hs.21691	ESTs	3.0
15	418883	AA604379	Hs.86211	hypothetical protein	3.0
	417933	X02308	Hs.82962	thymidylate synthetase	3.0
	434577	R37316	Hs.178769	Homo sapiens cDNA FLJ22487 fs, clone H	3.0
	430437	A1768801	Hs.169543	Homo sapiens cDNA FLJ13565 fs, clone PL	2.9
	427940	AA17812	Hs.38775	ESTs	2.9
20	456060	C14904	Hs.45194	Homo sapiens cDNA FLJ12284 fs, clone MA	2.9
	421988	AW450481	Hs.161333	ESTs	2.9
	448775	AB025237	Hs.398	nudix (nucleoside diphosphate linked mol	2.9
	436938	AW89843	Hs.326867	hypothetical protein MGC53178	2.9
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.9
25	451189	AA016019	Hs.40905	ESTs	2.9
	401558				2.9
	426207	BE390657	Hs.30026	HSPC182 protein	2.9
	404721				2.9
	401384				2.9
30	417288	A1884792	Hs.108812	hypothetical protein FLJ22004	2.9
	427648	A1376722	Hs.180105	prolactosome (prosome, macroprotein) subunit,	2.9
	435528	H54345	Hs.133951	ESTs	2.9
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	2.9
	428242	H55709	Hs.2260	leukemia inhibitory factor (cholinergic	2.9
35	438972	A1349100	Hs.124652	ESTs	2.9
	433112	AA075801	Hs.144583	ESTs, Weakly similar to unnamed protein	2.9
	423751	AW235633	Hs.48525	ESTs	2.9
	406748	AW339106	Hs.217453	annexin A2	2.9
	422154	T79045	Hs.126927	ESTs	2.9
40	405988				2.9
	443911	AA909536	Hs.143562	ESTs	2.9
	412420	AL036688	Hs.73853	bone morphogenetic protein 2	2.9
	445043	AW014413	Hs.195066	ESTs	2.9
	410114	AW590540	Hs.271280	ESTs	2.9
45	415217	AA504671		gbcx06012r1 NC1_CGAP_GCB1 Homo sapiens	2.9
	415849	R03028	Hs.5806	ESTs	2.9
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.9
	453331	A1240606	Hs.8895	ESTs	2.9
	432065	AA401039	Hs.2933	protein phosphatase 4 (formerly Xc, cate	2.9
50	433830	T05430	Hs.6194	chondroitin sulfate proteoglycan BEHA8b	2.9
	454377	AA070811		gb:7803C12 Chromosome 7 Fetal Brain cDNA	2.9
	421491	H99999	Hs.42736	ESTs	2.9
	452291	AF015592	Hs.28853	CDG7 (cell division cycle 7, S. cerevisi	2.8
	415446	P08809	Hs.66075	ESTs	2.8
55	439519	W15336		gbcx050x04r1 Soares_fetal_hear1_NbHH19W	2.8
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	2.8
	422403	AA474183	Hs.250173	hypothetical protein FLJ13158	2.8
	419461	AB07117	Hs.305335	synaptobrevin 1	2.8
	448789	BE339108	Hs.22051	hypothetical protein MGC15548	2.8
60	424126	AA335636	Hs.96917	ESTs	2.8
	458895	AV660159	Hs.282284	ESTs, Weakly similar to I39022 hypotheti	2.8
	418973	AA233066	Hs.191519	ESTs	2.8
	440471	A488146	Hs.307944	ESTs	2.8
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.8
65	433647	AA603367	Hs.222294	ESTs	2.8
	419817	U88867	Hs.75857	protein tyrosine phosphatase, receptor-t	2.8
	421723	AA420400	Hs.300717	sodium channel, voltage-gated, type III,	2.8
	434654	AB389550	Hs.130746	ESTs	2.8
	432622	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.8
70	400517	AF242388	Hs.149585	lensin	2.8
	433263	AW864793	Hs.57469	thrombospondin 1	2.8
	448134	BE114070	Hs.254416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	406736	A1254733	Hs.182426	ribosomal protein S2	2.8
	409207	AW373564	Hs.194637	BANP homolog, SMAR1 homolog	2.8
75	440196	N12847	Hs.126221	ESTs	2.8
	403561				2.8
	420193	AW955689	Hs.22509	ESTs	2.8
	425268	AB807883	Hs.180059	Homo sapiens cDNA FLJ20653 fs, clone KA	2.8
	440483	A1200836	Hs.150386	gb:PC0-MT0004-130300-011-c07 MT0004 Homo	2.8
80	412391	AW947710		ESTs	2.8
	448769	N68037	Hs.38173	ESTs	2.8
	411532	AW954829		gb:CV2-CT0261-201099-011-01 CT0261 Homo	2.8
	438221	A1798853	Hs.122224	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.8
	457578	AA578027		gbcx06012r1 NC1_CGAP_HSC1 Homo sapiens	2.8
	455110	AA422029	Hs.143640	ESTs, Weakly similar to hypoxanthine	2.8
	447169	AW673704	Hs.320831	Homo sapiens cDNA FLJ14597 fs, clone NT	2.8
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.8

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	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	2.8
	439662	H97552	Hs.26906	ESTs	2.8
	424694	U51333	Hs.159237	hexokinase 3 (white cell)	2.8
5	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis	2.8
	414598	AJ094221	Hs.135150	lung type-I cell membrane-associated gly	2.8
	447752	M73700	Hs.105358	lactoferrin	2.8
	400761	AA057264	Hs.238936	ESTs, Weakly similar to (beta1 not ava	2.8
	453350	AJ517771	Hs.61790	hypothetical protein FLJ21338	2.7
	456629	AWB91965	Hs.279789	histone deacetylase 3	2.7
10	439538	AA637323	Hs.104047	ESTs	2.7
	458914	AJ969857	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	2.7
	459029	BE255990	Hs.218239	hypothetical protein	2.7
	451129	BE072881		gb:RC2-BT0545-200300-012-e09 BT0548 Homo	2.7
	459412	AW749617	Hs.280776	kinase, TRF-1-interacting myosin-rela	2.7
15	453536	AA137000	Hs.62978	ESTs	2.7
	433378	AW910529	Hs.86404	hypothetical protein FLJ21816	2.7
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fls, clone H	2.7
	445322	N23033	Hs.155814	ESTs	2.7
	451652	AJ065416	Hs.213997	ESTs	2.7
20	429466	V85635	Hs.12827	ESTs	2.7
	429747	N87507	Hs.2490	carpase 1, apoptosis-related cysteine pr	2.7
	455514	AW983871		gb:RC1-HN0003-220300-021-h07 HN0003 Homo	2.7
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S	2.7
	444207	AJ855034	Hs.75752	cathepsin D (lysosomal aspartyl protease	2.7
25	427421	AA402414	Hs.30569	cohesin protein complex, subunit beta	2.7
	449655	AJ021987	Hs.59970	ESTs	2.7
	422648	D69693	Hs.118893	Meinoma associated gene	2.7
	428494	AA233439	Hs.184054	hypothetical protein FLJ20905	2.7
	404885	Y05946	Hs.172503	polyproteinase I acid binding protein (he	2.7
30	453295	AA278167	Hs.19215	Homo sapiens, clone IMAGE:3905822, mRNA	2.7
	427348	NM_014137	Hs.177288	PRO0550 protein	2.7
	435370	AB640474	Hs.225838	ESTs	2.7
	407892	BE543267	Hs.50734	Homo sapiens cDNA FLJ10534 fls, clone OV	2.7
	411874	AA096106	Hs.20403	ESTs	2.7
35	421192	AA833738	Hs.204529	KIAA1805 protein	2.7
	435699	V69033	Hs.189914	ESTs	2.7
	414603	R65394	Hs.25119	ESTs, Weakly similar to YEXQ_YEAST HYPOT	2.7
	453452	AJ037291	Hs.236655	ESTs, Moderately similar to A1LM_HUMAN A	2.7
	430654	AJ968810	Hs.301173	ESTs	2.7
40	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S	2.7
	403881				2.7
	431779	AW971178	Hs.268571	spolipoprotein C-4	2.7
	404584				2.7
45	448755	BE514434	Hs.20830	kinasin-like 2	2.7
	446839	BE031926	Hs.16244	mitotic spindle coiled-coil related prot	2.7
	411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.7
	404766				2.7
	447072	D61594	Hs.17279	tyrosine/protein sulfotransferase 1	2.7
	422176	N80977	Hs.29076	gb:yB9a1.1.s1 Soares fetal liver spleen	2.7
50	439627	BE821702	Hs.29076	hypothetical protein FLJ21641	2.7
	435632	AJ721522		gb:cw441.12.1 NCL_CoxAP_Ew1 Homo sapiens	2.7
	412833	AW930547	Hs.298262	ribosomal protein S19	2.7
	457245	AT45498	Hs.204579	ESTs	2.7
	446801	AJ695519	Hs.14427	Homo sapiens cDNA: FLJ21800 fls, clone H	2.7
55	432653	R91778	Hs.39309	ESTs	2.7
	450386	BE380047		gb:B01155362F2_HMG_NHC_53 Homo sapiens c	2.7
	438764	AA824524	Hs.336452	ESTs	2.7
	429285	AJ971081	Hs.20432	ESTs, Weakly similar to I30022 hypothet	2.7
	424653	BE549373	Hs.152967	Human EST clone 122807 marine invertebra	2.7
60	430017	BE409649	Hs.227789	mitogen-activated protein kinase-activat	2.7
	449892	N73608	Hs.550309	ESTs	2.7
	454201	AB023191	Hs.44131	KIAA0974 protein	2.7
	422279	AA296844	Hs.51260	hypothetical protein FLJ13164	2.7
	427354	J03050			2.7
65	400371	U80740	Hs.247551	metastin 1	2.7
	452449	AW068658	Hs.20943	ESTs	2.7
	431114	AA452400	Hs.291015	ESTs	2.7
	417098	ME4915	Hs.81110	pim-1 oncogene	2.7
70	447074	BE270540	Hs.151912	cyclic-dependent kinase 2	2.7
	403690				2.7
	454679	AW813110		gb:CM4-ST0189451099-021-005 ST0189 Homo	2.7
	411968	AZ07410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	2.6
	422240	HE0594	Hs.29002	KIAA1700 protein	2.6
	424368	AB037705	Hs.146085	KIAA1345 protein	2.6
75	405808				2.6
	419700	AF064933	Hs.52357	galactokinase 1	2.6
	435972	V95088	Hs.114158	ESTs	2.6
	435268	S70782	Hs.557	adrenergic, alpha-1D-, receptor	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
80	444156	AW900059	Hs.86437	ESTs, Highly similar to AF218140.1 gastr	2.6
	426205	AA424197	Hs.39947	ESTs, Weakly similar to S330466 hypox1	2.6
	437640	AA764893	Hs.727155	ESTs, Weakly similar to I30022 hypothet	2.6
	453948	AJ879797	Hs.64869	ESTs	2.6

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	415402	AA164687	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	2.6
	425397	J04388	Hs.193346	lysozymes (DNA) II alpha (LYOJ)	2.6
	418228	AA952181	Hs.111219	ESTs, Moderately similar to ALU1_HUMAN A	2.6
5	401324				2.6
	425234	AW152225	Hs.155939	ESTs, Weakly similar to I380222 hypothetical	2.6
	443210	A0192649	Hs.3951	hypothetical protein MGCI3168	2.6
	457244	AA581385	Hs.162473	ESTs, Weakly similar to I380222 hypothetical	2.6
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	2.6
	433933	A0754389	Hs.133494	Homo sapiens clone TCCCA00154 mRNA sequ	2.6
10	437437	AA276869	Hs.16520	hypothetical protein DKFZp762L0311	2.6
	434205	AW135973	Hs.288516	ESTs, Weakly similar to S01950 antigen	2.6
	400992				2.6
	455530	AW684744	glb1-RCN015-040400-011-003 HNO15 Homo	2.6	
15	436139	AA766786	Hs.120936	ESTs	2.6
	440330	AL038449	Hs.207163	ESTs	2.6
	412942	AL120344	Hs.75074	mitogen-activated protein kinase-activat	2.6
	432753	NM_014075	Hs.335938	Homo sapiens PRO0593 mRNA, complete cds	2.6
	433430	A0863735	Hs.186755	ESTs	2.6
20	436693	AW073223	Hs.303197	B-cell CLL/lymphoma 7C	2.6
	429482	A0707874	Hs.203952	transcription/translation domain-asso	2.6
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	2.6
	414217	A0309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fs, clone I	2.6
	434165	AA971528	Hs.95361	myosin VIIA (Usher syndrome 1B) (autosoma	2.6
	414655	AA156720	Hs.103342	ESTs	2.6
25	424489	148551	Hs.149250	D-galact precursor,	2.6
	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.6
	403797				2.6
	434573	AW372340	Hs.159717	ESTs	2.6
30	418841	NM_002332	Hs.89137	low density lipoprotein-related protein	2.6
	415785	R82419	Hs.23603	ESTs, Moderately similar to ALU3_HUMAN A	2.6
	450608	AA010365	Hs.193229	ESTs	2.6
	425304	AA463844	Hs.313389	fibroblast growth factor 11	2.6
	432268	B0311556	Hs.274230	3'-phosphoadenosine 5'-phosphosulfate sy	2.6
	410507	AA355288	Hs.40834	translational splicing response protein	2.6
	427343	A038044	Hs.176977	protein kinase C binding protein 2	2.6
35	420617	AW133716	Hs.117330	ESTs	2.6
	414399	147345	Hs.155202	transcription elongation factor II (SII)	2.6
	446009	A0180021	Hs.270651	ESTs, Moderately similar to A47582 B-cell	2.6
	440829	AF136407	Hs.7446	chromosome 6 open-reading frame 5	2.6
40	403475	AA315514	Hs.47986	hypothetical protein MGCI0940	2.6
	455946	AA374568	Hs.127683	ESTs, Moderately similar to Z109206A B c	2.6
	421462	AF016466	Hs.104624	avacuorin B	2.6
	434846	AW295389	Hs.119766	ESTs	2.6
	422887	A0751848	Hs.49215	ESTs	2.6
45	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	2.6
	437389	AL359367	Hs.271568	hypothetical protein DKFZp762M115	2.6
	408981	AW500797	Hs.49427	Gens-interacting protein	2.6
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	2.6
	418079	R40058	Hs.6911	ESTs	2.5
50	437620	AA769002	Hs.323836	ESTs, Weakly similar to alternatively sp	2.5
	436835	AW956751	Hs.283937	ESTs, Weakly similar to FOXO2_HUMAN FORKH	2.5
	426661	AB018297	Hs.159183	KIAA0754 protein	2.5
	435177	A018174	Hs.42936	ESTs	2.5
	437323	AA371145	Hs.226627	leptin receptor	2.5
55	422114	AW194651	Hs.111901	aspartate resistance protein ARS2	2.5
	448478	A1523218	Hs.203456	ESTs	2.5
	426623	AA382826	Hs.132793	ESTs	2.5
	446764	A0558807	Hs.182112	ESTs	2.5
	452385	A0551489	Hs.246214	ESTs	2.5
60	403726	N26939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5
	444888	A0551039	Hs.148559	ESTs	2.5
	456179	H75490	Hs.21930	ESTs	2.5
	424840	D75987	Hs.153479	nitrate sprind polase, S. carmelisae, homo	2.5
65	406273	NM_000919	Hs.83909	peptidylglycine alpha-amidating monooxyg	2.5
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.5
	445895	BE543594	Hs.51478	hypothetical protein FLJ22329	2.5
	454967	AW684375	Hs.226627	gbl3-CT0214-150200-074-E06 CT0204 Homo	2.5
	442303	AA680289	Hs.129169	ESTs	2.5
70	456583	AF179897	Hs.104105	Meis (mouse) homolog 2	2.5
	434263	N34895	Hs.44648	ESTs	2.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	2.5
	424526	AW073571	Hs.238564	ESTs, Weakly similar to KIAA1204 protein	2.5
	406038	Y14443	Hs.88719	zinc finger protein 200	2.5
	413495	Y12395	Hs.315177	interferon-related developmental regulat	2.5
75	423098	AA321900	Hs.204682	ESTs	2.5
	410817	AD62769	Hs.93559	protein disulfide isomerase related prot	2.5
	438941	AF138951	Hs.6710	mannose-6-phosphate utilization defect 1	2.5
	453828	AW970960	Hs.293821	ESTs	2.5
	445034	AW283376	Hs.143560	ESTs	2.5
80	446920	BE407797	Hs.223704	checkpoint with forkhead and ring finger	2.5
	406876	A1382296	Hs.180842	cholesterol protein L13	2.5
	412370	AW046514	glb1-RC2-ET0021-280400-011-005 ET0021 Homo	2.5	
	423642	AW452650	Hs.157148	hypothetical protein MGCI3204	2.5

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5	433357	AW876789	Hs.165607	ESTs	2.5
	414853	U31116	Hs.77780	saraglycan, beta (43kD dystrophin-assoc	2.5
	416097	BE387371	Hs.118954	hypothetical protein FLJ20085	2.5
	428619	AK020140	Hs.187378	hypothetical protein FLJ11278	2.5
	413976	BE254532	Hs.75655	procollagen-protein, 2-alpha1(I)coll-4 di	2.5
10	445223	AW291553	Hs.254953	ESTs	2.5
	423926	X03833	Hs.17722	interleukin 1, alpha	2.5
	410165	BE560228	Hs.71869	apoptosis-associated speck-like protein	2.5
	406474				2.5
	433808	AW298141	Hs.157975	ESTs	2.5
15	430765	AW748482	Hs.77873	B7 homolog 3	2.5
	437528	N99646	Hs.169745	crumbs (Drosophila) homolog 1	2.5
	420734	AW972872	Hs.293036	ESTs	2.5
	415346	Z43108		gb-HSC13E071 normalized infant brain cDN	2.5
	419337	AW291112	Hs.209978	ESTs	2.5
20	444606	R08478	Hs.19041	ESTs	2.5
	430061	AB037817	Hs.230188	KIAA1396 protein	2.5
	413407	A156293	Hs.75339	inositol polyphosphate phosphatase-like	2.5
	411965	BE467339	Hs.280115	ESTs	2.5
	403278	AJ346683	Hs.52763	anaphase-promoting complex subunit 7	2.5
25	403142				2.5
	425081	X74784	Hs.154443	minichromosome maintenance deficient (S	2.5
	416205	H65470	Hs.16004	ESTs	2.5
	431518	AA743462	Hs.155337	ESTs	2.5
	448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypothet	2.5
30	420301	AW628666	Hs.294430	ESTs, Weakly similar to I30022 hypothet	2.5
	404366				2.5
	449733	R74546	Hs.98438	Homo sapiens cDNA, FLJ112094 fls, clone HE	2.5
	456983	AB907673		gb:IL-8T152-080396-004 BT152 Homo sapien	2.5
	402856	AW839658		gb:RCO-DT0076-110100-031-c09 DT0076 Homo	2.5
35	420751	J03819	Hs.399113	adenergic, beta-1, receptor	2.4
	436005	AA791333	Hs.270751	ESTs	2.4
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN01_HUMAN Z	2.4
	453496	AA442103	Hs.333084	solute carrier family 2 (facilitated glu	2.4
	453563	ALD4000	Hs.188083	ESTs	2.4
40	407399	AW103886		gb:cd33606.v1 NCL_GCAP_Ov23 Homo sapiens	2.4
	454630	BE142075		gb:CM3-HT0137-170599-012-02 HT0137 Homo	2.4
	451026	AA013218	Hs.157492	car-D4 (mouse) homolog	2.4
	420779	L12958	Hs.93922	dopamine receptor D4	2.4
	430322	AB84170	Hs.221348	ESTs	2.4
45	455928	BE156306		gb:QW0-HT0067-150200-114-04 HT0367 Homo	2.4
	419625	U91616	Hs.311640	nuclear factor of kappa light polypeptid	2.4
	446773	AA362702	Hs.332041	Homo sapiens. Similar to RREN cDNA 2700	2.4
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	2.4
	447247	AW953351	Hs.287305	Homo sapiens cDNA, FLJ113090 fls, clone NT	2.4
50	429108	ALD08637	Hs.156352	neutrophil cytosolic factor 4 (AOK4)	2.4
	451802	AB17711	Hs.209374	ESTs	2.4
	419417	R92481	Hs.39429	ESTs	2.4
	407034	AF033574	Hs.22405	leukocyte immunoglobulin-like receptor,	2.4
	423567	BE252948	Hs.69331	hypothetical protein FLJ13633	2.4
55	427501	AB69280	Hs.131743	ESTs	2.4
	451773	Z42044	Hs.25996	KIAA1273 protein	2.4
	438845	AA732297	Hs.113928	ESTs	2.4
	431084	AW290121	Hs.265263	Homo sapiens cDNA FLJ114115 fls, clone MA	2.4
	440614	AA781533	Hs.127236	hypothetical protein FLJ112879	2.4
60	423271	AF176911	Hs.132004	cardiotrophin-like cytokine; neurotroph	2.4
	452125	BE312542	Hs.28077	GDP-mannose pyrophosphorylase B	2.4
	419508	AW967538	Hs.93786	ATP-binding cassette, sub-family C1 (CFTR	2.4
	453446	BE299996		gb:60094254F1 NH_MGC_17 Homo sapiens c	2.4
	419792	AA250890	Hs.190037	ESTs	2.4
65	432790	R01362	Hs.106642	ESTs, Weakly similar to T09052 hypothet	2.4
	410447	AW181634		gb:MG3-5T0220-230103-04-06-w4 ST0220 Homo	2.4
	438662	AA223569	Hs.63351	cleavage and polyadenylation specific fa	2.4
	402408				2.4
	443950	NM_001425	Hs.95999	epithelial membrane protein 3	2.4
70	414525	AA335738	Hs.76686	glutathione peroxidase 1	2.4
	403248				2.4
	432088	AA625454		gb:NM5-09.v1 NCL_GCAP_P120 Homo sapiens	2.4
	431692	AL021331	Hs.267749	unc33 (C.elegans) homolog A	2.4
	455023	AW689007		gb:IL3-CT0020-310100-065-H11 CT0020 Homo	2.4
75	426249	F06422	Hs.168352	nucleoside kinase protein 1	2.4
	446795	AF797713	Hs.156471	ESTs	2.4
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.4
	414252	AA346483	Hs.126191	ESTs	2.4
	417918	AA209205	Hs.153754	hypothetical protein FLJ12606	2.4
80	427550	BE242816	Hs.179636	nuclear RNA helicase, DECD variant of DE	2.4
	404020				2.4
	407846	AA426202	Hs.40403	Cbp300-interacting transactivator, wit	2.4
	417222	AB25424	Hs.42053	hypothetical protein MG2383	2.4
	443639	BE259142	Hs.91611	proteasome (prosome, macropain) subunit,	2.4
	452705	AW449390	Hs.297150	ESTs, Moderately similar to SUR1_HUMAN S	2.4
	401676				2.4

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452198	A097560	Hs.61210	ESTs, Weakly similar to 138022 hypothetical	2.3
411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	2.3
404054				2.3
430458	AA479300	Hs.225706	ESTs, Weakly similar to 138022 hypothetical	2.3
440210	AW674502	Hs.125296	ESTs	2.3
446727	AB011095	Hs.16032	KIAA0523 protein	2.3
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.3
438379	N23018	Hs.171591	C-terminal binding protein 2	2.3
448919	A074065	Hs.220045	ESTs	2.3
441293	R49462	Hs.106541	ESTs	2.3
411566	NM_000429	Hs.323715	methionine adenosyltransferase L, alpha	2.3
480203	AA053137	Hs.42390	nasopharyngeal carcinoma susceptibility	2.3
134641	AW072502	Hs.334825	Homo sapiens cDNA FLJ14752 fa, clone NT	2.3
450748	A073595	Hs.130016	ESTs	2.3
404195				2.3
418327	U70370	Hs.84136	paired-like homeodomain transcription fa	2.3
451370	A791929	Hs.300782	ESTs	2.3
403034				2.3
407723	AW071161	Hs.252873	ESTs	2.3
431320	AW969474	Hs.183070	ESTs	2.3
429271	AF039850	Hs.198515	dead ring (Drosophila)-like 1	2.3
453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, com	2.3
419225	U70073		gb:HSUT0073 Human Homo sapiens cDNA cton	2.3
444656	A027924	Hs.145199	ESTs	2.3
405741				2.3
405917				2.3
432657	AA736777	Hs.293770	ESTs	2.3
437949	U78519	Hs.41854	ESTs, Weakly similar to A-65010 X-linked	2.3
450514	AC005785	Hs.25069	A kinase (PRKA) anchor protein 8	2.3
418400	BE243026	Hs.301595	KIAA0246 protein	2.3
444019	BE173977	Hs.10096	putative nuclear RNA helicase	2.3
406326				2.3
412077	N51107	Hs.471999	ESTs, Weakly similar to FLJ000004 protein	2.3
427647	W19744	Hs.180069	Homo sapiens cDNA FLJ20653 fa, clone KA	2.3
414523	AA148590	Hs.188636	ESTs	2.3
414854	BE545797	Hs.51493	ESTs, Weakly similar to hypothetical pro	2.3
420352	BE258836		gb:60111737.f1 NIH_MGC_16 Homo sapiens c	2.3
438467	AW292275	Hs.155355	ESTs	2.3
402627				2.3
451711	AK000461	Hs.25990	cat eye syndrome chromosome region, c2nd	2.3
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S,	2.3
423869	BE405301	Hs.134012	Ctq-related factor	2.3
405915				2.3
431503	NM_012129	Hs.258576	claudin 12	2.3
423306	W85562	Hs.105198	ESTs	2.3
443232	AF161521	Hs.9031	phenylalanyl-tRNA synthetase beta subuni	2.3
433064	D79991	Hs.30002	SH3-containing protein SH3GLB2, KIAA1648	2.3
434437	A012556	Hs.197813	ESTs	2.3
436191	BE407866	Hs.170253	hypothetical protein FLJ23292	2.3
420006	H14429	Hs.94300	serologically defined colon cancer anlig	2.3
447942	F12523	Hs.334786	hypothetical protein MGC16040	2.3
403166				2.3
422119	A027829	Hs.111862	KIAA0590 gene product	2.3
403751				2.3
426451	A008165	Hs.169546	GATA-binding protein 3	2.3
427413	BE547847	Hs.177781	hypothetical protein MGC9518	2.3
405091	AW670386	Hs.269423	ESTs	2.3
404951	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.3
427722	AK000123	Hs.190479	hypothetical protein FLJ20115	2.3
405747				2.3
435210	AA780519	Hs.311601	EST	2.3
404652				2.3
423524	AF055989	Hs.129738	potassium voltage-gated channel, Shaw-re	2.2
426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.2
444424	A654894	Hs.196377	ESTs	2.2
434031	BE384165	Hs.23723	pseudouridylyl synthase 1	2.2
427650	AW501245	Hs.252759	ribosomal protein S3	2.2
435220	D50030	Hs.104	HGF activator	2.2
438279	AA085166	Hs.154762	HIV-1 rev binding protein 2	2.2
424668	D83702	Hs.151573	cytochrome 1 (phylloquinone-like)	2.2
429961	BE246829	Hs.226770	DNFZ5565C0424 protein	2.2
442065	A031229	Hs.128417	hypothetical protein FLJ14009	2.2
415198	AW005480	Hs.943	natural killer cell transcript 4	2.2
420536	AL117435	Hs.275438	histone deacetylase 7A	2.2
411263	BE297802	Hs.69360	histone-like 6 (nucleic centromere-associ	2.2
443753	AW067578	Hs.134749	ESTs	2.2
423243	AA351938	Hs.23964	sin3-associated polypeptide, 18kD	2.2
446572	AA659151	Hs.282961	ESTs	2.2
412247	AF022375	Hs.73793	vascular endothelial growth factor	2.2
421040	AA715026	Hs.135280	ESTs	2.2
426212	S71824	Hs.167993	neural cell adhesion molecule 1	2.2
455584	BE307420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
406851	AA026794	Hs.180255	major histocompatibility complex, class	2.2

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5	444153	AK001810	Hs.10414	hypothetical protein FLJ10748	2.2
	419575	U43431	Hs.91175	topoisomerase (DNA) III alpha	2.2
	418672	L44284	Hs.159243	ESTs	2.2
	456281	AA210718	Hs.104157	ESTs, Weakly similar to KIAA0594 protein	2.2
	415737	AA176725	Hs.118743	ESTs	2.2
10	447554	AJ301598	Hs.36119	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	405159				2.2
	442777	AW661820	Hs.211413	ESTs	2.2
	440139	H71395	Hs.30749	ESTs	2.2
	458339	AW976853	Hs.172843	ESTs	2.2
15	401876				2.2
	439566	AF063637	Hs.2267	gb.Homo sapiens full length insert cDNA	2.2
	425879	H05963	Hs.12267	virionectin (serum spreading factor, som	2.2
	441837	AJ361743	Hs.175881	core-binding factor, beta subunit	2.2
	439644	AB015419	Hs.247710	preprocalcitonin-releasing peptide	2.2
20	431474	AL133990	Hs.190642	ESTs	2.2
	407739	NM_002285	Hs.38070	lymphoid nuclear protein related to AF4	2.2
	424244	AV547184	Hs.143801	hypothetical protein NCJA-1	2.2
	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORE MOUSE CORN1	2.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (gBIO)	2.2
25	422365	AF035637	Hs.115621	REV3 (yeast homolog-like, catalytic sub	2.2
	404170				2.2
	406902	M32074		gb.Human retinoic acid receptor gamma 2	2.2
	437902	AA770599	Hs.144055	ESTs	2.2
	401012				2.2
30	446502	AJ302654	Hs.208024	ESTs	2.2
	442554	AW467376	Hs.125540	ESTs	2.2
	443021	AJ368540	Hs.8904	Ig superfamily protein	2.2
	421141	AW117261	Hs.125914	ESTs	2.2
	443070	BE386662	Hs.8984	Homo sapiens chromosome 14 BAC 98L12	2.2
35	446565	H05741	Hs.17514	neurite-spanning 4-domains, subfamily A	2.2
	427695	R08483	Hs.172362	ESTs	2.2
	426503	AJ380153		gb.EST33093 Skin tumor 1 Homo sapiens cD	2.2
	431468	AW249431	Hs.255258	nuclear prelamin A recognition factor	2.2
	418185	AW975861	Hs.47367	KIAA1755 protein	2.2
40	437919	BE410556	Hs.564005	Homo sapiens cDNA FLJ113549 fs, clone PL	2.2
	402064				2.2
	413335	AJ613318	Hs.48442	ESTs	2.2
	406212	AA297567	Hs.43728	hypothetical protein	2.2
	402163				2.2
45	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	2.2
	407335	AA531047	Hs.158761	Homo sapiens cDNA FLJ13054 fs, clone NT	2.2
	409715	W42591	Hs.23892	ESTs	2.2
	413921	W46466	Hs.58879	ESTs	2.2
	443823	BE095782	Hs.8877	hypothetical protein	2.2
50	432458	AJ068598	Hs.78768	malignant cell expression-enhanced gene/	2.2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	2.2
	423178	AJ331440	Hs.124983	Homo sapiens mRNA: cDNA DKFZp564C142 (H	2.2
	451089	AJ393705	Hs.4139	Homo sapiens cDNA: FLJ23269 fs, clone C	2.2
	415216	AJ829905	Hs.193211	Homo sapiens cDNA FLJ11421 fs, clone HE	2.2
55	442242	AV547908	Hs.90424	Homo sapiens cDNA: FLJ23285 fs, clone H	2.2
	441830	AJ383104	Hs.42554	hypothetical protein DKFZp564D0372	2.2
	405600	X55371	Hs.172550	polyprotein-like tract binding protein (the	2.2
	443378	AV392550	Hs.5280	proteasome (prosome, macropain) subunit,	2.2
	432558	R97268	Hs.177269	ESTs	2.2
60	405146	R45621	Hs.81057	hypothetical protein MG2718	2.2
	419865	NM_000200	Hs.53592	U1-snRNP binding protein lamplog (70kD)	2.2
	439444	AJ277652	Hs.54576	ESTs, Weakly similar to U30022 hypothi	2.2
	438407	AJ457122	Hs.129673	eucaryotic translation initiation factor	2.2
	450184	W31096	Hs.237617	Homo sapiens, clone IMAGE:3447394, mRNA,	2.2
65	409130	BE074601	Hs.75658	phosphorylase, glycogen, brain	2.2
	428444	AW972635	Hs.301304	hypothetical protein FLJ115261	2.2
	429489	AF008203	Hs.204039	aristless-like homeobox 3	2.2
	433042	AV193534	Hs.281895	Homo sapiens cDNA FLJ11660 fs, clone HE	2.2
	440658	H25142	Hs.143032	ESTs, Weakly similar to neuronal tinase	2.2
70	405204	AA545651	Hs.43866	protein tyrosine phosphatase type IVA, m	2.2
	427498	NM_003526	Hs.178728	methyl-CpG-binding domain protein 3	2.2
	408006	H57654	Hs.303345	ESTs, Weakly similar to U30022 hypothi	2.2
	445703	AV554845	Hs.27	glycine dehydrogenase (decarboxylating,	2.2
	431446	AW284529	Hs.253369	Homo sapiens cDNA FLJ110285 fs, clone HE	2.2
75	456660	AA505249	Hs.112282	salute carrier family 30 cation transport	2.2
	433099	NM_002504	Hs.3187	nuclear transcription factor, X-box bind	2.2
	415857	AA666115	Hs.127797	Homo sapiens cDNA FLJ11381 fs, clone HE	2.2
	415245	N59650	Hs.27252	ESTs	2.2
	403557	R14913		gb.W4210.51 Soares fetal liver spleen	2.2
80	402521	AW501216	Hs.108945	KIAA0515 protein	2.2
	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	2.2
	446530	AV558909	Hs.282642	ESTs	2.2
	415767	AJ291596	Hs.72890	ESTs	2.2
	414812	XJ2755	Hs.77367	monokine induced by gamma interferon	2.2
	453028	AB000532	Hs.31442	RecQ protein-like 4	2.2
	412133	U83460	Hs.73614	separin carrier family 31 (copper transpo	2.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfat	2.2

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437033	AY248364	Hs.5409	RNA polymerase I subunit	2.2
422732	AA577455	Hs.24937	transferrin-2 alpha (htra-2 alpha)	2.2
416388	AI417358	Hs.73677	ESTs	2.2
452849	AF044924	Hs.30792	hook2 protein	2.2
446615	BE513202	Hs.15589	TFPII binding protein	2.2
429361	NV_015905	Hs.183658	transcriptional intermediate factor 1	2.2
446279	AA490770	Hs.182382	ESTs	2.2
429238	NV_001809	Hs.1594	centromere protein A (17A2)	2.2
403969				2.2
410423	AF042432	Hs.63489	protein tyrosine phosphatase, non-recept	2.2
429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	2.2
447091	AA085648	Hs.157779	ESTs, Weakly similar to CA17_HUMAN COLLA	2.2
422017	NM_003877	Hs.110776	STAT induced STAT1 inhibitor-2	2.2
427628	NM_007118	Hs.171957	single functional domain (FTPRF interact	2.2
436726	AB033103	Hs.6385	KIAA1277 protein	2.2
453315	BE544203	Hs.24831	ESTs	2.2
423244	AL035379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.2
433610	AA808322	Hs.112547	ESTs	2.2
429451	BE400861	Hs.202833	heme oxygenase (decycling) 1	2.2
417980	R32235		gb:ph6708.f1 Soares placenta Nb29P Homo	2.2
406347				2.2
414406	BE297904		gb:0117781.f41 NIH_MGC_17 Homo sapiens c	2.2
401827				2.2
446913	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr	2.2
452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cal	2.2
456786	AF002094	Hs.132851	hypothetical protein FLJ114222	2.2
455031	AI632091	Hs.116877	ESTs	2.1
442609	AL020995	Hs.8516	selenoprotein N	2.1
439732	AW629604	Hs.167841	hypothetical protein from EUROMAGE 1703	2.1
421506	BE302706	Hs.105950	thymidine kinase 1, soluble	2.1
439253	AF060504	Hs.332252	ESTs	2.1
409669	AW177551	Hs.220255	hypothetical protein MGC13058	2.1
429574	BE268321	Hs.208912	hypothetical protein MGC361	2.1
437470	AL359147	Hs.134742	hypothetical protein DXPZp547D005	2.1
428945	AW015088	Hs.4964	DXFZp5631.f24 protein	2.1
447687	AI275747	Hs.150186	hypothetical protein DXFZp566K1946	2.1
459584	AI910884	Hs.207898	ESTs	2.1
439130	AA306090	Hs.124707	ESTs	2.1
428160	AI129167	Hs.102674	guanine nucleotide binding protein (G pr	2.1
442028	AI239437	Hs.48945	ESTs	2.1
430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	2.1
443609	AV560231	Hs.282941	ESTs, Highly similar to A Chain A, Human	2.1
417164	AA336283	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.1
444534	AW271626	Hs.42294	ESTs	2.1
436391	AI262248	Hs.25027	ESTs	2.1
442003	AW207497	Hs.201891	ESTs	2.1
456278	BE300389	Hs.289038	hypothetical protein MGC4126	2.1
410976	BE243965	Hs.50560	major vault protein	2.1
417810	D28419	Hs.82609	hydroxymethylbilane synthase	2.1
445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
452712	AW638616		gb:RCS-LT0054-140200-013-D011 T0054 Homo	2.1
434026	BE543269	Hs.50292	mitochondrial ribosomal protein L32	2.1
421564	AB007864	Hs.105850	KIAA0404 protein	2.1
424927	AW973666	Hs.153850	hypothetical protein C32102.4	2.1
432742	AA564453	Hs.162339	ESTs	2.1
426958	IS6180	Hs.117975	ESTs	2.1
421531	AA713506	Hs.201769	ESTs	2.1
410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast h	2.1
420503	AI570943	Hs.337546	ESTs	2.1
448127	AA784616	Hs.282893	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
452897	BE040508	Hs.269323	ESTs, Moderately similar to I78855 sens	2.1
447112	HI7800	Hs.71154	ESTs	2.1
406577				2.1
437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.1
451460	AT97550	Hs.208652	ESTs	2.1
447402	IS4520	Hs.18490	hypothetical protein FLJ20452	2.1
435828	AA700705	Hs.13862	ESTs	2.1
436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.1
420562	BE047878	Hs.59093	Homo sapiens chromosome 19, contig R2837	2.1
452020	AA722012	Hs.255757	ESTs, Weakly similar to AT7A_HUMAN POTEN	2.1
415586	245481		gb:HSJC2QE04.1 normalized infant brain cDN	2.1
452620	AA435504	Hs.119286	ESTs	2.1
457066	BE244613	Hs.158272	ESTs, Weakly similar to CA13 MOUSE COLLA	2.1
435412	AW972330	Hs.283022	gigliering receptor expressed on myeloid	2.1
431741	AA514783	Hs.191701	ESTs	2.1
446840	AW294828	Hs.209203	ESTs	2.1
440818	AI147060	Hs.146726	ESTs	2.1
410174	AA306007	Hs.59461	DXFZp34C245 protein	2.1
404822				2.1
412760	AW379030	Hs.41324	ESTs	2.1
410653	BE383768	Is.65238	95 kDa retinoblastoma protein binding pr	2.1
426925	NM_001196	Is.315689	Homo sapiens cDNA: FLJ22373 flc, clone H	2.1

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426242	AA337476	His 293984	hypothetical protein MGC13102	2.1
452560	BE077084	His.336432	ESTs	2.1
456437	A9524228	His.115185	ESTs. Moderately similar to PCA259 feni	2.1
458922	DE501631	His.262053	ESTs	2.1
459321	AW581535	His.141480	Homo sapiens. mRNA: cDNA DKFZp434M079 (fr	2.1
419488	AA318241	His. 90651	nucleophosmin/nucleolysin 3	2.1
411829	AW665749		gb:OV3-SN0021-100500-185-c03 SN0021 Homo	2.1
457192	AL135682	His. 22452	Homo sapiens. mRNA for KIAA1737 protein,	2.1
422128	AW881145		gb:OV0-CT0033-010400-182-ad0 OT0033 Homo	2.1
452571	W01516	His.34665	ESTs	2.1
423659	H41850	His.131846	PCAF associated factor 61 alpha	2.1
406610				2.1
456338	AW614995		gb:MR1-ST0205-170400-024-009 ST0206 Homo	2.1
418365	AA362958		gb:EST172002-Ovary II Homo sapiens. cDNA 5	2.1
437623	D63880	His.5719	chromosome condensation-related SMC-asso	2.1
410908	AA121686	His.10592	ESTs	2.1
420221	N25591	His.43725	ESTs	2.1
424739	AA346108	His.221610	ESTs	2.1
425358	AL049685	His.155369	hypothetical protein similar to tenascin	2.1
424901	Z11933	His.182505	POU domain, class 3, transcription facto	2.1
411096	U80034	His.68583	mitochondrial intermediate peptidase	2.1
415635	F13168		gb:HSC3JF101 normalized rat brain cDN	2.1
418181	U37012	His. 83727	cleavage and polyadenylation specific fa	2.1
407103	AA424881	His.255301	hypothetical protein MGC13170	2.1
454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.1
400021				2.1
432228	NS1700		gbyyZ2001.s1 Soares_multiple_sclerosis_	2.1
455055	AA504595	His.111418	ESTs	2.1
405258				2.1
444645	A184564	His.101654	ESTs	2.1
430246	A126909	His.108265	hypothetical protein FLJ12552	2.1
456687	AW024815	His.170088	GLUT4 enhancer factor	2.1
403857				2.1
400258				2.1
422221	AA308649	His.168070	FYH oncogene related to SRC, FGR, YES	2.1
414054	A913901	His.126430	ESTs	2.1
452700	A1655390	His.268940	five-span transmembrane protein MB3	2.1
454606	AW807572		gb:MR4-ST0124-181299-020-006 ST0124 Homo	2.1
448954	AB014564	His.22616	KIA0054 protein	2.1
443148	A034357	His.211194	ESTs. Weakly similar to ALU6_HUMAN ALU S	2.1
453486	AL038201	His.173554	ubiquinol-cytochrome c reductase core pr	2.1
437695	AA769202	His.192142	ESTs	2.1
425449	XS2056	His.157441	spleen focus forming virus (SFFV) provir	2.1
447270	AC002551	His.331	general transcription factor IIC, poly	2.1
435677	AA984142	His.263726	ESTs. Weakly similar to TSGA RAT TESTIS	2.1
436382	AW977063	His.250161	ESTs	2.1
435837	A1689210	His.187276	Homo sapiens cDNA FLJ11431 fls, clone HE	2.1
458287	AA987556	His.12867	ESTs	2.1
423794	BE511781	His.231695	ESTs	2.1
408049	AW079098	His.74315	desmoplakin (DP1, DPI)	2.1
402721				2.1
451999	AW175401	His.27424	DEAD(H (Asp-Glu-Ala-AspHis) box polypep	2.1
417541	A9592191	His.180040	hypothetical protein FLJ22439	2.1
414857	AAW02389	His.520	modulator recognition factor I	2.1
435760	AF231922	His.213004	chromosome 21 open reading frame 62	2.1
428086	AL110153	His.224137	hypothetical protein	2.1
447853	AA343034	His.164285	ESTs. Weakly similar to AFG1_YEAST AFG1	2.1
419304	NM_022110	His.69565	hemopoietic cell kinase	2.1
431019	NM_005249	His.2714	forkhead box G1B	2.1
421064	A1245432	His.101382	tumor necrosis factor, alpha-induced pro	2.1
416435	AI413301	His.178703	KIAA0129 gene product	2.1
427014	AA808737	His.222531	ESTs. Weakly similar to S55501 interlo	2.1
459369	T83080		gby4d0e03.r1 Soares testis liver spleen	2.1
402239				2.1
412280	AW205116	His.272814	hypothetical protein DKFZp034E1723	2.1
426012	AA367507	His.737581	pregnancy-associated plasma protein A	2.1
438845	A1865558	His.184587	ESTs	2.1
426076	AW962714		gb:EST374787 MAGE resequencs, MAGG Homo	2.1
404561				2.1
442532	AA457211	His.8858	bromodomain adjacent to zinc finger doma	2.1
405175	W29089	His.19566	hypothetical protein DKFZp66G12416	2.1
423857	AA331896		gb:EST35757 Embryo, 8 week I Homo sapien	2.1
458604	W37944	His.4007	Sarcotomal-associated protein	2.1
409650	T08490	His.288969	HSCARG protein	2.1
401725				2.1
433675	AW977653	His.75319	ribonucleotide reductase M2 polypeptide	2.1
456741	W37608	His.184492	ESTs	2.1
417037	DE083636	His.80676	antigen identified by monoclonal antibod	2.1
415079	RA3179	His.22895	hypothetical protein FLJ23548	2.1
439262	AA832333	His.333045	ESTs	2.1
403108				2.1
436718	AW015227	His.289053	hypothetical protein FLJ14733	2.1
440696	A1762157	His.187660	putative Rab5 GTP/GDP exchange factor ho	2.1

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425186	247825_1	H16622 R17322 AA351965
425517	252729_1	AF121179 BE162736 AA358827
426076	260604_1	AW952714 AA365277 AA366278
426413	264650_1	AA377823 AW554494 A020968
426503	265202_1	AA380153 AA390283 AW553526
426531	266760_1	AA381071 AA381084 AA380652
429875	310034_1	A051815 AA460162 AA460751
430968	326269_1	AW572830 AA527647 AA489820 AA570362
432068	341195_1	AA525454 AW5335 RB5052 777379
433532	368950_1	AW953367 AA598607 AA740735
434559	38888_1	AF147315 AW173079 T53029
435065	393228_1	BE064391 BE064395 AA663613 N99644
436190	41555_1	AK001059 AA633055
436395	41965_1	AJ227090 AW494533 AW551119 F00947
436532	421802_1	AA721522 AW975443 T30070
436722	425758_1	AW575977 AA729465 AA747132
436872	42851_1	X15624
437034	431713_1	AA742543 AA809675 AW576568
439086	46852_1	AF085947 H70891 H76855
439228	47001_1	N51700 AF086051 N51752
439518	47334_1	W63226 AF086341 W72300
439546	47360_1	AF085056 W75297 W72446
439556	47387_1	AF085387 W77684 W72711
439710	47550_1	AF086543 W56291 W56225
443657	576685_1	R14973 R14967 A081006
444158	593828_1	AW373679 AJ102655 H12014
444386	604004_1	BE265183 AJ143268 BE053367
451129	658070_1	BE072681 BE072946 AJ762181
452712	928309_1	AW638616 AW638660 BE144343 AJ914520 AW688910 BE184854 BE184784
453446	957533_1	BE299996 BE297115 BE270415 BE296214 BE296526
453528	975645_1	AW614958 AL047199 AW550579
453746	979731_1	AL120611 BE006190 BE006189
454377	114761_1	AA076811 AW614764
454389	115662_1	AW675251 AW847602 A0779719
454606	1226149_2	AW020752 AW610271 AW805944 AW610310 AW610215 AW610368 AW610167
454630	1227352_1	BE142075 BE142148 BE142189 AW616245 BE142147 BE142002 BE142406 BE142094 BE142020 BE142074 BE142247 BE142000 BE142375
454631	1227443_1	AW611165 BE142133
454631	1227443_1	AW611324 AW611325 AW611326 AW611333 AW611329 AW611332 AW611339 AW611335
454679	1228529_1	AW613110 AW613112
454967	1247021_1	AW846276 AW846416 AW848160 AW847545 AW847547 AW848063 AW848113
455023	1249188_1	AW650307 AW650301 AW550877
455302	1276542_1	AW957641 AW651777
455470	1252845_1	AW947952 AW947957 AW947950 AW947957 AW947953 AW947973 AW947966 AW947971 AW947947 AW947970 AW947955 AW947975 AW947952
455514	1321549_1	AW947955
455530	1322298_1	AW553871 BE090302 AW963867 AW963845 AW963860 AW963853 AW963852
455584	1334741_1	AW984744 AW984759
455776	1364505_1	BE007420 BE007419 BE007421 BE007422
455908	1382301_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
456072	1470255_1	BE156306 BE156198 BE156230 BE156377 BE156374
456094	1504780_1	HS4381 HA4463 BE393262
457374	328758_1	HS5081 C01228
457578	359618_1	AA493662 AW697396 BE154814
457730	359065_1	AA570027
457730	359065_1	AW753613 AW753857 BE150274 BE150693 BE150394 AA808651 AA550159 AA654653 BE150419

TABLE 9C:

Ref: Unique number corresponding to an E-ess probe set.
Sequence source: The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al" refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:499-495.
Strand: Indicates DNA strand from which exons were predicted.
NT_position: Indicates nucleotide positions of predicted exons.

Pley	Ref	Strand	NT_position
400822	7465000	Plus	166223-186402,186878-167275
400859	9757499	Minus	518583-52010,58131-58294,99474-99570
405917	7263186	Plus	172358-172631
405952	6095628	Plus	140330-140822
401012	7230638	Minus	735-1137
401048	7232177	Plus	132430-132761
401125	8570296	Minus	126953-126964
401324	9883751	Plus	234557-234744
401384	6850539	Minus	58360-58545
401555	7135678	Plus	103510-104030
401626	8579543	Minus	238100-238432
401676	9965536	Plus	3851-4651
401714	6715702	Plus	96404-96681
401729	8134856	Minus	90651-90878
401827	2262095	Plus	94725-94960,98452-98660
401876	6099107	Plus	55513-96641
402028	7139781	Plus	88749-89237
402064	8117294	Plus	100159-100350,100445-100912
402239	7690131	Plus	38175-38304,42133-42265
402408	9796235	Minus	110326-110451

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	402404	9796344	Minus	64925-65873
	402516	9798099	Minus	193342-195511
	402604	9509420	Plus	20393-20767
	402627	9531216	Plus	12136-12272, 16487-16628, 17654-17798, 18494-18621, 18933-19089, 20669-20790, 21134-21296, 22866-22973, 23686-23820, 28626-28695, 29279-29469
5	402721	8969253	Minus	144426-144715
	402798	3355547	Plus	23566-23867
	402856	9801288	Minus	90119-90411
	403048	4210391	Plus	44275-44592, 49656-49955
10	403108	8999955	Plus	92523-93867
	403142	9444521	Plus	89286-90131
	403166	9638127	Minus	67752-67940, 68935-68856, 70394-70507
	403178	9989298	Plus	116458-116564
	403680	7331517	Minus	57184-157415
15	403751	7229815	Minus	158794-160509
	403790	8084957	Minus	87826-87947, 89835-90002
	403797	8093986	Minus	123065-125008
	403957	7708910	Minus	2524-3426
	403981	7710245	Minus	107250-107685, 108524-109213
20	403961	7596976	Minus	110393-110603
	403969	8569909	Plus	31237-31375, 32405-32506
	404020	8655966	Minus	174449-174963
	404054	3648785	Plus	62713-69755
	404084	9944055	Plus	2795-2969
25	404108	8247074	Minus	63603-64942
	404170	9330783	Plus	168836-169248
	404185	4572394	Minus	129171-129327
	404240	5002624	Minus	116132-116407, 116653-116922
	404255	9856663	Minus	75747-75947
30	404299	5738652	Minus	3626-4025
	404366	9964577	Plus	95589-96801
	404554	7243861	Plus	42537-42839
	404561	9795980	Minus	69039-70100
35	404584	9857511	Plus	13851-139153
	404589	9531665	Minus	32824-32985
	404642	9796810	Plus	102999-103145
	404652	9795969	Minus	108172-108296
	404721	9856648	Minus	173763-174294
40	404756	7706327	Plus	82849-83027
	404802	4581357	Minus	32053-32600
	404884	6038882	Plus	87221-87505
	405159	9966252	Plus	79659-78804
	405258	7329310	Plus	129930-130076
	405288	6133075	Minus	26266-126436
45	405393	2811095	Plus	118526-118992
	405362	2337862	Minus	105008-105142, 105960-106091, 140445-140556, 142519-142541
	405558	1621110	Plus	4502-4644, 59383-6083
	405588	5002511	Plus	46180-46366
	405605	5836195	Minus	117070-117270
50	405701	4263751	Plus	33243-33364
	405741	9966947	Minus	156747-156875, 156936-157208
	405747	8469069	Minus	153933-154060
	405771	7018349	Plus	91181-91254, 91510-91589
	405808	9929207	Plus	109758-111166
55	405884	6758747	Plus	62363-62583
	405915	7712162	Minus	43717-43859
	406028	8312393	Minus	177469-177829
	406085	9123888	Plus	18655-18843
	406169	6684220	Minus	12620-14251
60	406267	7528342	Minus	2570-2731
	406326	9212385	Plus	84508-84655
	406347	9235981	Plus	90509-91091
	406474	9795567	Plus	52758-53211
	406577	7711730	Plus	11377-11509
65	406610	8312226	Plus	13096-13334

TABLE 10A. ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

70	Table 10A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix HG-U133 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.				
75	Play:	Unique Eos probeset identifier number			
	ExAcn:	Exemplar Accession number, Genbank accession number			
	UigeneID:	Uigene number			
	Uigene Title:	Uigene gene title			
	R1:	Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor			
80	Play	ExAcn	UigeneID	Uigene Title	R1
	453655	AW960427	Hs.79059	transforming growth factor, beta receptor	136.7
	417275	X63578	Hs.295449	parvalbumin	29.0
	430829	AW451999	Hs.194024	ESTs	25.7

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	410957	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polypeptide	22.6
	419954	D14720	Hs.93883	myosin protein zero (Charcot-Marie-Tooth)	21.2
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	18.5
	416133	NM_016863	Hs.89512	ATPase, Ca++ transporting, plasma membrane	15.5
5	416018	AW138239	Hs.75977	proteasome activator subunit 1	15.2
	417167	AW064337	Hs.4290	ESTs	14.8
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1
10	439830	AA266665	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEIN	12.5
	430968	AW148552	Hs.167398	ESTs	12.6
	412636	NM_004415	Hs.74316	desmoplakin (DPL, DP1)	12.5
	429396	AB011106	Hs.195012	KIAA0534 protein	12.2
	412538	AA310199	Hs.203838	ESTs	12.2
	423590	AA329498	Hs.23804	ESTs, Weakly similar to PNC099 src3 prot	12.1
15	456844	A1264155	Hs.152981	CDP-diacylglycerol synthase (phospholipase)	11.9
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.9
	442593	R39004	Hs.31961	ESTs	10.8
	446353	AZ060519	Hs.153661	ESTs	10.4
	420290	AW077318	Hs.154400	ESTs	10.3
20	414220	BE290094	gb.601118231F1 NIH_MGC	17 Homo sapiens c	10.3
	414290	A1568801	Hs.71721	ESTs	10.2
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	10.0
	414937	R26898	Hs.12382	ESTs	10.0
25	419643	F05066	Hs.91791	chromosome 11 open reading frame 25	9.5
	407173	T64349	gb.601118231F1 NIH_MGC	17 Homo sapiens c	9.5
	412454	R5745	Hs.167330	ESTs	9.5
	438365	AF100143	Hs.6540	fibroblast growth factor 13	9.4
	415315	F12240	Hs.250655	prothymosin, alpha (gene sequence 2B)	9.3
	441790	AW294909	Hs.132208	ESTs	9.2
30	448117	H49129	Hs.127982	ESTs	9.1
	400681				9.0
	437558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypothetical	9.0
	412453	R20205	Hs.167330	ESTs	9.0
35	408920	AL120071	Hs.48598	fibronectin leucine rich transmembrane p	8.9
	409031	AA376836	Hs.75728	ESTs	8.7
40	421806	BE20016	Hs.182470	PTD10 protein	8.3
	446544	AB31932	Hs.7047	ESTs, Weakly similar to Unknown (H-sap)	8.2
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	8.2
	438400	AL038511	Hs.125316	ESTs, Weakly similar to S33960 finger pr	8.2
	416036	Z37916	Hs.63382	latent transforming growth factor beta b	8.0
	454490	U83111	Hs.57303	small inducible cytokine subfamily A (C)	8.0
	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0
45	408428	NM_014787	Hs.44695	Homo sapiens mRNA; cDNA DKFZP564B1264 (f	7.9
	437073	A1885508	Hs.94122	DnaI (Hsp40) homolog, subfamily B, membe	7.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	7.9
	440209	H05049	Hs.22269	neurexin 3	7.8
50	405119	V02613	Hs.101672	ESTs, Weakly similar to T00331 hypothetical	7.8
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	7.8
	410587	AA370706	Hs.86412	chromosome 9 open reading frame 5	7.8
	429611	A1895077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from 7q	7.7
	405800				7.7
55	421750	AK000758	Hs.107872	hypothetical protein FLJ20781	7.7
	426156	BE539836	Hs.98882	hypothetical protein FKSG32	7.7
	423440	R25234	Hs.143434	contactin 1	7.6
	445148	AZ14510	Hs.146304	ESTs	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
60	424087	N69333	Hs.143434	contactin 1	7.6
	437479	R61866	Hs.101277	ESTs	7.5
	405071				7.5
	421224	AW402154	Hs.125812	ESTs	7.4
	442025	AW887434	Hs.11810	CD411 protein	7.4
65	459476	BE189644		gb.154170731.110500-087-c08 H10731 Homo	7.2
	430573	AA744550	Hs.136345	ESTs	7.1
	401836				7.1
	448958	AB020651	Hs.22553	KIAA0344 protein	7.1
	430152	AB001325	Hs.234642	aquaporin 3	7.1
	419474	AW958619	Hs.155849	ESTs	7.1
70	401780				7.1
	446052	AA358760	gb.EST167599 Fetal lung II Homo sapiens c	7.0	
	423605	AF047825	Hs.129887	cadherin 19, type 2	7.0
	433098	AW190593	Hs.151143	ESTs	7.0
	449511	A1436187	Hs.226261	guanine nucleotide binding protein (G pr	6.9
	451285	AW137912	Hs.227553	Homo sapiens chromosome X map Xp11.23L-	6.9
	428414	AL049989	Hs.194216	DKFZP564C152 protein	6.8
	419273	BE271180	Hs.253490	ESTs, Weakly similar to 138022 hypothetical	6.8
	443155	R54485	Hs.23772	ESTs	6.8
	450561	R49674	Hs.25909	ESTs	6.8
80	433068	NM_005456	Hs.285215	sialyltransferase	6.8
	440729	AA904738	Hs.128204	ESTs	6.8
	448426	BE018315	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	6.7
	423689	AA328082	Hs.209569	ESTs	6.6

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	415661	A379882	Hs.72530	ESTs	6.5
	413510	F13044		gb HSC3H8101 normalized infant brain cDN	6.4
	427992	Y15014	Hs.181353	UDP Gal4betaGalNAc beta 1,3-galactosyltr	6.4
5	453344	BE349075	Hs.44571	ESTs	6.4
	450642	R39773	Hs.7130	corin IV	6.4
	432251	AW972983	Hs.232155	polycythemia rubra vera 1, cell surface	6.4
	429322	D86984	Hs.199243	KIAA0231 protein	6.4
	444827	AW016637	Hs.199425	ESTs	6.4
	441482	AB033359	Hs.18705	KIAA1233 protein	6.4
10	400332	565407	Hs.245012	FLT4	6.3
	440703	AL.137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp44G227 (lr	6.3
	446129	AW244073	Hs.145946	ESTs	6.3
	454576	AW204712	Hs.61957	ESTs	6.3
	425226	AA359933		gb:EST69040 Fetal lung II Homo sapiens c	6.3
15	421913	A1934365	Hs.109439	osteoglycin (osteoleinductive factor, mime	6.3
	434273	AA913143	Hs.26303	ESTs	6.2
	409480	A350357	Hs.164568	fibroblast growth factor 7 (keratinocyte	6.2
	451301	A176514	Hs.209800	EST	6.2
20	430754	AW862610	Hs.157068	ESTs	6.2
	438356	AA805530	Hs.48527	ESTs	6.2
	422743	BE304678	Hs.119598	ribosomal protein L3	6.2
	453535	AW255374	Hs.31412	Homo sapiens cDNA FLJ11422 fa. clone HE	6.2
	426388	AW091304	Hs.87103	ESTs	6.2
	425502	A1904296		gb:PM-BT046-220195-286_1 BT046 Homo sapi	6.1
25	402546				6.1
	457534	A1761307	Hs.232226	ESTs	6.1
	408168	AL137573	Hs.4343	Homo sapiens mRNA; cDNA DKFZp564A2463 g	6.1
	440588				6.1
	432501	BE546532	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	6.1
30	442979	AW440782	Hs.174743	ESTs	6.0
	422262	AL022315	Hs.113887	lectin, galactoside-binding, soluble, 2	6.0
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0
	454065	BE394588		gb:501311808F1 NIH_MGC_44 Homo sapiens c	5.9
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9
35	401521				5.9
	425007	R62424	Hs.126058	ESTs	5.9
	446298	AF187813	Hs.14637	kidney- and liver-specific gene	5.9
	417761	R13727	Hs.21435	ESTs	5.9
40	424800	AA326523	Hs.105698	MS1P031 protein	5.9
	441695	T12411	Hs.153745	hypothetical protein FLJ13465	5.8
	457483	AB034694	Hs.272558	endomucin-1	5.9
	417175	R44558	Hs.94002	ESTs	5.8
	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J1184	5.8
45	436427	A344378	Hs.143399	ESTs	5.8
	411638	AC065085	Hs.146246	ESTs	5.8
	458003	AB007052	Hs.210361	ESTs	5.7
	411052	AW814950		gb:MR1-ST0206-130400-023-006 ST0206 Homo	5.7
	431063	Z98949	Hs.326843	hypothetical protein bk12942.1	5.7
50	492382	AA307858	Hs.60257	Homo sapiens cDNA FLJ13598 fa. clone PL	5.7
	408478	NM_000806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7
	442676	A1733585	Hs.130897	ESTs	5.7
	446443	AV690082	Hs.134228	ESTs	5.7
	400865				5.7
55	495080	AW192083	Hs.290855	ESTs	5.6
	407952	A1215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6
	431984	AL080238	Hs.272284	Human DNA sequences from clone GS1-256022	5.6
	425705	AF007833	Hs.155265	xruppel-related zinc finger protein hcr4	5.6
	442239	AW135374	Hs.270940	ESTs, Moderately similar to F41925 hypot	5.6
60	422994	AW981902	Hs.296276	ESTs	5.6
	457148	AF091835	Hs.184627	KIAA0118 protein	5.6
	428335	AL046991	Hs.10338	ESTs	5.6
	415927	AL129168	Hs.79819	Kell blood group precursor (McLeod pheno	5.5
	402052				5.5
65	440526	AB82243	Hs.211471	ESTs	5.5
	444409	AF192140	Hs.492565	ESTs	5.5
	417877	AB25626	Hs.86320	ESTs	5.4
	458238	AW071521	Hs.333541	beta-amyloid binding protein precursor	5.4
	430702	U56979	Hs.250651	H factor 1 (complement)	5.4
	456188	HF1010	Hs.44840	ESTs	5.4
70	427424	AA402853	Hs.113011	ESTs	5.4
	437354	AA742215	Hs.291688	ESTs	5.4
	455617	BE078070		gb:CM1-BT0614-160300-149-02 BT0614 Homo	5.4
	425090	AF203332	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3
75	427861	AA813185	Hs.98183	ESTs	5.3
	408556	UA0516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3
	444209	AT573134	Hs.146494	ESTs	5.3
	422831	R02504	Hs.332943	ESTs	5.3
	403180				5.3
	416326	BE379727	Hs.83213	thy acid binding protein 4, adipocyte	5.3
80	430339	W28608	Hs.239625	integral membrane protein 2e1	5.2
	431586	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	5.2
	431930	AB035301	Hs.272211	cathepin 7, type 2	5.2
	437403	AT08145	Hs.121196	ESTs	5.2

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5	438285	AA782845	Hs.22790	ESTs	5.2
	439901	N73865	Hs.124169	ESTs	5.2
	438607	AA809052	Hs.211275	ESTs	5.2
	445222	AW293384	Hs.197821	ESTs	5.2
10	422634	AK001507	Hs.326984	Homo sapiens clone FLB8914 PRO1821 mRNA	5.2
	419042	T81429	Hs.221055	ESTs	5.2
	436777	AA731199	Hs.293130	ESTs	5.2
	445071	A280246	Hs.149504	ESTs	5.1
15	400616	AW138527	Hs.256096	ESTs	5.1
	412047	AK034349	Hs.49696	ESTs	5.1
	438533	AW959074	Hs.23646	Homo sapiens cDNA FLJ13097 fls, clone NT	5.1
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1
20	409263	AA069573	Hs.50319	ESTs	5.1
	453830	AA534296	Hs.20953	ESTs	5.1
	455890	AA022880	Hs.176065	ESTs	5.1
	417616	R07728	Hs.286868	ESTs	5.1
25	423457	F08208	Hs.283844	similar to rat thicarbonylate carrier-1	5.1
	441535	AL133735	Hs.17885	phosphatidylethanol binding cathepsin as	5.0
	416490	AF090116	Hs.79348	regulator of G-protein signalling 7	5.0
	417284	N82889	Hs.107242	Homo sapiens cDNA FLJ12965 fls, clone NT	5.0
30	447335	T58148	Hs.171597	gcyb9g96s.1 Stratagene lung (S37210) H	5.0
	446605	AL109878	Hs.201336	Homo sapiens mRNA full length insert cDN	5.0
	442240	AJ791883	Hs.282719	ESTs	4.9
	458399	BE407712	Hs.153596	creatine kinase, mitochondrial 1 (ubiqui	4.9
35	427972	AA864870	Hs.181304	putative gene product	4.9
	432944	AA570587	Hs.36512	ESTs	4.9
	440180	BE360293	gb:601345159F1 NIH_MGC_8 Homo sapiens cD	4.9	
	440477	A097452	Hs.153095	ESTs	4.9
40	416040	AW819158	Hs.289044	Homo sapiens cDNA FLJ12048 fls, clone HE	4.9
	444922	AJ821750	Hs.144871	Homo sapiens cDNA FLJ13752 fls, clone PL	4.9
	438678	AJ690021	Hs.24908	ESTs	4.8
	448072	AI459306	Hs.293549	ESTs	4.8
45	408936	AL130043	Hs.293549	ESTs	4.8
	412822	AW664708	Hs.171959	ESTs	4.8
	414943	Q80647	Hs.124153	ESTs	4.8
	429254	H10133	Hs.91846	hypothetical protein DKFZp781C121	4.8
50	453567	AJ742835	Hs.33368	hypothetical protein FLJ11175	4.8
	407906	AI336655	Hs.41185	Homo sapiens mRNA: cDNA DKFZp564O1262 (l	4.8
	441020	AJ333860	Hs.17558	Homo sapiens cDNA FLJ14446 fls, clone HE	4.8
	405130	AW996689	gb:CV3-BN0046-150400-151:q9s BN0046 Homo	4.7	
55	446218	AV657159	gb:AV657159 GLC Homo sapiens cDNA clone	4.7	
	434347	AJ052543	Hs.79381	metanoma-derived leucine zipper, extra-n	4.7
	402178	BE063207	Hs.296543	grancalcin	4.7
	438221	AK001781	Hs.296543	Homo sapiens cDNA FLJ10919 fls, clone OV	4.7
60	420480	AL137361	Hs.58173	hypothetical protein	4.7
	400900	Y10282	Hs.46525	eyes absent (Drosophila) homolog 3	4.7
	435161	AF124150	Hs.272091	ESTs	4.6
	404793	U66581	Hs.248121	G protein-coupled receptor 22	4.6
65	430895	U66581	Hs.56022	ESTs	4.6
	438571	AW020775	Hs.164168	ESTs	4.6
	445824	AJ254671	Hs.6594	ESTs	4.6
	421044	AF061871	Hs.311738	Human DNA sequence from clone RP1-238D15	4.6
70	418274	AJ485887	Hs.128677	Human DNA sequence from clone RP1-50C24	4.6
	425475	V86339	Hs.107057	ESTs	4.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fls, clone MA	4.6
	414272	AJ651603	Hs.46368	ESTs	4.5
75	445236	AJ640222	Hs.138207	ESTs	4.5
	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24035 hypotheti	4.5
	414630	BE103957	gb:60130177F1 NIH_MGC_21 Homo sapiens c	4.5	
	414456	H74314	gb:yu5610.1r1 Soares fetal liver spleen	4.5	
80	401024	AI815523	Hs.76330	synectin, alpha (non A4 component of am	4.5
	414699	AI815523	Hs.33067	ESTs	4.5
	423449	AI497900	Hs.33067	ESTs	4.5
	405138	BE147225	Hs.24144	ESTs	4.4
85	413544	BE147225	Hs.27151	ESTs	4.4
	453880	AI803166	Hs.28462	neurexin 1	4.4
	433521	T68087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4
	441184	AA922909	Hs.150269	ESTs	4.4
90	429876	AJ028977	Hs.225974	KIAA1054 protein	4.4
	445481	AW661846	Hs.148836	ESTs	4.4
	452340	NM_002202	Hs.905	ISL1 transcription factor, LIMhomeodoma	4.4
	404789	AW153342	Hs.24144	ESTs	4.4
95	444331	AW153342	Hs.27151	ESTs	4.4
	429726	AW626326	Hs.27151	ESTs	4.4
	446093	AE030356	Hs.22998	neurexin 1	4.4
	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	4.4
100	415716	N59204	Hs.179652	nucleosome assembly protein 1-like 1	4.4
	417888	R23053	gb:ghy31a05.r1 Soares placenta Nb2HP Homo	4.4	
	419656	AB022314	Hs.92025	KIAA0316 gene product	4.4
	425864	U56420	Hs.159933	olfactory receptor, family 5, subfamily	4.4

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5	435078	AW518888	Hs.40937	ESTs	gb.MRO-HT0168-141199-002-409 HT0168 Homo
	413493	BE144444		ESTs	sterol-C5 desaturase (fungal) ERG3, delta
	432712	AB016247	Hs.288031	ESTs	
	459560	R25754	Hs.301185	ESTs	
	404628				
	423782	JA472209	Hs.323117	ESTs	
	426867	AA60967	Hs.22668	ESTs	
	426802	AA365182	Hs.46699	ESTs	
	457353	J55533	Hs.248144	metacardin 2 receptor (adrenocortical)	
10	417112	BE180342	gb.RC3-HT0522-130400-012-a07 HT0522 Homo	CGI-35 protein	
	401522	N47812	Hs.306198	Homo sapiens cDNA FLJ11570 fs, clone HE	
	419055	AJ365384	Hs.11571	ESTs	
	410171	H07892	Hs.12431	ESTs	
	415564	U09899	Hs.91139	solute carrier family 1 (neuronal)SLP16	
15	458789	AL157468	Hs.325625	Homo sapiens cDNA FLJ20648 fs, clone AD	
	455040	AV852286	gb.CVO-CT0225-100000-187-d08 CT0225 Homo	gb.CVO-CT0225-100000-187-d08 CT0225 Homo	
	438533	AI440296	Hs.170673	ESTs, Weakly similar to T24832 hypobell	
	455025	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	
20	433389	AF038171	gb.Homo sapiens clone 23871 mRNA sequenc	hypothetical protein from Xq28	
	454356	AW930363	Hs.11522	ESTs, Weakly similar to 1901303A Lew zip	
	442339	BE299568	Hs.227591	gb.HTR277 HTTCDL1 Homo sapiens cDNA ST3	
	421249	AA265362	Hs.296276	ESTs	
	443998	AI620661	Hs.232048	ESTs	
	452197	AW023596	Hs.232048	ESTs	
	451117	AA015752	Hs.205173	ESTs	
	404501	AW047252	Hs.75514	nucleoside phosphorylase	
	410378	R23324	Hs.41893	Onal (Hsp40) homolog, subfamily B, membe	
	422528	AB011182	Hs.118087	KIAA0610 protein	
	440323	AA970614	Hs.127992	ESTs	
	425767	AF054178	Hs.153483	chromosome 1 open reading frame 7	
	434460	AA478496	Hs.3852	KIAA0368 protein	
	410362	H04811	Hs.53154	proprotein convertase subtilisin/kexin 1	
	413121	T96090	Hs.142878	ESTs	
	409403	AA668224	Hs.6534	Homo sapiens cDNA: FLJ22547 fs, clone H	
	452235	AA007512	Hs.17538	ESTs	
	449754	H00820	Hs.30977	ESTs, Weakly similar to B34007/hypohe	
	421813	BE048255	gb.t249605.y1 NCL_CGAP_Bm52 Homo sapien	gb.t249605.y1 NCL_CGAP_Bm52 Homo sapien	
	408496	AI803302	Hs.136182	ESTs	
	432051	AA309127	Hs.231225	hypothetical protein HT023	
	434101	AA625205	Hs.255599	KIAA1622 protein	
	451837	T92157	Hs.16970	ESTs	
	411772	BE170301	gb.Q4-H-070536-040500-193-05 HT0536 Homo	SWAP-70 protein	
45	437630	AI525782	Hs.153029	gb.ncs104.s1 NCL_CGAP_Py1 Homo sapiens	
	430212	AA469153			
	400216				
	429830	AI537278	Hs.225841	DKFZP434D193 protein	
	453165	ST4727	Hs.32042	aspartacylase (aminocyclase 2, Cerevan	
	418047	R31833	Hs.4847	ESTs	
	405354				
	427931	AW206512	Hs.186996	ESTs	
	428775	AA434579	Hs.143691	ESTs	
	449422	AA001373	Hs.59821	ESTs	
	453864	AW021407	Hs.21068	hypothetical protein	
	456407	AI968814	gb.EST80690 MAGE resequences, MAGI Homo	gb.EST80690 MAGE resequences, MAGI Homo	
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	
	420784	T65158	Hs.102399	ESTs, Moderately similar to S65657/alpha	
	421585	AJ352026	Hs.94319	VP510 domain receptor protein	
	429628	H09604	Hs.13268	ESTs	
	410087	F12079	Hs.332579	ESTs	
	409840	AW502122	gb.U-HF-BR07-ajr-c-08-D-Ulr1 NIH_MGC_5	gb.U-HF-BR07-ajr-c-08-D-Ulr1 NIH_MGC_5	
	423854	AA437061	Hs.14060	prokineticin 1 precursor	
	419910	AA662013	Hs.190173	ESTs, Weakly similar to A46010 X-linked	
	427443	AA402713	Hs.97872	ESTs	
	414890	C17758	Hs.221652	Homo sapiens cDNA FLJ14323 fs, clone PL	
	412678	AA115575	Hs.114914	ESTs	
	405629				
	420299	AI056871	Hs.15276	ESTs	
	453098	Z25935	Hs.86379	ESTs	
	435752	AFZ08001		gb.Homo sapiens growth hormone receptor	
	441005	Z41305	Hs.303172	Homo sapiens mRNA, cDNA DKFZ547G133 (fr	
	414516	AB378027	Hs.135560	ESTs, Weakly similar to T43458 (hypohe	
	442257	AW503831	Hs.323370	Human EST clone 25267 mirror transposon	
	422663	BE295342	Hs.19348	hypothetical protein FLJ13119	
	406697	U21388	Hs.123017	Human unproductively rearranged y-mu-ch	
	443850	AW014723	Hs.334612	ESTs	
	412677	AW029606	Hs.17384	ESTs	
	422788	AL117352	Hs.120828	Human DNA sequence from clone RPS-676B10	
	405377				
80	414378	BE333858	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [
	453341	AI758912	Hs.296341	adenylyl cyclase-associated protein 2	
	431960	AW241821	Hs.301927	c6.1A	
	416854	H40164	Hs.80295	Purkinje cell protein 4	

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427264	AA001117	Hs.125747	ESTs	3.9
427246	NM_004484	Hs.119551	glypican 3	3.9
452346	BE743534		gb:TCBAP1D00885 Pediatric pre-B cell acute	3.9
414655	NM_004455	Hs.75828	glypican 5	3.8
418217	A1010647	Hs.13442	ESTs	3.8
419118	AA234223	Hs.139204	ESTs	3.8
445017	A1705493	Hs.176860	ESTs	3.8
405957				3.8
427760	BE402651		gb:60129986SF1 NHP_MGC_21 Homo sapiens c	3.8
453853	X02544	Hs.572	oroscromucoid 1	3.8
457821	H47156	Hs.124322	ESTs, Weakly similar to A47582 B-cell	3.8
457330	AB013618	Hs.247220	peroxisome biogenesis factor 10	3.8
435600	AL047034	Hs.119747	ESTs	3.8
456003	U46922	Hs.77252	fragile histidine triad gene	3.8
413341	H78472	Hs.191325	ESTs, Weakly similar to T18957 hypotheti	3.8
449057	AB037784	Hs.27941	KIAA1363 protein	3.8
471955	P06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8
414764	AW013987	Hs.72047	ESTs	3.8
404391				3.7
433629	R13140	Hs.13359	ESTs	3.7
424738	A963740	Hs.46826	ESTs	3.7
421315				3.7
407708	AA191085	Hs.25612	ESTs, Moderately similar to S23950 retro	3.7
440530	AA388646	Hs.174187	ESTs	3.7
433930	AA620338	Hs.273781	ESTs	3.7
409552	AW452320	Hs.279728	ESTs	3.7
437258	A1754847	Hs.273751	regulator of G-protein signaling 4	3.7
445688	A1248205	Hs.153244	ESTs	3.7
408503	R19566	Hs.197817	ESTs	3.7
417091	AA193283	Hs.291590	ESTs	3.7
446568	AW885605	Hs.5084	ESTs	3.7
423135	N87655	Hs.29411	ESTs	3.7
400135				3.7
459150	BE155335		gb:PM1-HT0350-160300-005-005 HT0350 Homo	3.7
457221	AW362197	Hs.218250	ESTs	3.7
451660	A1807927	Hs.249601	ESTs	3.7
401500	BE247275	Hs.151787	US snRNP-specific protein, 116 kD	3.7
446816	A1342686	Hs.279765	ESTs	3.7
447795	AW265151	Hs.163612	ESTs	3.7
427632	RS5424	Hs.26834	ESTs	3.6
412258	AA376758	Hs.324841	hypothetical protein FLJ22622	3.6
454329	AW381980		gb:OV4-HT0016-091199-026-005 HT00316 Homo	3.6
439274	AF086092	Hs.45372	ESTs	3.6
452381	I23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
422897	AA679784	Hs.4290	ESTs	3.6
429656	X05608	Hs.211584	neurofilament, light polypeptide (88kD)	3.6
421908	AW935200	Hs.285814	sprouty (Drosophila) homolog 4	3.6
407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	3.6
429432	AW614271	Hs.121647	ESTs, Highly similar to AC009014 6 sim	3.6
406085				3.6
417154	A1874701	Hs.21368	ESTs	3.6
447176	Z42549	Hs.163953	ESTs	3.6
423953	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	3.6
449231	BE410360	Hs.298573	KIAA1720 protein	3.6
411607	AW853498		gb:RC1-CT0252-170200-025-002 CT0252 Homo	3.6
405977				3.6
441470	BE403874	Hs.301988	ESTs	3.6
423569	NM_005256	Hs.129818	growth arrest-specific 2	3.6
441235	A084586	Hs.135570	Homo sapiens cDNA: FLJ21268 fls, clone C	3.6
450236	AW162998	Hs.24684	KIAA1376 protein	3.6
425364	AF052150	Hs.155659	Homo sapiens clone 24533 mRNA sequence	3.6
429715	AA384564	Hs.108919	ESTs	3.6
414831	M31158	Hs.77439	protein kinase, CAMP-dependent, regula	3.6
416876	AW501916	Hs.117897	ESTs	3.6
404878				3.6
425153	AW023193	Hs.27045	ESTs	3.6
452222	A104995		gb:an03c03.x1 Stratogene schizo brain S1	3.5
415047	F13142		gb:HSC3M0031 normalized infant brain cDN	3.5
401532				3.5
445456	D69923	Hs.153490	ESTs	3.5
431326	AW026751	Hs.5794	ESTs, Weakly similar to 2109250A B cell	3.5
445858	AF070523	Hs.13423	Homo sapiens clone 74455 mRNA sequence	3.5
455901	BE155527		gb:PM1-HT0350-190400-013-008 HT0350 Homo	3.5
415421	AA134005	Hs.75305	eukaryotic translation initiation factor	3.5
455697	BE067952		gb:CM0-BT0365-051299-172-g05 BT0365 Homo	3.5
405678				3.5
418207	C14685	Hs.34772	ESTs	3.5
425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5
417027	AA192305	Hs.23925	brachin	3.5
428357	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5
417702	R09935	Hs.191146	ESTs	3.5
445687	W80382	Hs.149297	ESTs	3.5
408776	AA057355	Hs.63355	ESTs, Weakly similar to I36022 hypotheti	3.5

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413164	BE068494	gb:MR1-BT0371:050500-009 a12 BT0371 Homo	3.5
414593	BE367664	gb:601273249F1 NIH_MGC_20 Homo sapiens c	3.5
453220	AB033089	Hs.32452 Homo sapiens mRNA for KIAA1263 protein,	3.5
415521	AB48602	Hs.55498 ESTs	3.5
454437	AG28173	Hs.191460 hypothetical protein MGC12936	3.5
446066	AG343931	Hs.149383 ESTs	3.5
423374	AB037770	Hs.127656 KIAA1340 protein	3.5
419347	C15944	Hs.90005 superoincervical ganglia, neural specific	3.5
418516	NM_006218	Hs.85701 phosphoinositide-3-kinase, catalytic, α	3.5
451776	W45679	Hs.169854 hypothetical protein SP102	3.5
423905	M62402	Hs.274313 insulin-like growth factor binding prote	3.5
456995	T89832	Hs.170278 ESTs	3.5
403323			3.5
425222	M56724	Hs.154207 centromere protein C 1	3.5
439394	AA149250	Hs.56105 ESTs	3.4
433803	AI823593	Hs.27588 ESTs	3.4
450715	AI266484	Hs.31570 ESTs, Weakly similar to KIAA1324 protein	3.4
411474	AV984427	gb:IL3-CT0214-150200-075-A10 CT0214 Homo	3.4
415076	NM_000857	Hs.77890 guanylate cyclase 1, soluble, beta 3	3.4
423626	U20325	Hs.1707 cocaine- and amphetamine-regulated trans	3.4
459495	BE544159	gb:601076707F1 NIH_MGC_12 Homo sapiens c	3.4
427173	BE265017	Hs.97540 ESTs	3.4
408112	AW451982	Hs.248613 ESTs	3.4
446092	N33522	Hs.145894 ESTs	3.4
416868	AB688856	Hs.292597 ESTs	3.4
455234	BE551408	Hs.127196 ESTs	3.4
415555	AA244416	gb:0097411.s.1 NC1 CGAP_Pv1 Homo sapiens	3.4
414314	BE312991	gb:601150275F1 NIH_MGC_19 Homo sapiens c	3.4
400425	AY004252	Hs.287385 PR domain containing 12	3.4
414366	BE548143	gb:601076456F1 NIH_MGC_12 Homo sapiens c	3.4
434053	AW445136	Hs.136495 ESTs	3.4
449997	AB83052	Hs.201577 KIAA1829 protein	3.4
433461	AI636047	Hs.197623 ESTs	3.4
428006	AA418743	Hs.38306 KIAA1852 protein	3.4
424695	U58331	Hs.151899 sarcoglycan, delta (35kD dystroglycan-asso	3.4
443294	AI733625	Hs.133053 ESTs	3.4
428212	AW444451	Hs.134812 ESTs	3.4
457673	AA551569	Hs.272034 hypothetical protein PR02822	3.3
440390	AA233933	Hs.14652 hypothetical protein FLJ11151	3.3
428536	AI143139	Hs.2228 insulin-like 1	3.3
426597	AA382250	Hs.145601 ESTs	3.3
410366	AI257589	Hs.302689 hypothetical protein	3.3
458258	AW406546	Hs.127971 ESTs	3.3
401738			3.3
429039	TS7490	Hs.50002 small inducible cytokine subfamily A (C)	3.3
425785	T27017	Hs.155828 Homo sapiens clone 24400 mRNA sequence	3.3
433328	AW298159	Hs.23644 ESTs, Weakly similar to S55824 reverse t	3.3
414841	BE293116	Hs.76392 aldehyde dehydrogenase 1 family, member	3.3
434998	AW975157	Hs.26037 ESTs	3.3
456359	AI967391	Hs.93574 homeo box D3	3.3
426527	NM_001037	Hs.170238 sodium channel, voltage-gated, type I, b	3.3
454287	AA437199	Hs.6556 cell division cycle 25C	3.3
400302	LA8056	Hs.19115 klatin hydrolase (prostate-specific memb	3.3
434077	AF1116059	Hs.321151 Homo sapiens PRO1412 mRNA, complete cds	3.3
436602	AI793222	Hs.166817 ESTs	3.3
449204	AB000039	Hs.23251 Down syndrome critical region gene 4	3.3
417935	RS3697	Hs.170044 ESTs	3.3
423310	AA325225	Hs.124023 Homo sapiens cDNA FLJ14218 fs, clone NT	3.3
436624	TS4297	Hs.5241 fatty acid binding protein 1, liver	3.3
453406	AI192987	Hs.61784 hypothetical protein FLJ14451	3.3
420164	AV330037	Hs.24908 ESTs	3.3
447826	AW775317	Hs.265666 ESTs	3.3
419875	AA853410	Hs.93557 proenkephalin	3.3
444612	AW138111	Hs.22992 ESTs	3.3
418504	BE159718	Hs.85335 Homo sapiens mRNA; cDNA DKFZp664D1462 (f	3.2
415242	RA6986	Hs.295014 ESTs	3.2
418188	AW139413	Hs.151880 ESTs	3.2
430355	NM_006219	Hs.239818 phosphoinositide 3-kinase, catalytic, be	3.2
421640	AW966652	gb:EST1378726 MAGE resequencs, MAGI Homo	3.2
423289	AB076049	Hs.274415 Homo sapiens cDNA FLJ10229 fs, clone HE	3.2
408806	AW487814	Hs.289005 Homo sapiens cDNA FLJ21532 fs, clone C	3.2
400409	AF153341	Hs.283954 Homo sapiens winged helix/forkhead trans	3.2
446015	T30968	Hs.125311 hypothetical protein FLJ10971	3.2
425495	AA358454	Hs.78026 ESTs, Weakly similar to similar to ankyr	3.2
403092			3.2
452971	AI873878	Hs.31789 ESTs	3.2
454186	BE141030	gb:MRD-HT0067-201099-002-h11 HT0067 Homo	3.2
401485			3.2
401949			3.2
457452	AW072675	gb:EST384766 MAGE resequencs, MAGI Homo	3.2
454100	AI693231	Hs.126043 chromosome 21 open reading frame S1	3.2
448440	AA173467	Hs.62402 p21Cdc42/Rac1-activated kinase 1 (yeast	3.2
421200	AA284811	Hs.264433 ESTs	3.2

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	430142	NM_000437	Hs.234362	platelet-activating factor acetylhydrolase	3.2
	433197	AB040889	Hs.281022	KIAA1456 protein	3.2
	443509	AV645470		go AV645470 GLC Homo sapiens cDNA clone	3.2
	440827	U793110	Hs.128128	ESTs	3.2
5	432799	NM_016161	Hs.278950	alpha-1,4-N-acetylglucosaminyltransferase	3.2
	409257	AW370362	Hs.278950	gb:RC1-BT0255-181099-012-07 BT0255 Homo	3.2
	459235	BE246010	Hs.271468	Homo sapiens mRNA for FLJ000338 protein,	3.2
	416789	FA222439	Hs.799333	cyclin I	3.2
10	429809	AL162010	Hs.223603	Homo sapiens mRNA, cDNA DKFZp751D09121 (3.2
	420156	AW445258	Hs.6187	ESTs	3.2
	455577	BE006341		gb:RC2-EN0127-240300-011-b05 EN0127 Homo	3.2
	400617	AF151084	Hs.36069	hypothetical protein	3.2
	437129	AL943327	Hs.302057	Homo sapiens mRNA, cDNA DKFZp564E016 (h	3.2
	451820	AW655357	Hs.337353	ESTs	3.2
15	457535	AA609685	Hs.279672	membrane component, chromosome 11, surf	3.2
	419956	AL137939	Hs.40096	ESTs	3.1
	456235	AA203637		gb:zx58b.t2.r1 Soares_fetal_liver_spleen_	3.1
	423930	AA332697	Hs.42721	ESTs	3.1
	403796				3.1
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.1
20	445886	AJ793176	Hs.145596	ESTs	3.1
	414401	AJ760159	Hs.124833	ESTs	3.1
	441573	BE563966	Hs.6529	ESTs, Weakly similar to T8885 serineoth	3.1
	450725	R71389	Hs.175951	ESTs	3.1
	458805	AJ262933	Hs.23254	hypothetical protein FLJ14393	3.1
	417868	AJ076534	Hs.122592	ESTs	3.1
	458391	AJ764208	Hs.133273	ESTs	3.1
	423446	AJ267677	Hs.127416	synapjanin 1	3.1
30	454486	AW857077	Hs.RC1-CT0302-140300-016-04 CT0302 Homo	3.1	
	408341	AW182952	Hs.249597	ESTs	3.1
	410559	AW905749	Hs.318685	superoxide dismutase 2, mitochondrial	3.1
	404907				3.1
	434910	AJ333863	Hs.215474	ESTs, Moderately similar to alternative	3.1
35	436990	AJ149729	Hs.120657	ESTs	3.1
	441521	AJ733376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1
	454673	AW812807	Hs.378950	gb:RC3-ST0186-070100-016-04 ST0186 Homo	3.1
	429470	AJ878901	Hs.203862	guanine nucleotide binding protein (G pr	3.1
	404345	AA730407	Hs.159156	protocadherin 11	3.1
40	408217	AJ433201	Hs.279860	tumor protein, translationally-controlled	3.1
	417313	AJ195602	Hs.279860	gb:zx20291.1 Soares_HuMPu_S1 Homo sapi	3.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1
	411003	AA181018	Hs.13056	hypothetical protein FLJ13920	3.1
	425339	AA596330	Hs.198113	ESTs	3.1
	426716	NM_005379	Hs.171521	zona domain, immunoglobulin domain (Ig)	3.1
45	449076	AK001256	Hs.229275	KIAA1576 protein	3.1
	429608	U49250	Hs.210862	T-box, brain, 1	3.1
	442308	AA895402	Hs.111	fibroblast growth factor 9 (gila-activel	3.1
	428465	AW670576	Hs.29353	ESTs	3.1
	411696	AF106564	Hs.71246	neurofilament 3 (150kD medium)	3.1
	447965	AW292577	Hs.94445	ESTs	3.1
	413918	AW019898	Hs.71245	ESTs	3.1
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.1
	425610	AJ236227	Hs.31903	ESTs	3.1
55	427865	AA416931	Hs.125065	ESTs	3.1
	425060	AW139155	Hs.194995	hypothetical protein DKFZp434C03020	3.1
	430708	U73308	Hs.278485	olfactory receptor, family 1, subfamily	3.1
	448084	AJ467800	Hs.271000	ESTs, Weakly similar to 38022 hypot	3.1
	454506	AW647346	Hs.271000	go:RC3-CT0205-240999-021-e01 CT0205 Homo	3.1
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocytic/macrophage	3.0
60	422963	M79141	Hs.13234	ESTs	3.0
	417696	BC241624	Hs.82401	CD59 antigen (p60, early T-cell activat	3.0
	448175	BC295174	Hs.225169	hypothetical protein FLJ13102	3.0
	414696	BC409757	Hs.23189	ESTs, Moderately similar to TB22_HUMAN T	3.0
	458360	A027207	Hs.132263	ESTs	3.0
65	451829	AW964081	Hs.247377	ESTs	3.0
	445179	AB94743	Hs.224760	ESTs	3.0
	433050	AJ720050	Hs.145362	immortalization-upregulated protein	3.0
	432018	AA524447	Hs.152377	ESTs	3.0
	407988	NA7760	Hs.285107	hypothetical protein FLJ13397	3.0
70	405911				3.0
	418808	AB21836	Hs.10359	ESTs	3.0
	431900	AW972048	Hs.192534	ESTs	3.0
	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0
75	423652	AW877787	Hs.136102	KIAA0853 protein	3.0
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0
	405793				3.0
	410711	AB002316	Hs.65746	KIAA0318 protein	3.0
	411279	AW854776	Hs.404-010067-010300-121-001 OT0067 Homo	3.0	
80	423957	AW918309	Hs.136235	Homo sapiens cDNA FLJ13542 fs, clone PL	3.0
	427071	AA397958	Hs.152719	ESTs	3.0
	434961	AW974956	Hs.152719	gb:EST387061 MAGE resequences, MAGN Homo	3.0

TABLE 10B

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	Key:	Unique Eos proset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
5	Key	Accession
	406257	1172994_1
	406840	1156071_1
	411052	1230374_1
	411279	1227516_1
	411474	1247047_2
10	411607	1251251_1
	411772	1257386_1
	412112	1277883_1
15	413164	1351422_1
20		
25	413493	1373553_1
	413510	1374377_1
	413544	1375671_1
	414220	1426940_1
	414314	1435028_1
	414366	1438636_1
	414456	1447555_1
	414593	1464909_1
	414630	1468003_1
	415047	1517450_1
	417213	165644_1
35	417888	1706022_1
	419555	185884_1
	421249	206640_1
	421640	204633_1
40	421813	207654_1
	422760	221034_1
	425256	252776_1
	430212	314437_1
	432222	343347_1
45	433369	36497_1
	434961	396357_1
	435752	41050_1
	437403	437156_1
	441196	48524_2
50	443509	571199_1
	446525	65988_1
	445218	65986_1
	447135	70963_1
	452346	912206_1
55	452602	919733_1
	454065	959407_1
	454186	1049791_1
60	454339	1122972_1
	454486	1125053_1
	454505	1219657_1
	454673	1278669_1
	455040	1250028_1
65	455225	1262318_1
	455577	1333898_1
	455617	1346117_1
	455697	1351148_1
	455901	1381569_1
	456235	168886_1
70	456407	184896_1
	457452	339381_1
	459150	919196_1
75	TABLE 10C:	
	Key:	Unique number corresponding to an Eos proset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:		Indicates DNA strand from which exon was predicted.
NI_positon:		Indicates nucleotide positions of predicted exons.
80	Key	Strand
	406861	8118474
		Plus
		NI_positon
		81912-85187

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	400685	8118768	Minus	72969-73050,73713-73800
	400685	1845037	Minus	44482-45526
	400878	9864757	Plus	31493-32042
	401024	8117489	Plus	60551-60802
5	401315	9212516	Minus	189890-199619
	401485	7341723	Plus	68009-68200,68841-69077
	401521	7705251	Plus	3127-3234
	401532	7799378	Plus	124414-124950,125058-125418
	401738	2982169	Minus	41547-41757
10	401780	7249190	Minus	28307-28617,28920-29045,29135-29296,29411-29567,29105-29787,30224-30573
	401836	7534063	Plus	71981-72084
	401949	3492899	Plus	16028-161650
	402092	7249154	Minus	107533-108094
	402176	7543687	Minus	10-750
15	402546	7637346	Plus	24673-25170
	403052	8954241	Plus	174720-175016,175104-175406,175508-175813
	403180	7523276	Minus	63003-63759
	403323	8340882	Minus	120366-120845
	403796	8099896	Minus	75073-77654
20	404391	3135305	Minus	26030-26173,27852-27997
	404769	8099713	Minus	175801-176823
	404793	7232206	Minus	61087-61590
	404828	6580415	Minus	26291-27253
25	404907	7331453	Minus	102880-103828
	404958	7407941	Minus	2731-4531
	405071	7708797	Minus	11115-11552
	405130	8516045	Plus	150235-150440
	405138	8576241	Plus	90303-90516
	405354	2642452	Plus	52213-53089
30	405377	5640375	Plus	216556-216948
	405629	4508116	Minus	101678-101866
	405678	4079670	Plus	151821-152027
	405733	1405887	Minus	89197-89453
	405800	2791346	Plus	10271-10813
35	405867	6758731	Minus	74553-75173
	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

40 TABLE 11A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES
 Table 11A lists about 533 CNS-enriched genes significantly down-regulated in glioblastomas compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix Eos HUG3 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.
 Pkey: Unique Eot probe identifier number
 ExAcen: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor
 R2: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue

55	Pkey	ExAcen	UnigeneID	Unigene Title	R1	R2
	417275	X83578	Hs.29540	pirinibornin	29.0	30.0
	435829	AW45199	Hs.194024	ESTs	25.7	5.2
	410557	AF063228	Hs.65248	dynein, cytoplasmic, intermediate polypeptide	22.6	25.8
	419554	D14720	Hs.33883	myosin protein zero (Charcot-Marie-Tooth)	21.2	30.3
60	416133	NM_001083	Hs.83512	ATPase, Ca++ transporting, plasma membrane	15.5	16.8
	416018	AW138239	Hs.78977	prothion convertase subtilisin/kexin 1	15.2	18.0
	417167	AW206437	Hs.42390	ESTs	14.8	17.7
	433840	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
	413324	U00571	Hs.75296	cardiotropin releasing hormone	13.1	18.0
65	430830	AA046666	Hs.151489	ESTs, Weakly similar to XET_HUMAN PROTEIN	12.6	16.5
	408068	AW148552	Hs.162398	ESTs	12.6	16.9
	429096	AB011106	Hs.196012	KIA00534 protein	12.2	21.1
	412638	AA910199	Hs.200380	ESTs	12.2	16.0
	442593	R33804	Hs.31361	ESTs	10.8	15.0
70	446353	A200919	Hs.153661	ESTs	10.4	13.2
	426365	AA376667	Hs.10283	RNA binding motif protein 88	10.0	5.9
	414937	R38698	Hs.12382	ESTs	10.0	10.8
	419643	F06066	Hs.91791	chromosome 11 open reading frame 25	9.5	10.9
	412454	R55045	Hs.167330	ESTs	9.5	14.1
75	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
	441790	AW294309	Hs.132208	ESTs	9.2	3.2
	448117	H49129	Hs.172982	ESTs	9.1	12.8
	433558	AA333757	Hs.200769	ESTs, Weakly similar to T24435 hypothesis	9.0	14.7
	412453	R20005	Hs.167330	ESTs	9.0	13.7
80	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9	17.3
	405031	AA376836	Hs.76728	ESTs	8.7	8.6
	446544	AG31332	Hs.7047	ESTs, Weakly similar to Unknown [H.sapi	8.2	20.0
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger p	8.2	6.3

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	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0	8.9
	408428	NM_014787	Hs.44896	DnaI (Hsp40) homolog, subfamily B, member	7.9	9.6
	437073	A085608	Hs.94122	ESTs	7.9	11.3
	408434	AW195537	Hs.107716	hypothetical protein FLJ22344	7.9	16.4
5	440209	H03491	Hs.22288	neurexin 3	7.8	34.3
	408119	VQ6213	Hs.101672	ESTs, weakly similar to T00331 hypothetical	7.8	9.0
	429611	A088077	Hs.213388	Homo sapiens BAC clone C18-60N22 from 7q	7.7	5.0
	423440	R25234	Hs.143434	contactin 1	7.7	9.9
	445148	A1214510	Hs.1462804	ESTs	7.6	9.1
10	415294	D65880	Hs.75170	KIAA0227 protein	7.6	7.6
	424087	N69333	Hs.143434	contactin 1	7.6	10.3
	437479	R61656	Hs.101277	ESTs	7.5	9.3
	430573	AA144650	Hs.136345	ESTs	7.1	2.8
	448958	A002061	Hs.22853	KIAA0584 protein	7.1	10.4
15	419474	AW968619	Hs.155849	ESTs	7.1	3.0
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0	6.9
	433598	AW190593	Hs.151143	ESTs	7.0	9.2
	449511	A1036187	Hs.216201	guanine nucleotide binding protein (G pr	6.9	3.1
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.8	5.0
20	443155	R54485	Hs.23772	ESTs	6.8	3.5
	450561	R49674	Hs.25909	ESTs	6.8	8.1
	433568	NM_006456	Hs.266215	slit/Transferrase	6.8	2.0
	423588	AA320082	Hs.205569	ESTs	6.6	10.5
	415681	A1379882	Hs.72630	ESTs	6.5	9.0
25	413510	F13044		gh.HSC3HH101 normalised infant brain cDN	6.4	7.1
	427992	Y15614	Hs.181353	UDP-Gal-betaGlcNAc-beta 1,3-galactosyltr	6.4	9.5
	450442	R39773	Hs.7130	caprin IV	6.4	5.7
	429322	D65984	Hs.199243	KIAA0231 protein	6.4	8.2
30	447482	AB033059	Hs.18705	KIAA1233 protein	6.4	2.3
	446129	AW244073	Hs.145546	ESTs	6.3	8.3
	421913	A1054355	Hs.109439	osteoglycin (osteopontin-like factor, mem	6.3	2.1
	434273	FA913143	Hs.26303	ESTs	6.2	10.3
	408480	A1350337	Hs.164568	fibroblast growth factor 7 (heparinocyte	6.2	3.5
35	451301	U1769514	Hs.205990	EST	6.2	12.4
	438558	AA305330	Hs.46387	ESTs	6.2	3.1
	426388	AW051384	Hs.57103	ESTs	6.2	8.6
	452502	A1904296		gt:PM-BT046-220199-286_1 BT046 Homo sapi	6.1	2.8
	439155	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp566A2463 (f	6.1	6.3
40	442379	AW040982	Hs.174743	ESTs	6.1	6.3
	420713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	6.0	8.8
	430004	U27768	Hs.227571	regulator of G-protein signaling 4	5.9	21.4
	425067	R62424	Hs.126059	ESTs	5.9	8.1
	441695	112411	Hs.183745	hypothetical protein FLJ11456	5.9	3.1
45	417175	R44558	Hs.94002	ESTs	5.8	12.5
	437483	AL300174		gt:Homo sapiens mRNA; cDNA DKFZp547J184	5.8	2.2
	436427	A1344378	Hs.143399	ESTs	5.8	13.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13986 fs, clone PL	5.7	4.4
	408478	NM_008006	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7	12.5
50	442376	A1733395	Hs.130897	ESTs	5.7	6.8
	446443	AV859082	Hs.134228	ESTs	5.7	6.4
	450380	AW192083	Hs.290855	ESTs	5.6	15.6
	431954	AL080239	Hs.272284	Human DNA sequence from clone GS1-256022	5.6	8.2
	428356	AL048991	Hs.10238	ESTs	5.6	6.2
55	417877	A0225829	Hs.86320	ESTs	5.4	4.9
	429290	AF203032	Hs.195760	neurofilament, heavy polypeptide (200kD)	5.3	13.1
	408556	U48616	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3	6.6
	431390	AB035361	Hs.272211	cadherin 7, type 2	5.2	6.0
	438265	AA782845	Hs.227590	ESTs	5.2	7.3
60	439501	N73885	Hs.126169	ESTs	5.2	2.7
	445222	AW253894	Hs.197621	ESTs	5.2	8.1
	408616	AW138627	Hs.255098	ESTs	5.1	2.5
	430523	AW950704	Hs.22648	Homo sapiens cDNA FLJ13097 fs, clone NT	5.1	9.0
	436773	AW078629	Hs.82110	PC4 and SFRS1 interacting protein 1	5.1	7.3
65	409263	AA095753	Hs.50319	ESTs	5.1	12.9
	452630	AA534296	Hs.20953	ESTs	5.1	3.4
	441535	AL135736	Hs.7885	phosphotyrosyl-binding clathrin as	5.0	4.8
	416460	AF090116	Hs.79348	regulator of G-protein signaling 7	5.0	20.1
	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fs, clone NT	5.0	3.9
70	446955	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0	6.1
	442440	A1791863	Hs.292179	ESTs	4.9	6.7
	427972	AA064870	Hs.181304	retinoid gene product	4.9	9.0
	416040	AW819158	Hs.289344	Homo sapiens cDNA FLJ12048 fs, clone HE	4.9	2.8
	444922	A1921750	Hs.144871	Homo sapiens cDNA FLJ13752 fs, clone PL	4.8	3.7
	408936	AL138043	Hs.293549	ESTs	4.8	6.6
75	414943	D06547	Hs.124193	ESTs	4.8	3.1
	429254	H10133	Hs.91846	hypothetical protein DKFZp761C121	4.8	2.3
	407906	AA369655	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564C1262 (f	4.8	9.1
	416577	BE063207	Hs.79381	granulysin	4.7	2.2
	420460	AL137361	Hs.58173	hypothetical protein	4.7	2.8
80	404763				4.6	2.2
	430895	U66581	Hs.248121	G-protein-coupled receptor 22	4.6	7.4
	438571	AW020775	Hs.56022	ESTs	4.6	5.4
	444585	AW170015	Hs.6594	ESTs	4.6	6.0

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414272	A1851603	Hs.46988	ESTs	4.5	2.2
414699	A1815523	Hs.76930	synuclein, alpha (non A4 component of am	4.5	30.9
423449	AA497900	Hs.33067	ESTs	4.5	20.8
435251	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4	2.0
429876	AB028677	Hs.225874	KIAA1054 protein	4.4	19.2
429726	AW628326	Hs.27151	ESTs	4.4	10.2
449393	AB035356	Hs.22998	neuroxin 1	4.4	9.4
415716	N59254	Hs.179662	nucleosome assembly protein 1-like 1	4.4	15.1
419556	AB022514	Hs.92025	KIAA0376 gene product	4.4	8.2
425864	US6420	Hs.155903	olfactory receptor, family 5, subfamily	4.4	2.4
435078	AW510888	Hs.40537	ESTs	4.4	5.7
437212	AB016247	Hs.288031	sterol C5-desaturase (lungal ERG3, delta	4.3	5.9
428867	AA460567	Hs.27568	ESTs	4.3	6.0
412112	BE180342	gp.RC3-110622:130400-812-507	HT0622 Homo	4.3	5.2
410171	H07892	Hs.12431	ESTs	4.3	5.3
442339	BE296668	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2	5.0
421249	AA285362	gp.H11277	HTCDL1 Homo sapiens cDNA 53'	4.2	3.5
422528	AB011182	Hs.118087	KIAA0510 protein	4.1	4.7
434460	AA478486	Hs.3852	KIAA0368 protein	4.1	8.3
410362	H04811	Hs.53164	proprotein convertase subtilisin/texin 1	4.1	7.0
449754	H070820	Hs.50877	ESTs, Weakly similar to B34087 hypophth	4.1	3.9
408496	AK638002	Hs.136182	ESTs	4.1	4.7
434101	AA625205	Hs.255599	KIAA1622 protein	4.1	6.3
430212	AA469153	Hs.32042	glnb65704 s1 NC0_CGAP_P1 Homo sapiens	4.0	2.5
453165	374727	Hs.32042	aspartylase (aminocyclase 2, Caraway	4.0	7.4
454407	A1958614	gp.EST380650	MAGEC2, MAGEC2, MAGEC2	4.0	5.1
441963	NM_003947	Hs.8004	hurdlein-associated protein interaction	4.0	32.3
429628	H09604	Hs.13268	ESTs	4.0	4.5
410087	F12079	Hs.332578	ESTs	4.0	6.8
419910	AA562913	Hs.130173	ESTs, Weakly similar to A48010 K-linked	4.0	2.6
441005	ZA1305	Hs.30317	Homo sapiens mRNA, cDNA DKFZp451G133 (fr	3.9	21.7
412677	AV029608	Hs.17384	ESTs	3.9	2.2
453341	A1758912	Hs.296341	adenylyl cyclase-associated protein 2	3.9	7.2
416854	H04164	Hs.80296	Purkinje cell protein 4	3.9	2.2
414686	NM_004466	Hs.76528	phycyanin 5	3.8	6.2
418217	A910547	Hs.13442	ESTs	3.8	3.2
421855	F06504	Hs.27384	ESTs, Moderately similar to ALUM_HUMAN A	3.8	2.2
414764	AW013887	Hs.72047	ESTs	3.8	10.7
453629	R13140	Hs.13359	ESTs	3.7	2.7
424738	AB93740	Hs.46826	ESTs	3.7	3.7
407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7	5.3
437268	A1754847	Hs.227571	regulator of G-protein signalling 4	3.7	50.7
423135	N07655	Hs.26411	ESTs	3.7	21.7
448618	A140568	Hs.277765	ESTs	3.7	2.6
427562	RS5424	Hs.26534	ESTs	3.6	3.6
439274	AF086392	Hs.48372	ESTs	3.6	34.5
452381	H23329	Hs.239880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6	6.0
422897	AA477374	Hs.42280	ESTs	3.6	5.1
429656	XG5608	Hs.211584	neurofilament, light polypeptide (58kD)	3.6	24.6
417154	A1674701	Hs.21388	ESTs	3.6	5.8
417176	Z42549	Hs.160893	ESTs	3.6	6.4
405977				3.6	3.9
423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6	2.5
441235	AB84586	Hs.135670	Homo sapiens cDNA FLJ21269 fs, clone C	3.6	5.4
426775	AA384564	Hs.108829	ESTs	3.6	3.4
414831	N31158	Hs.77439	protein kinase, cAMP-dependent, regula	3.6	2.8
425153	AV022193	Hs.27046	ESTs	3.6	4.9
446496	D60923	Hs.153460	ESTs	3.5	9.8
445898	AF070823	Hs.13423	Homo sapiens clone 24468 mRNA sequence	3.5	16.6
416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.5	5.0
418207	C14685	Hs.34712	ESTs	3.5	16.0
425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5	6.5
417027	AA192306	Hs.23926	triatin	3.5	2.5
408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5	5.3
408776	AA607365	Hs.63256	ESTs, Weakly similar to 138022 hypophth	3.5	5.5
453220	AB033389	Hs.32462	Homo sapiens mRNA for KIAA11253 protein,	3.4	4.4
419347	C15944	Hs.90005	superior cervical ganglia, neural specifi	3.5	42.3
433803	AB23593	Hs.27688	ESTs	3.4	3.6
450715	AC064484	Hs.31370	ESTs, Weakly similar to KIAA1324 protein	3.4	4.1
415076	NM_008857	Hs.77890	guanylate cyclase 1, soluble, beta-3	3.4	8.8
423826	U03025	Hs.1707	cocaine- and amphetamine-regulated trans	3.4	4.7
427173	BE255017	Hs.97540	ESTs	3.4	2.4
446092	N33622	Hs.145894	ESTs	3.4	3.5
416888	AB558866	Hs.292597	ESTs	3.4	4.5
458234	BE351408	Hs.121155	ESTs	3.4	4.4
434053	AW445136	Hs.134946	ESTs	3.4	3.9
428536	A1143139	Hs.2268	visinin-like 1	3.3	42.3
410366	AD27589	Hs.30269	hypothetical protein	3.3	14.4
425785	T27017	Hs.155528	Homo sapiens clone 24400 mRNA sequence	3.3	4.6
434998	AW975157	Hs.26037	ESTs	3.3	4.7
456359	A1967991	Hs.93574	homeo box D3	3.3	4.4
426527	NM_001037	Hs.170238	sodium channel, voltage-gated, type 1, b	3.3	5.2
400302	NA8006	Hs.1915	krate hydratase (prostate-specific memb	3.3	9.0

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	419558	AW963679		Hs 18057	gb:EST365749 MAGE resequences, MAGC Homo	2.7	3.1
	446318	A949309	Hs 12805	ESTs		2.7	4.1
	445183	AB007877	Hs 12385	KIAA0417 gene product		2.7	5.3
5	457012	R41480	Hs 127630	ESTs		2.7	19.0
	431908	AC020302	Hs 17702	protein kinase C, beta 1		2.7	7.2
	432223	NM_002514	Hs 235535	nephroblastoma overexpressed gene		2.7	2.8
	447832	AAB37474	Hs 20021	vesicle-associated membrane protein 1 (s		2.7	3.8
	450214	BE459763	Hs 227571	regulator of G-protein signalling 4		2.7	6.9
	434731	AA548049	Hs 121518	ESTs		2.7	5.0
10	430793	AU777556	Hs 82202	Homo sapiens cDNA FLJ141814 fs, clone NT		2.7	5.2
	407709	AA456135	Hs 23023	ESTs		2.7	2.5
	422420	U03398	Hs 1524	tumor necrosis factor (ligand) superfamily		2.7	3.3
	434305	AI065883	Hs 133318	ESTs		2.7	5.9
	435648	H24347	Hs 27524	ESTs		2.7	15.0
15	418407	AL044818	Hs 84528	nuclear transcription factor Y, beta		2.7	2.7
	436771	AW975687	Hs 282579	ESTs		2.7	6.0
	428689	NM_014351	Hs 159810	sulfonamide family 4A, member 1		2.7	4.8
	442503	NM_006539	Hs 17235	calcium channel, voltage-dependent, gamma		2.7	4.4
20	441056	AW605267	Hs 7627	CGI-60 protein		2.7	3.1
	410330	AW023630	Hs 46786	ESTs		2.6	29.5
	434398	AA121098	Hs 3638	serum-inducible kinase		2.6	2.6
	438831	BE632273	Hs 8439	synapsin II		2.6	7.8
	415566	Z94492	Hs 8875	PRO1073 protein		2.6	3.4
	412643	AW571239	Hs 251982	ESTs		2.6	2.2
25	430456	AA314998	Hs 241503	hypothetical protein		2.6	17.9
	416498	U33632	Hs 79351	potassium channel, subfamily K, member 1		2.6	2.9
	401421					2.6	2.0
	419530	X98330	Hs 90821	ryanodine receptor 2 (cardiac)		2.6	4.2
30	441817	AW969706	Hs 283332	ESTs		2.6	3.8
	439203	AA448930	Hs 8453	KIAA1587 protein		2.6	4.2
	426504	U12431	Hs 168109	FLAV (conlytic) lethal, abnormal vision,		2.6	5.1
	444583	AW684403	Hs 100861	hypothetical protein FLJ141600		2.6	3.7
	417919	A1828203	Hs 86379	ESTs		2.6	3.0
	434293	NM_004445	Hs 3796	EphB6		2.6	3.2
35	431716	D89053	Hs 268912	fatty acid-Coenzyme A ligase, long-chain		2.6	6.4
	443337	AW505305	Hs 259166	synaptin 7		2.6	2.2
	440736	D95919	Hs 265848	myomegalin		2.6	7.1
	404648					2.6	3.0
	429955	AA463571		gb:z7269.01 Soares_totat_fetus_Nb2HF8_		2.6	3.5
40	438520	AW604391	Hs 121121	ESTs, Weakly similar to 500755 pleckstr		2.6	3.9
	441190	H09073	Hs 25046	ESTs		2.6	3.1
	432278	AL137506	Hs 274256	hypothetical protein FLJ23563		2.6	2.9
	447431	AB68167	Hs 131044	ESTs		2.6	4.1
	416836	D54745	Hs 80247	cholecystokinin		2.6	14.9
45	440371	NM_005872	Hs 22960	breast carcinoma amplified sequence 2		2.6	2.4
	436321	AA709133	Hs 180144	ESTs		2.5	2.8
	439693	AU741816	Hs 125897	ESTs		2.5	3.6
	443212	AW269515	Hs 102500	hypothetical protein FLJ20481		2.5	2.8
	422861	AL121104	Hs 130564	Homo sapiens mRNA, cDNA DKFZp434A1627 (l		2.5	3.8
50	407868	NM_000950	Hs 40537	proline-rich Gla (G-carboxyglutamic acid		2.5	3.1
	443992	AW022228	Hs 322922	ESTs		2.5	27.9
	444124	RM3097	Hs 6818	ESTs		2.5	5.3
	411379	AU163444	Hs 12554	ESTs, Weakly similar to NPFL4_HUMAN NUCLE		2.5	38.0
55	443474	AU207936	Hs 7195	gamma-aminobutyric acid (GABA) A recepto		2.5	3.8
	446277	AU284218	Hs 159204	ESTs		2.5	2.2
	410111	AU60206	Hs 189647	ESTs		2.5	3.5
	445182	AB011131	Hs 12376	piccolo (presynaptic cytoskeletal protein)		2.5	4.8
	410718	A1520783	Hs 191435	ESTs		2.5	4.5
60	417261	T60432	Hs 269034	ESTs, Moderately similar to AF097994 1 L		2.5	2.9
	420274	AW988000	Hs 143389	ESTs, Weakly similar to T14318 ubiquitin		2.5	2.8
	432496	AF064264	Hs 49765	VLCS-H1 protein		2.5	4.7
	437331	AL353533	Hs 21710	hypothetical protein DKFZp761G0313		2.5	4.7
	437368	AA71969	Hs 182606	ESTs		2.5	3.0
	441985	BE047625	Hs 169815	ESTs		2.5	3.6
65	410025	BE220489	Hs 113592	ESTs, Moderately similar to I54374 gene		2.5	9.2
	414880	AA143331	Hs 272572	hemoglobin, alpha 2		2.5	3.6
	429866	A1374851	Hs 22542	ESTs		2.5	23.9
	429028	AA443439	Hs 48797	ESTs		2.5	2.8
	438109	AU016621	Hs 71367	ESTs, Moderately similar to ALU7_HUMAN A		2.5	3.1
70	438780	AL109688	Hs 112237	gb:Homo sapiens mRNA full length insert		2.5	2.3
	440888	H45600	Hs 326880	ESTs		2.5	3.9
	445246	AU217113	Hs 147586	ESTs		2.5	2.6
	440152	AB002376	Hs 7006	KIAA0378 protein		2.4	23.6
	432740	AF061634	Hs 278898	tumor necrosis factor alpha-inducible ce		2.4	2.1
75	415722	D60706	Hs 22245	ESTs		2.4	3.9
	432298	AL115812	Hs 274293	Homo sapiens mRNA, cDNA DKFZp761G1111 (f		2.4	9.8
	437948	AA772920	Hs 303527	ESTs		2.4	9.8
	421360	AA297012	Hs 103839	erythrocyte membrane protein band 4.1-H		2.4	2.8
	427115	AW987263	Hs 112237	ESTs		2.4	2.2
80	432074	BE294935	Hs 27147	G-protein-coupled receptor 37 (endotheli		2.4	10.0
	436639	AL148138	Hs 1111	thrombin growth factor 9 (glia-activat		2.4	3.5
	434520	AA205273	Hs 177011	hypothetical protein		2.4	3.1
	411529	AA430348	Hs 317596	Homo sapiens cDNA FLJ12927 fs, clone NT		2.4	3.0

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5	442272	AA588302	Hs.129172	ESTs	2.4	2.1
	429297	AW247388	Hs.301423	calcium binding protein 1 (calbain)	2.4	2.7
	444647	H14718	Hs.11506	Human clone Z389 mRNA sequence	2.4	2.8
	415827	H17462	Hs.23079	ESTs	2.4	15.0
	451397	AA017432	Hs.84329	ESTs. Weakly similar to Z302_HUMAN ZINC	2.4	3.9
10	445200	AA064460	Hs.12409	somatostatin	2.4	3.7
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKF3566AC1416 (l	2.4	2.4
	420328	Y19062	Hs.96870	staufen (Drosophila, RNA-binding protein	2.4	4.3
	432122	AA526514	Hs.118121	glcnv0902.s1 NCL_CGAP_Ov2 Homo sapiens	2.4	4.3
	444125	A1124852	Hs.118121	ESTs	2.4	3.5
15	430538	AB032435	Hs.242821	differentiation-associated Na-dependent	2.4	10.8
	467519	X89438	Hs.3052	early growth response 4	2.4	2.4
	400371	R51736	Hs.12381	ESTs	2.4	2.1
	452303	AA224872	Hs.115088	ESTs	2.4	3.2
	440105	AA694010	Hs.6932	Homo sapiens clone Z389 mRNA sequence	2.4	23.4
20	400979				2.4	4.1
	432296	R49685	Hs.24980	ESTs	2.4	6.5
	408950	AA707814	Hs.14945	long lathy acyl-CoA synthetase 2 gene	2.4	16.5
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	2.4	2.2
	432098	AF252297	Hs.91546	cytochrome P450 related metabolizing pr	2.4	2.7
25	408974	AW015456	Hs.297017	ESTs	2.4	2.5
	412177	Z23591	Hs.73734	glycosylprotein V (retinoid)	2.4	2.6
	415153	H94205		gbc027a08.1 Soares fetal liver spleen	2.4	2.5
	417583	AA668782	Hs.191264	ESTs. Weakly similar to ALU1_HUMAN ALU S	2.4	2.6
	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	3.0
30	424940	AA050308	Hs.194327	ESTs	2.3	6.3
	431709	AB116086	Hs.260241	acetylcholinesterase-associated protein 2	2.3	4.1
	419125	AA542452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger) pro	2.3	2.9
	423641	AL137256	Hs.130469	ATPase, aminophospholipid transporter-II	2.3	8.7
	436407	T88803	Hs.271507	ESTs. Weakly similar to TIM_HUMAN PROBAB	2.3	3.2
35	446861	AL109761	Hs.21754	Homo sapiens mRNA full length insert cDN	2.3	5.2
	415669	NM_095025	Hs.78569	serine (or cysteine) proteinase inhibito	2.3	5.4
	410765	AB64972	Hs.66180	nucleosome assembly protein 1-like 2	2.3	9.1
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfat	2.3	5.0
	442668	AA158651		gbc25905.1 Soares_pregnant uterus_nBH	2.3	2.4
40	445566	AF510241	Hs.12887	actin-related protein 3 beta	2.3	6.5
	444562	U07616	Hs.173034	amphiphysin (Sjögren-Mann syndrome with b	2.3	26.3
	444562	AA186715	Hs.335429	RKEN cDNA 9130422N15 gene	2.3	2.5
	423420	A517384	Hs.128382	Homo sapiens mRNA; cDNA DKF37611224 (l	2.3	7.8
	428450	RS1613	Hs.128304	ESTs	2.3	26.3
45	427127	AW802262	Hs.22265	pyruvate dehydrogenase phosphatase	2.3	2.2
	447179	AW015633	Hs.157299	ESTs	2.3	3.8
	414711	A310440	Hs.288735	Homo sapiens cDNA FLJ13522 ls, clone PL	2.3	2.3
	433449	AW772262	Hs.157299	gbcv07105.s1 NCL_CGAP_Kcd11 Homo sapien	2.3	3.8
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	2.5
50	416778	M16505	Hs.75876	steroid sulfatase (microsomal), arylsulf	2.3	7.6
	425130	AA446208	Hs.99163	ESTs	2.3	4.1
	456644	AW963354	Hs.334029	metallothionein 1G	2.3	2.5
	432623	AA68031	Hs.37282	ESTs	2.3	4.2
	417455	AW007066	Hs.18949	ESTs. Weakly similar to CA26_HUMAN COLLA	2.3	3.0
55	412100	AW692731		gb CMO-NN0005-100300-279-c02 NN0005 Homo	2.3	3.7
	446881	AF668719	Hs.195387	ESTs	2.3	3.2
	416101	RA4854	Hs.268086	ESTs	2.3	6.5
	439731	AB951335	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
	415734	NM_014747	Hs.78748	KIAA0227 gene product	2.3	40.1
60	424596	AB020639	Hs.151017	estrogen-related receptor gamma	2.3	2.6
	420230	AL034344	Hs.264188	breastfold box C1	2.3	2.4
	451559	AL119980	Hs.26535	hypothetical protein DKF37610221	2.3	5.7
	404835				2.3	2.1
	456765	AA597900	Hs.33067	ESTs	2.3	4.1
65	455517	AW984068		gb RCD-NN0006-169300-011-e05 NN0006 Homo	2.3	2.4
	405006	AF541853	Hs.43670	kinesin family member 3A	2.2	16.8
	411770	NM_014278	Hs.71992	heat shock protein (pop110 family)	2.2	3.9
	430105	X70297	Hs.2540	cholinergic receptor, nicotinic, alpha p	2.2	2.6
	456694	F12632	Hs.13298	ESTs	2.2	4.9
70	415081	AL044872	Hs.778192	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2	4.4
	439642	W81441	Hs.153967	ESTs	2.2	2.4
	450138	AW152104	Hs.200679	ESTs	2.2	4.9
	454222	BE144344	Hs.7589	ESTs. Weakly similar to A46010 X-linked	2.2	3.7
	405326				2.2	2.7
75	431342	AW971018	Hs.21659	ESTs	2.2	5.2
	453101	AW962776	Hs.94943	ESTs	2.2	3.3
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	2.2	2.8
	451398	AF793124	Hs.144479	ESTs	2.2	4.6
	433026	AL041224	Hs.65379	ESTs	2.2	10.4
80	406449	NM_004408	Hs.166161	dynamitin 1	2.2	6.1
	414130	AB670831	Hs.71592	Homo sapiens cDNA: FLJ21893 ls, clone H	2.2	3.1
	445016	U79716	Hs.127248	retin	2.2	3.9
	424375	AF070547	Hs.146312	Homo sapiens clone 24820 mRNA sequence	2.2	2.3
	424645	NM_014682	Hs.151449	KIAA0535 gene product	2.2	11.7
	409729	DS1315	Hs.106289	ESTs	2.2	4.9
	432809	AA565509	Hs.131703	ESTs	2.2	19.9
	422690	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.2	10.4

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	428532	AF157326	Hs.184786	TBP-interacting protein	2.2	6.5
	413074	A1871368	Hs.8417	hypothetical protein DKFZp761M0423	2.2	3.4
	414442	AA156238	Hs.32501	ESTs	2.2	3.2
5	452766	AW069459	Hs.61539	ESTs	2.2	2.0
	450440	AB024334	Hs.25901	lysine 3-monoxygenase/tyrosophan 5-mu	2.2	3.2
	426281	AK000987	Hs.169111	oxidation resistance 1	2.2	2.3
	428411	AW291464	Hs.10338	ESTs	2.2	2.3
	413787	A352558	Hs.75544	lysine 3-monoxygenase/tyrosophan 5-mu	2.2	3.1
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	2.2	8.5
10	435105	AW163034	Hs.5467	synaptotagmin 3	2.2	7.9
	405385				2.2	2.4
	447285	A1371849	Hs.200696	ATPase, Class VI, type 11C	2.2	2.2
	452667	T87219	Hs.13219	ESTs	2.2	3.1
	422234	AF119818	Hs.113287	fosc, large (Drosophila) homolog associ	2.2	3.2
15	410339	A1916499	Hs.298258	ESTs	2.1	3.2
	413231	D87461	Hs.75244	BCL2-like 2	2.1	4.5
	447104	R19305	Hs.210705	Homo sapiens cDNA FLJ13162 fs, clone NT	2.1	2.2
	451952	AL120173	Hs.301953	ESTs	2.1	36.5
	415841	Z45637	Hs.7093	ESTs	2.1	2.4
20	4141066	A1926489	Hs.213490	ESTs, Weakly similar to N33_HUMAN N33 PR	2.1	2.2
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.1	6.6
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.1	5.3
	440712	R56245	Hs.8100	ESTs	2.1	4.5
	409660	AW452065	Hs.258905	ESTs	2.1	2.1
25	430434	AL049548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	2.1	5.4
	434138	AA625104		gbr2u8907.11 Soares_testis_NHT Homo sap	2.1	3.0
	448510	NM_006157	Hs.21602	mel (epicrion) like 1	2.1	4.8
	418948	A1217057		gbrp43h07.x1 Soares_testis_hearHH19W	2.1	2.9
	414876	AW950925	Hs.924	crystallin, mu	2.1	3.4
30	440426	A115980	Hs.7181	Homo sapiens cDNA FLJ13663 fs, clone PL	2.1	3.7
	411249	AA016227	Hs.27260	ESTs	2.1	4.1
	451475	119093	Hs.26450	KIAA0725 protein	2.1	2.1
	448743	AB032362	Hs.21896	KIAA1136 protein	2.1	29.7
35	430814	U85336	Hs.247953	NG5 protein	2.1	2.7
	426990	AL044315	Hs.172054	Homo sapiens mRNA for KIAA1750 protein,	2.1	2.3
	426642	AW059223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.1	4.5
	427335	AA448542	Hs.251677	G anilin 7B	2.1	2.2
	450809	F13036	Hs.27373	Homo sapiens mRNA: cDNA DKFZ56401763 (f	2.1	2.3
40	453832	AA425868	Hs.41641	Bruno (Drosophila)-like 4, RNA binding	2.1	5.9
	445383	TG5116	Hs.525111	ESTs	2.1	2.9
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	2.1	2.1
	453976	BE463630	Hs.163714	ESTs	2.1	4.2
	451111	R39036	Hs.328455	EST	2.1	3.3
	452236	F01611	Hs.107631	ESTs	2.1	4.9
45	445279	RA1901	Hs.22245	ESTs	2.1	9.6
	448799	A1937094	Hs.179080	ESTs	2.1	3.1
	418338	NM_002522	Hs.84154	neuronal pentraxin 1	2.1	8.3
	445725	AK000596	Hs.13209	hypothetical protein FLJ10094	2.1	5.4
50	443537	D13305	Hs.203	cholecystikinin B receptor	2.1	4.1
	454066	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	2.1	6.4
	429954	A1918130	Hs.21374	ESTs	2.1	7.2
	415292	H29016	Hs.200576	ESTs	2.1	3.9
	423563	R24734	Hs.75209	protein kinase (cAMP-dependent, cataly	2.1	3.1
55	424906	A1565386	Hs.153716	Homo sapiens mRNA for Hmnb33 protein, 3	2.1	4.7
	458309	AA040620	Hs.5672	hypothetical protein AF140225	2.1	2.2
	435340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	2.1	4.7
	402596	BE314624	Hs.31128	polymerase (RNA) II (DNA directed) polp	2.1	5.4
	454046	F26619	Hs.4814	calcium/calmodulin-dependent protein kin	2.1	6.6
60	448792	RA1250	Hs.12826	ESTs	2.1	4.1
	448500	AW956345	Hs.12926	ESTs	2.1	2.4
	441134	W20592	Hs.7678	cellular retinoic acid-binding protein 1	2.1	5.8
	433361	AW465373	Hs.300141	ubonin protein L35	2.1	2.2
	452946	X95425	Hs.31092	EphA5	2.1	5.0
	426167	AF039023	Hs.167496	RYAN binding protein 6	2.0	2.2
65	453666	AW015681	Hs.135229	ESTs, Weakly similar to A29F_HUMAN ATAX	2.0	3.1
	424632	AB014522	Hs.151406	KIAA0623 gene product	2.0	2.8
	448589	AF017090	Hs.21554	KIAA1107 protein	2.0	4.1
	430416	AC005531	Hs.57806	Homo sapiens PAC clone RP4-701016 from 7	2.0	2.3
	445627	AW18475	Hs.7363	ESTs	2.0	2.1
	417092	H97508	Hs.181165	eukaryotic translation elongation factor	2.0	2.5
70	433623	AW056554	Hs.144559	ESTs	2.0	4.7
	435850	AF206847	Hs.283514	mitochondrial ceramidase	2.0	3.7
	435086	AW975243	Hs.122596	ESTs	2.0	2.1
	423181	D61506	Hs.8417	hypothetical protein DKFZp761M0423	2.0	2.1
75	411562	AL950201	Hs.70768	hypothetical protein DKFZp586E1923	2.0	2.8
	431645	AF070849	Hs.266483	dyenin light chain-A	2.0	2.5
	428634	A1929645	Hs.225936	synapsin I	2.0	3.6
	439607	BE540565	Hs.155480	ESTs	2.0	17.5
	436033	AW138045	Hs.242256	ESTs	2.0	4.0
80	430317	AB026645	Hs.239169	glutaminase	2.0	2.7
	419631	AW188117	Hs.303154	popery protein 3	2.0	2.6
	432660	AJ288130	Hs.64004	ESTs	2.0	2.3
	454048	H05626	Hs.6921	ESTs	2.0	15.9

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5	426917	AA913814	Hs.172854	DKFZP5660923 protein	2.0	3.1
	423246	AL119114	Hs.77196	spectrin, alpha, non-erythrocytic 1 (alp)	2.0	2.9
	415989	AI257700	Hs.317584	ESTs	2.0	4.8
	420275	AA290308	Hs.190561	ESTs, Highly similar to SORL1_HUMAN SORT1	2.0	5.1
	424983	AI242434	Hs.169911	ESTs	2.0	15.9
	446295	AA955662	Hs.63131	Homo sapiens cDNA FLJ13155 fs, clone NT	2.0	2.7
	450005	AI241555	Hs.60171	ESTs	2.0	3.5

TABLE 11b:

Play:	Unique Eos probe/identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

15	Play	CAT Number	Accession
	408274	104999_1	R17315 Z43964 AA053547
15	412100	1277224_1	AW892731 HB0502 Z45826
	412112	1277883_1	BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901699 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180222 AW901891 BE180345 AW903614 AW903615 HB5799 HB3501 BE180220
20	413153	1350849_1	N94205 BE067565 DE067556
	413510	1374377_1	F13044 T77009 BE145525 BE145493
25	414628	145963_1	AA159551 AA159622 R14472
	415949	180800_1	A1217097 AW386056 W38035 W38792 AA232835 AW9036943
25	419558	185904_1	AW953679 AW953680 AA244436 HB2527 AA361046 AA244483 HB2526
	421249	200649_1	AA285362 AW753386 AW847156 AA285373 AW875575 AW875558
25	421640	204833_1	AW966552 AW966653 AA294989 AA385977
	422955	311735_1	AA463871 A277645 AL118763
30	430212	314437_1	AA469153 AW18503 AA459225
	432122	341756_1	AA526514 AW973343 AA554293
30	433449	365332_1	AW772280 AA362974
	434138	380572_1	AA528504 AW16187 AW9074833 AW575642 AI933368
35	474283	43765_1	AL301074 AW988817
	439780	47673_1	AL109688 P23665 P26578
35	452502	919733_1	A1904296 BE007223 R30687
	455517	1321762_1	AW984058 AW984072 AW984077
35	456407	184986_1	AW986614 AA24209 AA281411

TABLE 11c:

Play:	Unique number corresponding to an Eos probe/identifier
Ref:	Sequence source. The 7 digit numbers in the column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:469-495
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

45	Play	Ref	Strand	NL_position
	400979	807254	Plus	160842-161028
45	401213	9588408	Plus	98243-98380,98489-98619
	401421	745289	Minus	142291-142461
50	403082	8554241	Plus	174720-175016,175104-175406,175508-175813
	404648	9795894	Minus	115334-116220
50	404793	7232206	Minus	61087-61590
	404635	6970743	Plus	85462-85684,88139-88287,90338-91018,94827-94990
55	455326	4379875	Plus	10633-10709,30895-30983,38078-38253,55112-55327,57718-57818,65696-656841
	465385	6552172	Plus	48332-48454
55	405793	1405887	Minus	89197-89463
	405911	6758795	Plus	101008-101643
55	405977	8247789	Minus	135548-136177

TABLE 12a: ABOUT 678 GENES UP-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 12a lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal central nervous system (CNS). These were selected from 5590 probesets on the Affymetrix HG-U133 GeneChip array such that the ratio of "average" LGG to "average" CNS tissues was greater than or equal to 2.5. The "average" LGG level was set to the 85th percentile amongst various LGG tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

65	Play:	Unique Eos probe/identifier number
	Ex/Accession:	Exemplar Accession number, Genbank accession number
65	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
70	R1:	Ratio of LOWER GRADE GLIOBLASTOMA to normal CNS

75	Play	Ex/Accession	UnigeneID	Unigene Title	R1
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	20.3
75	424800	AL035588	Hs.153203	MyoD family inhibitor	19.5
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	18.5
75	402504			Target Exon	16.9
	444190	AW878918	Hs.10526	cysteine and glycine-rich protein 2	15.0
80	409638	AW450420	Hs.21335	ESTs	14.0
	443721	AB082926	Hs.145418	ESTs	14.0
80	456759	BE289150	Hs.127792	delta (Drosophila)-like 3	13.5
	441342	AI199268	Hs.19322	Homo sapiens. Similar to RIKEN cDNA 2010	12.2
80	433001	AF217513	Hs.279905	clone HCC310 PRO0310p1	10.3
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	9.5

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425187	AW014406	Hs.22509	ESTs	9.0
440210	AW674562	Hs.125296	ESTs	8.8
448769	N56037	Hs.38173	ESTs	8.4
437034	AA742453		gb:ny91c01 n1 NC1_OGAP_GCB.1 Homo sapiens	8.2
440539	W80383	Hs.58446	ESTs	8.1
417061	AI575944	Hs.188591	Homo sapiens cDNA FLJ120333 fs, clone HE	8.0
435020	AW505076	Hs.301855	DGeorge syndrome critical region gene B	7.8
414217	AI030958	Hs.279868	Homo sapiens cDNA FLJ23185 fs, clone L	7.7
440300	AI555869	Hs.346514	ESTs	7.6
449509	AW25142	Hs.180187	Homo sapiens cDNA FLJ14337 fs, clone PL	7.5
452372	AI855742	Hs.228474	ESTs	7.2
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi)	7.2
417308	H63720	Hs.81892	HA0101 gene product	7.2
447604	AW296968	Hs.157538	ESTs	7.1
418113	AI272141	Hs.83484	SRV (pex determining region Y)-box 4	7.1
424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fs, clone PL	7.1
406478			Target Exon	7.1
425726	NM_015625	Hs.191381	hypothetical protein	6.9
414761	AI077228	Hs.77265	enhancer of zeste (Drosophila) homolog 2	6.9
428037	N47474	Hs.89230	potassium intermediate/small conductance	6.7
423343	AA324643	Hs.245105	ESTs	6.7
418097	R45137	Hs.21868	ESTs	6.7
431553	X78075	Hs.2799	cartilage linking protein 1	6.6
412326	R07556	Hs.73817	small inducible cytokine A3 (homologous	6.6
425387	JO4088	Hs.156345	topoisomerase (DNA) II alpha (170KD)	6.4
419189	AW851980	Hs.262346	ESTs; Weakly similar to S72482 hypothel	6.4
431117	AF003522	Hs.256500	delta (Drosophila)-like 1	6.4
445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	6.3
402855			NM_001839 Homo sapiens calpain 3, acid	6.2
424009	F11690		gb:HS300041 normalized infant brain cDN	6.2
403419	AF094545		Target	6.2
446588	US3445	Hs.15432	downregulated in ovarian cancer 1	6.0
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	6.0
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	5.9
427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	5.9
416658	U03272	Hs.79432	Rhavin 2 (congenital contractural ara	5.8
405238			Target Exon	5.7
421977	W94197	Hs.110165	ribosomal protein L26 homolog	5.7
405348			C7D01664 gb:12608061 gb:184821849.11 (AB	5.6
428755	R45503	Hs.97459	ESTs; Highly similar to A39769 N-acetyl	5.4
426722	X12784	Hs.119129	collagen, type IV, alpha 1	5.3
403349	NM_001406		ophrin-B3	5.3
453941	U03817	Hs.36820	Bloom syndrome	5.2
425139	F05092	Hs.65087	ESTs	5.2
454880	AW835787		gb:Q4-LT0016-240200-110-b08 LT0016 Homo	5.2
452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.1
418030	BE207573	Hs.83321	neurexin B	5.1
425489	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.1
450539	AF031186	Hs.277174	ESTs	5.1
412811	H06382		ESTs	5.1
442832	AW206550	Hs.253569	ESTs	5.1
436608	AA628980		down syndrome critical region protein DS	5.1
408161	AW952912	Hs.300383	hypothetical protein M023032	5.1
443744	AI084326	Hs.271548	ESTs; Weakly similar to 178885 serpinth	5.1
447497	AW167254	Hs.205722	ESTs	5.0
450811	AI739486	Hs.245497	ESTs	5.0
433244	AB049493	Hs.271285	KIAA1510 protein	4.9
438458	AW975186		gb:EST387294 MAGE resequences; MAGN Homo	4.9
438456	AA913381	Hs.20594	ESTs	4.9
411048	AK001742	Hs.57991	hypothetical protein DkfZp434G0522	4.9
456304	AE020973		gb:nc21002 ys NC1_OGAP_P11 Homo sapiens	4.9
442547	AA306997	Hs.217484	ESTs; Weakly similar to ALU1.1 HUMAN ALU S	4.8
419991	AK000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.8
402274			C19000498* gb:14567179 gb:AA023067.1AC00	4.8
420092	AA814043	Hs.88045	ESTs	4.8
436282	R81913	Hs.272104	ESTs; Moderately similar to ALU1.1 HUMAN A	4.8
438099	AF751150	Hs.252009	ESTs; Moderately similar to 138022 hypoth	4.8
455104	BE064963		gb:RC1-BT0313-110300-015-006 BT0313 Homo	4.8
403961			Target Exon	4.8
424954	NM_005546	Hs.18495	tumor protein p53 (Li-Fraumeni syndrome)	4.8
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	4.7
447891	R41754	Hs.6495	ESTs	4.7
423529	T87318	Hs.120411	ESTs	4.7
422737	M06509	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.7
428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	4.6
437698	R61837	Hs.7990	ESTs; Moderately similar to 184505 calci	4.6
403481			Target Exon	4.6
425075	AW513691	Hs.270149	ESTs; Weakly similar to 2109260A B cell	4.6
422170	AF791949	Hs.112432	anti-Mullerian hormone	4.6
415379	N38657	Hs.263933	ESTs	4.5
406481			Target Exon	4.5
455052	BE311901	Hs.28935	gb:501142514f11 NR1_MGC_14 Homo sapiens c	4.5
423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKF Z6664C142 (tr	4.5

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411642	NM_014932	Hs.71132	neureglin 1	4.5
428282	N34905	Hs.44653	Human sapiens cDNA: FLJ22669 fs, clone H	4.5
432625	A1243506	Hs.34830	ESTs, Moderately similar to T03094 A.kin	4.5
452994	AW562597	Hs.31305	KIAA1547 protein	4.6
469961	AW256334	Hs.133100	ESTs	4.4
401454		NM_0142267	Human sapiens renal tumor anti	4.4
406395			Target Exon	4.4
432281	AK001239	Hs.274263	hypothetical protein FLJ10377	4.4
453732	AL134539	Hs.254129	KIAA1076	4.4
415131	DE1119		gb:HMU15SC11B Context human fetal brain	4.4
437695	AA769202	Hs.192142	ESTs	4.4
422081	AW136820	Hs.196011	ESTs	4.3
437746	AF234882	Hs.5814	suppression of tumorigenicity 7	4.3
433323	AA605132	Hs.159142	ESTs	4.3
420352	BE258835		gb:60111737.4f1 NH_MGC_16 Homo sapiens c	4.3
444218	AF070541	Hs.10684	Human sapiens clone 24421 mRNA sequence	4.3
441036	AI694309	Hs.126458	ESTs	4.3
443636	BE271613	Hs.140553	ESTs	4.3
425292	NM_006824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.3
450106	AA429504		ESTs	4.3
429149	AW193350	Hs.197962	ESTs, Weakly similar to 138022 hypotheti	4.2
422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
451254	AI571016	Hs.172967	ESTs	4.2
409189	AA125984		gb:zn2706.0.1 Stratiogene neuroepithelium	4.2
445118	AI208762	Hs.345572	ESTs	4.2
444326	AI933357	Hs.270710	ESTs	4.2
450360	C14904	Hs.45184	Human sapiens cDNA FLJ12284 fs, clone NA	4.2
404120			CS0005537"gb:32985959gb:ACCA1376.11(AFO	4.2
436899	AA764852	Hs.291567	ESTs	4.1
407624	AW157431	Hs.248941	ESTs	4.1
453361	AA035197	Hs.107375	ESTs	4.1
447439	AA313686	Hs.145020	ESTs, Weakly similar to KIAA1206 protein	4.1
438372	AI140189	Hs.123191	ESTs	4.1
438624	AA889055	Hs.123468	ESTs	4.1
422493	AW474163	Hs.250173	hypothetical protein FLJ13158	4.1
426972	A762023		gb:nc0906.x1 NC1_GCAP_CLL1 Homo sapiens	4.1
425295	AA431366	Hs.37251	ESTs	4.1
425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	4.1
434206	AW136973	Hs.180479	ESTs, Weakly similar to S69990 mitogen i	4.0
420802	AF086877	Hs.59236	regulator of G-protein signalling 20	4.0
402645			Target Exon	4.0
455306	AA225313	Hs.222886	ESTs, Weakly similar to TRIRY_HUMAN TRIC	4.0
413326	W94915	Hs.42419	ESTs	4.0
414348	C15240	Hs.182155	ESTs	4.0
422198	W91833	Hs.1634	cell division cycle 25A	4.0
411537	BE073250		gb:MR0-BT0551-060300-102-c05 BT0551 Homo	4.0
427137	AF035290	Hs.106300	Human sapiens clone 23556 mRNA sequence	3.9
439231	AW581935	Hs.141480	Human sapiens mRNA; cDNA DKFZp434N073 (fr	3.9
429433	AA452029	Hs.213596	ESTs, Weakly similar to KIAA1353 protein	3.9
424186	AI538021	Hs.288706	Human sapiens cDNA FLJ10218 fs, clone HE	3.9
449932	AI675444	Hs.263024	ESTs	3.9
434072	H70954	Hs.283559	Human sapiens PRO1082 mRNA, complete cds	3.9
434784	AA649051	Hs.164007	ESTs	3.9
425146	AW694527		gb:EST356697 MAGE resequences, MAGC Homo	3.9
428538	AA445440	Hs.98463	ESTs	3.9
443318	AI051603	Hs.133141	ESTs	3.9
416857	AA198775	Hs.292453	ESTs	3.9
411688	AW953440		gb:EST356510 MAGE resequences, MAGC Homo	3.9
447343	AA256641	Hs.236894	ESTs, Highly similar to S02292 alpha-2-m	3.9
425005	AB032959	Hs.318584	novel C3HC4 type Zinc finger (zinc finger	3.8
403696			C4001100"gb:5852342gb:AA054015.11(AFO	3.8
415884	HT22966	Hs.13471	ESTs	3.8
432646	AW753310	Hs.157697	gb:RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
447057	AI423407		ESTs	3.8
400814			Target Exon	3.8
441329	AI023675	Hs.46621	hypothetical protein FLJ20086	3.8
416864	HT7790	Hs.20269	ESTs	3.8
426044	AA502490	Hs.170290	ESTs	3.8
455646	BE064420		gb:RC4-B10311-241199-012-c08 BT0311 Homo	3.8
419043	T19167	Hs.89566	ets variant gene 1	3.8
445075	AW51827	Hs.347017	ESTs	3.8
457211	AW072565	Hs.32369	ESTs, Weakly similar to S51797 vasodilat	3.8
420004	AW075532	Hs.164039	ESTs, Moderately similar to 138022 hypot	3.8
428060	AA420616	Hs.249483	ESTs	3.7
416427	BE244030	Hs.78307	Rac/Cdc42 guanine exchange factor (GEF)	3.7
453038	AW024215	Hs.20503	HIV pX associated protein-8	3.7
404584			Target Exon	3.7
447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv	3.7
453438	AA469395	Hs.22792	ESTs	3.7
429643	AA455880	Hs.187279	FYVE-finger-containing Rab5 effector pro	3.7
458072	AB890347	Hs.271923	Human sapiens cDNA: FLJ22785 fs, clone K	3.7
459660	M79082		ESTs	3.7
432188	A352952	Hs.2928	solute carrier family 7 (cationic amino	3.7

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	430744	AA485229	Hs.105649	ESTs	3.7
	454392	8E260893	Hs.236131	homeodomain-interacting protein kinase 2	3.7
	454457	AW753456		gb:QV2-CT0261-1-261059-011-d11 CT0261 Homo	3.7
	435095	AA021160	Hs.4750	hypothetical protein DRF.zp564M082?	3.7
5	434205	AA780385	Hs.187885	ESTs	3.7
	418967	NM_001725	Hs.89535	bacteriocidal/permeability-increasing pro	3.7
	427809	M26380	Hs.180878	lipoprotein lipase	3.7
	427722	AK000123	Hs.180879	hypothetical protein FLJ20116	3.7
	412985	Z43567		gb:HSC1F0221 normalized infant brain cDN	3.7
10	438898	A819863	Hs.106243	ESTs	3.7
	418483	W26076	Hs.221847	ESTs	3.7
	419049	R20529	Hs.6906	ESTs	3.6
	433380	T05430	Hs.6154	chromodulin sulfate proteoglycan DEHABs	3.6
	440296	D30829	Hs.180610	splicing factor proline/glutamine rich (3.6
15	438025	AW051360	Hs.258910	ESTs	3.6
	458970	AW246119	Hs.25300	phosphatidylinositol 4-kinase type II	3.6
	446002	Y15227	Hs.20149	detected in lymphocytic leukemia, 1	3.6
	430558	AW665996	Hs.130729	ESTs, Weakly similar to ALUJ1_HUMAN ALU S	3.6
	409557	BE182896	Hs.211193	ESTs	3.6
20	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	3.6
	425331	AW962128		gb:EST374201 MAGE resequences, MAGE Homo	3.6
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZ596J1922 (I	3.6
	404185			Target Exon	3.6
	427517	AA644142	Hs.7107	ESTs, Weakly similar to ALUJ7_HUMAN ALU S	3.6
25	421094	AW978202	Hs.289054	hypothetical protein FLJ22251	3.6
	440388	A893520	Hs.223000	ESTs	3.6
	419334	NM_000028	Hs.592	phospholipase A2, group IB (pancreas)	3.6
	428292	AW178363		gb:RC3-HT105-01099-002+106 HT105 Homo	3.6
	442432	8E093599	Hs.38178	hypothetical protein FLJ23468	3.6
30	451826	AA020741	Hs.171611	ESTs	3.6
	427375	AL035450	Hs.177538	metallocarboxypeptidase CPX-1	3.6
	419485	AA489023	Hs.59807	ESTs, Weakly similar to unnamed protein	3.6
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	3.6
	418400	BE243026	Hs.301989	KIAA0246 protein	3.6
35	430674	AA725002	Hs.272018	low molecular mass ubiquitin-binding pr	3.5
	407013	U35637		gb:human netulin mRNA, partial cds	3.5
	403108			ENSP0000024115: Hypothetical 67.7 kDa p	3.5
	427564	A1148006	Hs.222120	ESTs	3.5
	450287	AP901347	Hs.36592	Hypothetical protein FLJ23342	3.5
40	436338	W62147	Hs.118394	ESTs	3.5
	447458	A741082	Hs.159861	ESTs	3.5
	457364	AW971037		gb:EST383123 MAGE resequences, MAGE Homo	3.5
	458814	A498587	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.5
	441701	AW339828	Hs.127497	ESTs	3.5
45	405558			Target Exon	3.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	3.5
	434589	AF147363		gb:Homo sapiens full length insert cDNA	3.5
	443282	T47764	Hs.132917	ESTs	3.5
50	405183			NM_016358? Homo sapiens inqouos homeobo	3.5
	410064	X53416	Hs.195454	fibrin A, alpha (actin-binding protein-	3.5
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	3.5
	404272			Target Exon	3.5
	428808	AA436007	Hs.188780	ESTs	3.5
55	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.4
	450475	AW805634	Hs.205015	ESTs	3.4
	454451	AW848706		gb:QV3-CT0192-211099-008-g02 CT0192 Homo	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	440948	AW188311	Hs.128619	ESTs	3.4
60	449611	A1970394	Hs.197075	ESTs	3.4
	445666	R59960	Hs.262386	ESTs	3.4
	445828	R05802	Hs.81907	ESTs	3.4
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	3.4
	442927	A1024347	Hs.121519	ESTs	3.4
	451130	A1762250	Hs.345554	ESTs	3.4
65	454765	AW819629		gb:RCS-ST0293-140200-014-H05 ST0293 Homo	3.4
	459200		Hs.30148	homeodomain-interacting protein kinase 3	3.4
	433791	AA719352	Hs.112718	ESTs	3.4
	444911	U06117	Hs.250	xanthine dehydrogenase	3.4
	439753	8E762223	Hs.7423	hypothetical protein from EUR0MAGE 2168	3.4
70	449833	A0208217	Hs.143879	ESTs	3.4
	447726	AL137638	Hs.19368	metlinin 2	3.4
	403849			Target Exon	3.4
	422418	AK001383	Hs.116385	hypothetical protein FLJ10521	3.3
	439533	W76021		gb:refSeq04.1 Soares_test_Heart_HbNH19W	3.3
75	415422	W64457		ESTs, Moderately similar to ZN61_HUMAN Z	3.3
	441668	A1611973	Hs.136313	ESTs	3.3
	432890	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	3.3
	412135	AW895309	Hs.81256	gb:CVA-MN0038-300300-155-e07 MN0038 Homo	3.3
	417130	AW276859	Hs.12155	S100 calcium-binding protein-A4 (calciu	3.3
80	447854	AW1138454	Hs.11594	ESTs	3.3
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cell	3.3
	404532			NM_022493 Homo sapiens hypothetical prot	3.3
	411965	AW851728		gb:NR2-CT0222-Q11199-007-g05 CT0222 Homo	3.3

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	403212		NM_019595 Homo sapiens intersectin 2 (IT	3.0
	422757	A909935	Hs 65551 Homo sapiens, Similar to DNA segment, Ch	3.0
	427624	AA406245	Hs 24895 ESTs	3.0
5	445626	AA050500	Hs 59847 ESTs	3.0
	411543	AW851248	gb:U3.CT0226-150200-066-F01 CT0220 Homo	3.0
	409112	BE243971	Hs 50549 quinone oxidoreductase homolog	3.0
	414403	AW965511	Hs 76054 ribosomal protein L27a	3.0
	427818	AA02587	Hs 32520 LAT1-3TM protein	3.0
10	455481	AW948317	gb:RC0-MT0015-283000-021-a09 MT0015 Homo	3.0
	444396	TS5213	Hs 4257 ESTs	3.0
	407235	D20569	Hs 165407 SAC2 (suppressor of actin mutations 2, y	3.0
	413431	AL096711	Hs 252953 Human DNA sequence from clone RP3-403A15	3.0
	461391	AA017410	Hs 40558 ESTs	3.0
	433261	AA629246	Hs 181451 ESTs	3.0
15	420658	AW965215	Hs 130707 ESTs	3.0
	442786	H50733	Hs 256261 ESTs, Moderately similar to ALUR_HUMAN A	3.0
	440897	AW104275	Hs 148348 ESTs	3.0
	444605	AW511659	Hs 278081 ESTs	3.0
	433062	AK001757	Hs 281348 hypothetical protein FLJ10895	3.0
20	406523	AW833259	Hs 314287 ESTs	3.0
	434377	R32325	Hs 221754 ESTs	3.0
	423869	BE409301	Hs 134012 C14-related factor	3.0
	405488		ENSP00000220888* ZINC FINGER TRANSCRIPTI	3.0
25	414988	C17535	gb:C17535 Human placenta cDNA (Tfajiwara	3.0
	440471	AA886148	Hs 307944 ESTs	3.0
	416355	H48875	Hs 268096 ESTs	3.0
	408265	AF171725	Hs 49002 Owen syndrome cell adhesion molecule	3.0
	424028	AF555084	Hs 153692 Homo sapiens cDNA FLJ14354 fs, clone Y7	2.9
	438201	AA780243	Hs 54647 ESTs	2.9
30	413851	AW897510	Hs 137387 ESTs	2.9
	422229	BE262054	Hs 282385 mitochondrial ribosomal protein S2	2.9
	441415	BE153823	Hs 282385 ESTs, Weakly similar to 2004399A chromos	2.9
	423770	AW576766	Hs 132776 Homo sapiens cDNA FLJ10077 fs, clone HE	2.9
	439627	BE521702	Hs 29076 hypothetical protein FLJ21841	2.9
35	414232	WB9646	Hs 238246 hypothetical protein FLJ22479	2.9
	405633		ENSP0000020376* PREX5 protein (Fragmen	2.9
	440483	A1200836	Hs 150386 ESTs	2.9
	443502	A1074528	Hs 133949 ESTs	2.9
40	448667	AB023227	Hs 23860 KIAA1010 protein	2.9
	446509	AW091711	Hs 101413 ESTs	2.9
	408788	AL134947	Hs 213956 Homo sapiens BAC clone RP11-10205 from Y	2.9
	413627	BE182082	Hs 246973 ESTs	2.9
	449655	AA021987	Hs 59970 ESTs	2.9
45	407376	AA295254	Hs 57776 ESTs, Moderately similar to 380222 hypot	2.9
	400090		Ecos Control	2.9
	454968	AW643046	gb:U3.CT0214-150300-085+H06 CT0214 Homo	2.9
	423352	AA324808	Hs 193576 ESTs	2.9
	426197	AA004410	Hs 100009 acyl-Coenzyme A oxidase 1, palmitoyl	2.9
50	421002	U04343	Hs 27954 CD86 antigen (CD28 antigen ligand 2, B7-	2.9
	415346	Z43108	gb:HSC136071 normalized infant brain cDN	2.9
	436726	AA324975	Hs 198689 ESTs, Weakly similar to T00079 hypothesi	2.9
	442513	AF150207	Hs 207949 ESTs	2.9
	425012	T77666	Hs 92414 Homo sapiens cDNA: FLJ22030 fs, clone H	2.9
55	402322		Target Exon	2.9
	427235	A126288	Hs 192232 ESTs	2.9
	456412	AW749617	Hs 280776 tektyrase, TRF1-interacting ankyrin-rela	2.9
	431196	AW974436	Hs 154928 ESTs	2.9
	439379	AA635002	Hs 125611 ESTs	2.9
60	423757	AL049337	Hs 132571 Homo sapiens mRNA; cDNA DKFZp564P016 (tr	2.9
	446134	AW161234	Hs 13993 TEPlike 1	2.9
	426645	AB052789	Hs 133263 ESTs	2.9
	440385	AB504711	Hs 347200 ESTs	2.9
	444161	NS2543	Hs 142940 ESTs	2.9
	405635	U07162	gb:Human clone LNA11 anti-antibody Ig hea	2.9
65	419239	AA468183	Hs 184598 Homo sapiens cDNA: FLJ2241 fs, clone C	2.9
	456760	AA498531	Hs 111534 fibrin, light polypeptide	2.9
	427245	AA421022	Hs 97739 ESTs	2.9
	400658		ENSP00000237081* KIAA1217 PROTEIN (FRAGM	2.9
	437071	A0760833	Hs 293971 ESTs	2.9
	435294	T64064	Hs 196008 Homo sapiens cDNA FLJ17223 fs, clone HE	2.9
70	429927	NM_001115	Hs 2522 adenylyl cyclase 8 (brain)	2.9
	446160	AW392197	Hs 218003 ESTs	2.9
	420674	NM_000055	Hs 1322 butyrylcholinesterase	2.9
	426430	AW073953	Hs 333396 Homo sapiens cDNA FLJ13595 fs, clone PL	2.9
75	418915	AA741778	Hs 118877 ESTs	2.9
	429622	AL157466	Hs 162751 Homo sapiens mRNA; cDNA DKFZp761E2423 (f	2.9
	447512	AW958148	Hs 129544 ESTs	2.9
	446990	A4279010	Hs 44821 ESTs	2.8
	423779	AW071837	Hs 57871 ESTs	2.8
80	427595	AW286741	Hs 97861 ESTs, Moderately similar to 380222 hypot	2.8
	416188	BE157260	Hs 79070 v-myc avian myelocytomatous viral oncog	2.8
	426746	JC3626	Hs 2057 uridine monophosphate synthetase (orotid	2.8
	403962	AF368294	Hs 272414 Homo sapiens HDCHMSP mRNA, partial cds	2.8

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	457579	AB020816	Hs.36761	HRA5-like suppressor	2.8
	451059	AW297465	Hs.267150	KIAA1409 protein	2.8
	403903			C500153Z-gj10645308gthAA/G21430.1A/C00	2.8
5	444491	A151081	Hs.270714	ESTs	2.8
	455989	BE155112		gb:PM1.H170350.151299.003-s03.N10350 Homo	2.8
	457282	AG521270	Hs.281462	hypothetical protein FLJ14251	2.8
	426305	AA446628	Hs.2799	cartilage linking protein 1	2.8
	435375	H1733610	Hs.187832	ESTs	2.8
	409078	AW327515	Hs.345269	ESTs	2.8
10	436109	AA022153	Hs.132760	hypothetical protein MGC15729	2.8
	444656	A1277924	Hs.145199	ESTs	2.8
	426384	AA72078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	2.8
	424200	AA337221		gb:EST14944 Endometrial tumor Homo sample	2.8
	438243	A581311		ESTs	2.8
15	434012	AA621425	Hs.186256	ESTs	2.8
	402711			Target Exon	2.8
	424955	AB803534	Hs.131583	ESTs	2.8
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.8
20	438934	BE220137	Hs.124232	ESTs	2.8
	438689	AW129261	Hs.181672	ESTs	2.8
	420083	AA478847	Hs.42484	hypothetical protein FLJ10618	2.8
	400315	U46120	Hs.153352	Human expressed unknown mRNA	2.8
	433693	A172637	Hs.277901	ESTs	2.8
25	458993	A1207788	Hs.343626	sialyltransferase 4b (beta-galactosidase	2.8
	409157	AA064631		gb:z172603.1 Scores_pineal_gland_N3HPG	2.8
	450597	A1701635	Hs.207077	ESTs	2.8
	425300	AW601773	Hs.270259	ESTs	2.8
	458617	Z25900	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F053 (lr	2.8
30	418312	AW972468	Hs.170207	Rat guanine nucleotide exchange factor R	2.8
	430335	D80007	Hs.239499	KIAA0185 protein	2.8
	454551	AW608189		gb:MR4-STO118-261099-612-e10.STO118 Homo	2.8
	419735	AW760456	Hs.169577	Homo sapiens cDNA FLJ14743 fs, clone NT	2.8
35	436265	AA731331	Hs.190668	ESTs	2.8
	439481	AF086294	Hs.128844	ESTs	2.8
	441954	AA972619	Hs.20506	ESTs, Weakly similar to 138022 hypothesis	2.8
	422548	D80893	Hs.118983	Melanoma associated gene	2.8
	430503	AA533574	Hs.152274	ESTs	2.8
	403942			Target Exon	2.8
40	420565	A1806770	Hs.30258	ESTs	2.8
	435095	AB51344	Hs.194178	ESTs, Weakly similar to ALUB_HUMAN !!!	2.8
	438480	AJ271643	Hs.87469	putative acid-sensing ion channel	2.8
	408137	A1694131	Hs.29002	KIAA1706 protein	2.8
	451892	AL137422	Hs.26549	Homo sapiens mRNA; cDNA DKFZp761A1623 (f	2.8
45	419713	AW568536	Hs.52381	nuth (nucleoside diphosphate linked mol	2.8
	457286	VQ8637	Hs.280740	hypothetical protein MGC3040	2.8
	414300	A1004870	Hs.188690	ESTs	2.8
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.8
	437933	A1276132	Hs.146155	ESTs	2.7
	402941			Target Exon	2.7
50	443210	A1692649	Hs.9451	hypothetical protein MGC13168	2.7
	450551	W79000	Hs.44545	ESTs, Weakly similar to B34087 hypothesis	2.7
	426765	AA743603	Hs.172108	nucleoporin 89D	2.7
	418086	AA932807	Hs.130558	ESTs	2.7
55	429483	AA474532	Hs.126708	ESTs	2.7
	430426	AA478807	Hs.121713	ESTs	2.7
	439019	AF085902	Hs.271737	ESTs	2.7
	400924			Target Exon	2.7
	458070	AW503578	Hs.209406	ESTs, Weakly similar to 138500 zinc fing	2.7
60	427799	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	442621	A1004333	Hs.130553	ESTs, Weakly similar to ALU1_HUMAN !!!	2.7
	431643	AL108028		gb: Homo sapiens mRNA full length insert	2.7
	425925	NM_001196	Hs.215699	Homo sapiens cDNA: FLJ23773 fs, clone H	2.7
	443352	A1055821	Hs.293420	ESTs	2.7
65	429972	A1700846	Hs.234518	ribosomal protein L23	2.7
	438875	AA827640	Hs.189059	ESTs	2.7
	422551	AW967284		gb:EST379359 MAGE resequences, MAGJ Homo	2.7
	445139	H17735	Hs.30749	ESTs	2.7
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14096 fs, clone MA	2.7
70	428612	AA770001	Hs.188778	ESTs	2.7
	436947	AB000627	Hs.6788	actinotinin	2.7
	436669	AF085334	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	438335	AF084221	Hs.243168	ESTs	2.7
	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (lr	2.7
75	412074	SA74983	Hs.73139	ADP-ribosyltransferase 1	2.7
	412225	AW902842		gb:GVO.NH1622-170400-193-c02.NH1022 Homo	2.7
	438801	AA825071	Hs.124284	ESTs	2.7
	447892	A1038379	Hs.131865	ESTs	2.7
	432964	AF118395	Hs.279865	trans-glycosyltransferase	2.7
80	403790			NM_001334*Homo sapiens cathepsin O (CTS	2.7
	403335	Y13187	Hs.249058	Homo sapiens dmd gene, intron 11	2.7
	415467	R60891	Hs.260274	ESTs	2.7
	428715	AW293716	Hs.53126	ESTs	2.7
	457750	A1651474	Hs.163944	ESTs	2.7

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42480	AA341442	Hs.205299	ESTs	2.7
444822	BE164351	Hs.252767	hypothetical protein FLJ23109	2.7
432651	AW973744	Hs.253100	ESTs	2.7
439823	AW965287	Hs.124514	ESTs	2.7
457021	AW568534	Hs.171108	Homo sapiens cDNA: FLJ21897 fl, clone H	2.7
440026	AA861299	Hs.160371	ESTs	2.7
466660	AW294936	Hs.156762	ESTs	2.7
435046	AA962772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
431599	AL133573	Hs.272322	Homo sapiens mRNA: cDNA DKFZp344Z235 (l	2.7
458527	AI550256	Hs.224875	ESTs	2.7
445899	AI263736	Hs.145626	ESTs	2.7
404254			ENSP000000082468" cDNA45P21.3 [butyrophilin	2.7
402344			Target Exon	2.7
426601	AA380153		gb:EST33053 Skin tumor 1 Homo sapiens cD	2.7
446420	AW015693	Hs.135614	ESTs	2.7
426914	AA393328	Hs.194303	ESTs	2.7
407903	AI287341	Hs.154029	bHLH factor Hes4	2.7
433909	AA761658		gb:nc24282.s1 MCL_CCAP_CCB1 Homo sapiens	2.7
403431			Target Exon	2.7
403290			CT0001011"gi4758212eflnp_004411.1) d	2.7
435143	R12375	Hs.194600	ESTs	2.7
416589	H64691		ghy168n03 r1 Scars fetal liver spleen	2.7
428650	AI948490	Hs.58765	ESTs	2.7
426128	BE561929	Hs.154718	tumor protein D62-like 2	2.7
443361	AI752628	Hs.133273	ESTs	2.7
404053			Target Exon	2.7
435113	AA665469	Hs.117136	ESTs	2.6
405717			CC000338.gi110092633reflnp_055314.1) pu	2.6
413998	BE065279		gb:RC1-BT0314-030500-016-s05 BT0314 Homo	2.6
444884	AI201194	Hs.148540	ESTs	2.6
415015	T77262	Hs.14463	ESTs	2.6
423234	AA323534	Hs.256162	AD037 protein	2.6
406871	AA938357	Hs.180842	ribosomal protein L13	2.6
428670	AA431642	Hs.134832	ESTs	2.6
403371	AF161546	Hs.44439	hypothetical protein	2.6
413920	BE501686	Hs.75617	collagen, type IV, alpha 2	2.6
408369	R38438	Hs.182575	solute carrier family 15 (solute transport	2.6
419817	AA743434	Hs.193778	ESTs	2.6
415788	AW626966	Hs.78851	KIAA0217 protein	2.6
427388	BE379510	Hs.177952	ribosomal protein, large, P1	2.6
451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	2.6
405863			Target Exon	2.6
454037	AW958716		gb:PM4-BN0067-250300-002-r11 BN0067 Homo	2.6
430147	BE5704	Hs.234434	hairpin/cancer-dt-spl related with YRP	2.6
425480	AB023198	Hs.158135	KIAA03981 protein	2.6
407182	AA312551	Hs.230157	ESTs	2.6
439538	AA837323	Hs.56407	ESTs	2.6
445249	T52285	Hs.153315	Homo sapiens mRNA for KIAA1764 protein,	2.6
425649	AA544953	Hs.138343	ESTs, Weakly similar to 178865 sense	2.6
402936			ENSP00000217246"DJ0803.15 (novel prote	2.6
420670	AW973577		ESTs	2.6
454049	AW938832		gb:PM2-DT0023-050400-003-A63 DT0023 Homo	2.6
413151	HA7969	Hs.141971	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
427484	AA568770	Hs.123158	Homo sapiens cDNA: FLJ12830 fl, clone NT	2.6
400780			NA_007325" Homo sapiens glutamate recept	2.6
429258	AA448765		gb:nc10609.r1 Scars_tetral_fetus_Mb2HF8_	2.6
448970	AW138582		gb:U-H-011-acw-a-06-G-U-1 r1 MCL_CCAP_3a	2.6
402615			CT000344"gi16512550eflnp_036483.1) ol	2.6
417059	BE537357	Hs.306995	hypothetical protein MGCS457	2.6
428359	AA428040	Hs.264165	gb:nc50602.r1 Scars_tetral_fetus_Mb2HF8_	2.6
449164	AI632772	Hs.74085	ESTs	2.6
415284	X54870	Hs.134214	DNA segment on chromosome 12 (unique) 24	2.6
443635	AI080230	Hs.134214	ESTs	2.6
402881			Target Exon	2.6
433258	AI060626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN !!!	2.6
428617	AA437337	Hs.168895	ESTs	2.6
418557	BE140602	Hs.246645	ESTs	2.6
445211	BE045601	Hs.118248	ESTs, Weakly similar to YC18_HUMAN HYPOT	2.6
404423			CB000067"gi110432400emb CAC10290.1) (A	2.6
435953	AI767687	Hs.141412	ESTs	2.6
435937	AA830853	Hs.115769	ESTs	2.6
439220	AW295340	Hs.130417	ESTs, Weakly similar to Z195_HUMAN ZINC	2.6
419597	W73652		gb:z50c01.s1 Scars_tetral_fetus_MbHH19W	2.6
436852	AI814817	Hs.269059	ESTs	2.6
435566	AC241254	Hs.178058	angiotensin I converting enzyme (peptidyl	2.6
443845	AI590084	Hs.143485	ESTs, Weakly similar to AA7161 Mac 2-bin	2.6
414223	AA954566	Hs.238246	hypothetical protein FLJ22475	2.6
443770	AW819524		gb:MR3-ST0216-151199-DT2-a10 ST0216 Homo	2.6
450443	AW009847	Hs.120744	ESTs	2.6
435523	T62849	Hs.110590	membrane-spanning 4-domains, subfamily A	2.6
404042			CT0001573"gi7302779gb:AA57827.1) (AE	2.6
450202	AW959756	Hs.34145	ESTs, Weakly similar to B49647 GTP bindi	2.6
416845	H55279	Hs.253788	gb:pc22H2.s1 Scars fetal liver spleen	2.6

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5	446423	AW139655	Hs.150120	ESTs	2.6
	447587	AW292139	Hs.115789	ESTs	2.6
	437014	AA808757	Hs.222531	ESTs, Weakly similar to S59501 interfero	2.6
	426411	AK000708	Hs.169764	hypothetical protein FLJ20701	2.6
	432668	AA558001	Hs.43296	ESTs	2.6
10	436682	A1590055	Hs.124110	ESTs	2.6
	426894	A1204209	Hs.143911	ESTs	2.6
	402605			Target Exon	2.6
	457554	AA570111	Hs.155873	ESTs, Weakly similar to ALUE_HUMAN III	2.6
	438166	N30158	Hs.122645	ESTs	2.6
15	443021	AA365546	Hs.8504	Ig superfamily protein	2.6
	427005	AA394228	Hs.97494	ESTs	2.6
	437085	AA743335	Hs.202329	ESTs	2.6
	R25283		Hs.258416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	2.6
	431019	NM_005249	Hs.2714	forkhead box G1B	2.5
20	437287	AA748180	Hs.159346	hypothetical protein FLJ21369	2.5
	458552	AW136139	Hs.245566	ESTs	2.5
	432350	AA713661	Hs.121091	ESTs	2.5
	421988	AW450481	Hs.161333	ESTs	2.5
	416704	H77795	Hs.39785	ESTs	2.5
25	447830	R98920	Hs.164314	ESTs	2.5
	413278	BE553085	Hs.833	interferon-stimulated protein, 15 kDa	2.5
	402789	A041403		ribosomal protein L29	2.5
	433583	A817723	Ilg.22678	hypothetical protein FLJ21832	2.5
	433523	N29882		ESTs	2.5
30	452296	T65535	Hs.111539	ESTs	2.5
	428678	AA432894	Hs.48926	ESTs	2.5
	442476	AF069475	gb:AF069475	Homo sapiens astrocytoma fib	2.5
	452785	AL359942	Hs.296434	erythroid differentiation and dendrocyte	2.5
	444422	A1788823	Hs.108264	ESTs	2.5
35	422973	AA278449	Hs.137429	ESTs	2.5
	416505	H66470	Hs.16004	ESTs	2.5
	402595		C1001578" gb:759903gb:AAF28093. II (AF1	2.5	
	447930	R44574	Hs.107510	ESTs	2.5
	455627	AW971556	Hs.291735	ESTs, Weakly similar to T8685 serine/th	2.5
40	458421	A1279978	Hs.22547	ESTs	2.5
	427527	A1809057	Hs.293441	immunoglobulin heavy constant mu	2.5
	436036	AA703679	Hs.106999	ESTs, Weakly similar to SVTS_HUMAN SYNAP	2.5
	453362	H14588	Hs.107375	ESTs	2.5
	423600	AK53359	Hs.310369	ESTs	2.5
45	433325	AW206986	Hs.143905	ESTs	2.5
	415983	A1436798	Hs.117078	Homo sapiens cDNA: FLJ23028 fs, clone L	2.5
	431198	AL047634	Hs.231913	ESTs	2.5
	430350	AA483670	Hs.47860	ESTs	2.5
	455276	BE176479		gb:RC3:HT0585-150300-022-b09 HT0585 Homo	2.5
50	416665	H72574		gb:yu28a10.s1 Soares fetal liver spleen	2.5
	422352	AA766296	Hs.93200	ESTs	2.5
	427613	AW273651	Hs.98025	ESTs	2.5
	453845	AL110003		gb:DKFZp564L0278_r1.564 (synonym: hlx2)	2.5
	450508	R37408	Hs.101654	ESTs	2.5
55	436361	AA825614	Hs.149065	ESTs	2.5
	427709	AH31811	Hs.180403	STRN protein	2.5
	432036	AF224266	Hs.27272	interleukin 20	2.5
	422752	BE247253	Hs.21261	suppressor of potassium transport defect	2.5
	413786	AW613780	Hs.135600	ESTs	2.5
60	439706	AW872527	Hs.579761	ESTs, Weakly similar to DAP1_HUMAN DEATH	2.5
	451533	NM_004857	Hs.26530	serum deprivation response (phosphatidyl	2.5
	414959	D59688	Hs.45184	Homo sapiens cDNA FLJ12284 fs, clone MA	2.5
	449919	A1674685	Hs.200141	ESTs	2.5
	458891	A1659166	Hs.207144	ESTs	2.5
65	427140	AA398487	Hs.97642	ESTs	2.5
	402519	U95281		oxidative 3 alpha hydroxysteroid dehydro	2.5
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.5
	443753	AW367578	Hs.134749	ESTs	2.5
	432888	T86623		gb:y81a08.s1 Soares fetal liver spleen	2.5
70	445965	AB036957	Hs.302294	glycoprotein beta-Gal 3'-sulfotransferase	2.5
	431202	AA495824	Hs.188822	ESTs, Weakly similar to A46010 X-linked	2.5
	445658	AA69362	Hs.172660	ESTs	2.5
	435330	R16769	Hs.173174	Homo sapiens cDNA FLJ14429 fs, clone HE	2.5
	453703	AW630133	Hs.83313	CHD3 protein	2.5
75	459232	AL040357		gb:DKFZp43400713_r1.434 (synonym: Ntss3)	2.5
	471955	AK000160	Hs.121576	Homo sapiens cDNA FLJ20153 fs, clone CO	2.5
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-asso	2.5
	425428	AL110261	Hs.157211	DKFZ55680621 protein	2.5
	437897	AW469275	Hs.257837	ESTs	2.5
80	408574	AA328046	Hs.45405	polymerase (RNA) II (DNA directed) poly	2.5
	418733	AA227714	Hs.179703	KIAA0129 gene product	2.5
	440473	BE562314	Hs.38711	Homo sapiens, clone IMAGE:3677165, mRNA,	2.5
	422106	DH4239	Hs.111732	Fe fragment of IgG binding protein	2.5
	411480	AW648022		gb:U3-C10214-231299-6C5-A09 C10214 Homo	2.5
	436391	AJ227892	Hs.146274	ESTs	2.5
	424947	R77952		ESTs, Weakly similar to alternatively sp	2.5
	450831	R37974	Hs.25255	ESTs	2.5

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447527 A102896 Hs. 42091 ESTs 2.5
 424686 AA345504 gh. EST51529 Gall bladder II Homo sapiens 2.5
 453385 AW296101 Hs. 252806 ESTs 2.5

5 TABLE 12B:

Play: Unique Ecol probe/seq identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

10	Play	CAT Number	Accession
	408292	1050507_1	AW178363 AWB48011 AWB45964 AWB45988 AWB45977 AWB46002
	409157	110363_1	AA04631 AA72200 AA048793
	409189	110681_1	AA125884 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA026764 AA038036 NB48229 NB48294 AA084752 AA076512 AA085119
15	411480	1247089_1	AWB48022 AWB48704 AWB48168 AWB48959 AWB48476 AWB48699 AWB48700 AWB48761
	411537	1248899_1	BE073250 BE073378 BE073379 AWB50523 AWB50529
	411543	1249127_1	AWB51248 AWB51425 AWB520805 AWB51021 AWB50905
	411565	1249756_1	AWB51728 AWB51607 AWB51621 AWB51702 AWB51647 AWB51727 AWB51658 AWB51617 AWB51628
	411671	125369_1	BE049094 AA077065 1865770 AA094546 R02483 C03868 N56170
20	411688	1254076_1	AWB95340 T08189 AWB57085
	412021	1272156_1	AWB85592 AWB55594 AWB85579 AWB85651
	412135	1279148_1	AWB95390 AWB95320 AWB95307 AWB95397 AWB95378 AWB95402 AWB95403 AWB95311 AWB95329 AWB95390 AWB95488 AWB95486 AWB95481 AWB95289
25	412225	1284108_1	AW902042 NT7591
	412811	132943_1	H03582 AW957370 AA320914 R13591 AA121201 D60420 BE763253 BE047862 T41952 AA243991 AA163507 AA635006 A091148 AA598669 R29687 AA813482 AW016432 H06383 R41807 AB364268 AA620526 A1241940 AWB09149 AWB09733 AWB08915 Z38240 AA121202 R11734
	413096	1349115_1	BE262797 BE063576 BE055164 BE065309
	413966	140720_1	Z43587 H24159 AA134240
	414988	1511316_1	C17535 D59244 D58878 D79090
30	415131	1523680_1	D61119 D61508 D61734
	415346	1534581_1	Z43108 F04265 R13085
	416422	1583811_1	H60457 H60709 H73528 H54335 R87154
	416569	1601567_1	H64991 R93444 R93458 R05530
	416665	1607797_1	H72974 W29867
35	416997	1803413_1	W73682 W73636 W96550
	423352	192979_1	BE259835 AWB68316 AA258918 AWB43305 R14744 A1580388 BE071923 R36280
	426702	195442_1	AW973577 AA533621 AA279187
	427551	211767_1	AW967284 AA312192 AA312203
40	428009	224177_1	F11690 AW963770 AA333586 C03830
	428200	225695_1	AA337221 AA336756 AW999196
	428686	24248_1	AA345504 AA345251 AW963243
	429497	265247_1	R77952 AA348808 AW959990 AW959962 A1565552 AW070702 AA793710 R05593
	429546	247244_1	AW954627 AW954629 AA351258 R25935
	429531	250199_1	AW962126 AA355363 AA427363
45	429503	268263_1	AA360163 AA360233 AW963520
	429397	290994_1	AA428040 AW989684 AA836434
	429828	301917_1	AA448765 C04967 C03045 AA658293
	429940	310894_1	W25215 AA661079 AA461391
	430163	31412_2	BE010030 AA670533 A011783 T68095 WE08032 BE064393 BE064394 BE157228 BE183282 A1936370 AA552514 T67280 AA039099
50	430535	319643_1	AW968485 AW968670 AA408922 BE350425
	432044	340773_1	AW972727 AA524829 AW972733
	432646	351909_1	AW753310 AW974000 AA557840 AA558570 AW751539
	432868	355700_1	T68623 A621425 A123232 A458959 AW785737
	433009	357371_1	AA781688 AA573621 R08214 R09670
55	433523	368873_1	H29882 AW665633 AW149901 A1572917 AA598500 AWB6456 A1336390 AWB64390 AWB64320
	433635	347158_1	A806185 AA810063 A893089 A8603075
	434059	36929_1	AF143633 T47219 T47216
	436038	42361_1	AA420860 A1126403 BE340035
	437034	4211713_1	AA742543 AA808575 AW976658
60	437643	43996_1	AL080280 T73124 H02689 AL080281
	438263	453072_1	A051311 AA781882 AA781678
	438458	457837_1	AW975185 AA801607 D25548
	439533	47349_1	W76021 AF088052 W77465
	442476	543547_1	AF069475 AF069477 AF069476
65	443770	579649_1	AW815924 AW815925 A1085174
	444016	58899_1	AA481514 AW647571
	44970	781254_1	AA138592 A638258 A633640 AWB38688 A611082
	450166	82677_1	AA429504 R41904 AA278467 H05648 AA007236
	453685	977734_1	AL110309 AW088119 H22681
70	454037	996267_1	AW996716 AW022148 N65320
	454177	1049351_1	AWB07321 AWB07322 AW177104 AWB07319 AWB07315 AWB07344 AWB07324 AW178116 BE141575 AWB84589 AWB07105 AWB45668 BE140942 AWB07178 AWB07167 AWB07338 AWB07320 AWB07306 AWB45666
	454451	1206502_1	AWB46706 AWB46703 AW752167 AWB46700 AWB46699 AW752176 AWB46694
	454457	1207274_1	AW753456 AW1753036 AWB54868 AWB54862
75	454581	125710_1	AWB09189 AWB092119 AWB113574
	454785	1233905_1	AWB19629 AWB54320
	454860	1237332_1	AWB53567 AWB53537 BE160187
	454968	1247029_1	AWB49046 AWB47956 AWB49039 AWB47957 AWB48679 AWB48698 AWB49034 AWB49033
	455104	1253737_1	BE064862 BE153898 AWB56751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AWB56622 BE155079 BE064651 BE153865 BE064609 BE064691
80	455276	1272541_1	BE176479 BE176578 BE176357 BE176550 AWB86079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362

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455409	1268335_1	AW936832 AW936809 AW936857 AW936861 AW936739 AW936734 AW936774 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW9
455481	1263182_1	AW948317 AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324
455646	1364567_1	BE068420 BE068426 BE068429 BE068414 BE064000 BE064517
455778	1364596_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
455899	1381547_1	BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452
456232	168294_1	AL00357 AA883621 AA203320
456304	176820_1	AB209373 AT470 BE005084 AA225796 AA225060 AA275101
457364	326154_1	AW971037 AA550819 AW952345

TABLE 12C:

Play:	Unique Eos probe set identifier number
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunkham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunkham, et al. (1998) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NI_position:	Indicates nucleotide positions of predicted exons.

20	Play	Ref	Strand	NI_position
	400492	9213749	Minus	123881-124090
	400533	6981826	Minus	277132-277595
	400645	8117693	Minus	58471-58716
	400658	8118459	Minus	73255-73544
	400780	8131663	Minus	118372-118619
25	400814	8569925	Minus	72849-72824,74761-74849
	400924	7107613	Minus	30309-30498
	401272	9797373	Minus	98314-98509
	401454	9186923	Minus	114559-114832
	401702	1871197	Minus	68182-68325
30	402229	9965022	Minus	15739-15951,16166-16779
	402274	2935596	Plus	5604-6257
	402282	7630369	Minus	75078-75203
	402344	8099256	Minus	76812-79040
35	402595	7705171	Plus	37870-37923,39664-39717,71711-71764
	402604	9959420	Plus	20393-20767
	402605	9959420	Plus	47650-47973
	402615	9926801	Plus	131390-132157
	402711	8901247	Minus	114305-115418
	402747	9212492	Minus	7105-7357
40	402855	9662953	Minus	59763-59969
	402936	8864303	Plus	51655-51771
	402981	9944246	Minus	45716-45889
	403108	8808955	Plus	93253-93667
45	403212	7630897	Minus	156037-156210
	403286	8281479	Plus	133763-133893,135813-135958
	403290	8083176	Plus	19288-20076
	403291	7230870	Plus	95177-95435
	403349	8569773	Minus	167815-168374
50	403431	7133839	Plus	56569-60580
	403481	9965004	Plus	33496-93633
	403696	3135242	Minus	143467-143634
	403790	8084957	Minus	87826-87947,89835-90002
	403849	7708855	Plus	95043-95519
55	403903	7710474	Minus	101166-102597
	403942	7711825	Minus	99606-99757
	403961	7996976	Minus	110093-110603
	404053	3548785	Plus	61797-64205
	404120	7242152	Plus	157776-158000
60	404185	4572584	Minus	129171-129327
	404254	9367203	Plus	129350-129873
	404272	9885189	Plus	83207-83365,84358-84496,90519-90720,91371-91447
	404423	7407859	Plus	34439-34618
	404584	9867511	Plus	138651-139153
65	404592	9843965	Minus	39067-39225
	404632	9796668	Plus	45095-45229
	405046	7958629	Minus	4373-4528
	405183	7209340	Plus	12335-12553
	405238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144464,144690-144836,151750-151883,152407-152484
70	405348	2914717	Minus	43310-43662
	405488	7131455	Minus	75771-75883,105295-105358,134754-134875
	405558	1621110	Plus	4502-4644,5983-6083
	405717	9588573	Plus	11275-11973
	405760	6066938	Minus	37424-38045
75	405863	7657810	Plus	49410-49620
	405941	6759796	Plus	2798-3444
	406395	9256242	Minus	20805-20960
	406478	9857507	Plus	68314-68523,68853-68950
80	406481	9864741	Minus	91439-91579

TABLE 13A: 964 GENES UP-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
 Table 13A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal normal adult tissues. These were selected from 9880 probesets on the Affymetrix Eos Hu3 GeneChip array such that the ratio of "average" LGG to "average" normal tissues was greater than or equal to 3.0. The "average" LGG level was set to the 85th

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percentile amongst various LGG tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

	PKay:	Unique Esq probe identifier number			
	ExAccn:	Exonig Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of LOWER GRADE GLOBLASTOMA to NORMAL ADULT TISSUES			
5					
10	PKay	ExAccn	UnigeneID	Unigene Title	R1
	427343	A1860044	Hs.116777	protein kinase C binding protein 2	67.6
	409399	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	58.2
	418375	NM_003081	Hs.84399	synaptonemal-associated protein, 250k	55.8
	431917	D16181	Hs.2868	peripheral myelin protein 2	50.6
15	428321	A1699994	Hs.2868	peripheral myelin protein 2	48.3
	426325	D26114	Hs.169339	myelin-associated oligodendrocyte basic	44.3
	435147	AL133731	Hs.4774	Homo sapiens mRNA, cDNA DKFpZp61C1712 (f	44.2
	456759	BE739150	Hs.127792	delta (Drosophila)-like 3	43.8
	419817	U6966.7	Hs.78667	protein tyrosine phosphatase, receptor	40.1
20	429007	D80642	gb:HUM092E09	Human fetal brain (TF44w)	38.8
	417183	RS2089	Hs.172717	ESTs	36.8
	433038	N46664	Hs.169339	hypothetical protein FLJ12015	34.9
	413472	BE242870	Hs.75379	solute carrier family 1 (glut high aff)	34.4
	425088	AA663372	Hs.165095	hypothetical protein FLJ12015	33.9
25	429276	AF566085	Hs.198612	G protein-coupled receptor 51	33.8
	424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	32.8
	450133	AW969799	Hs.102021	ESTs	32.8
	423849	AL157425	Hs.133315	Homo sapiens mRNA, cDNA DKFpZ61U1324 (f	32.8
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	31.3
30	449494	AW237014	Hs.315399	Homo sapiens cDNA: FLJ23075, clone L	30.3
	426204			Target Ecor	28.8
	412733	AA984472	Hs.74554	KIAA0090 protein	28.2
	416829	AB013805	Hs.80220	catenin (cadherin-associated protein), d	27.9
	439239	A031540	Hs.235331	ESTs	27.1
35	444378	R41339	Hs.47860	neurotrophin tyrosine kinase, receptor,	25.2
	429415	F05538	Hs.4273	ESTs	25.5
	429048	H05468	Hs.164502	ESTs	25.3
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	25.0
40	425057	AA826434	Hs.1019	achate-scute complex (Drosophila) homol	23.5
	426799	T08133	Hs.182936	Homo sapiens mRNA for KIAA1872 protein,	23.5
	447659	NM_012093	Hs.18208	adenylate kinase 5	23.2
	425842	A0587490	Hs.159623	NK-2 (Drosophila) homolog B	23.2
	423853	AB011537	Hs.133466	slt (Drosophila) homolog 1	22.9
45	432708	A302949	Hs.75169	ESTs	21.6
	437268	A754947	Hs.227571	regulator of G-protein signalling 4	21.1
	409395	U46745	Hs.335678	dystrobrevin, alpha	20.4
	441285	NM_002374	Hs.167	microtubule-associated protein 2	20.0
	422656	A1870435	Hs.1569	LIM homeobox protein 2	19.7
50	425523	A007946	Hs.154244	KIAA0478 protein	19.5
	437204	AL110216	Hs.22826	ESTs, Weakly similar to 155214 salivary	19.4
	416370	N90470	Hs.203697	ESTs, Weakly similar to 138022 hypotheti	19.1
	441497	RS1064	Hs.231172	ESTs	18.9
	453392	U23752	Hs.32864	SRY (sex determining region Y) box 11	18.8
55	408024	OE1408	Hs.21925	ESTs	18.6
	413597	AW302885	Hs.117183	ESTs	18.2
	422980	N46569	Hs.76722	CCAAT/enhancer binding protein (CEBP),	18.2
	428392	H10233	Hs.2205	secretory granule, neuroendocrine protei	18.2
	429466	AB6835	Hs.12827	ESTs	17.4
60	448302	AA80208	Hs.182936	Homo sapiens mRNA for KIAA1872 protein,	17.4
	439199	R40373	Hs.25299	ESTs	17.4
	448743	AE032952	Hs.21996	KIAA1136 protein	17.2
	418338	NM_002522	Hs.84151	neuronal pentraxin I	17.1
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	16.8
	444783	AK001468	Hs.62180	anillin (Drosophila Scrapes homolog), act	16.1
65	447004	AW296968	Hs.157539	ESTs	15.7
	425994	AW836277	Hs.156836	hypothetical protein DKFpZp61C07121	15.6
	448672	AA85511	Hs.226106	ESTs	15.8
	453772	A1885742	Hs.228474	ESTs	15.7
	424120	T80579	Hs.290270	ESTs	15.4
70	424581	M62022	Hs.150517	catenin (cadherin-associated protein), d	15.2
	424790	AL119344	Hs.15336	ESTs, Weakly similar to 204339A chromos	15.2
	426769	H11502	Hs.168950	Homo sapiens mRNA, cDNA DKFpZ666A1046 (f	15.2
	446592	Z44514		Homo sapiens mRNA for KIAA1763 protein,	14.9
	453642	A1370936	Hs.34074	dipeptidylpeptidase VI	14.7
75	428237	X18105	Hs.194765	H. sapiens GEMX-5624 mRNA, 3' UTR	14.6
	441440	A1827981	Hs.30495	ESTs	14.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	14.2
	415849	R20529	Hs.6806	ESTs	14.0
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	13.9
80	434277	X77748	Hs.13786	glutamate receptor, metabotropic 3	13.7
	409638	AW450420	Hs.21335	ESTs	
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	
	415734	NM_014747	Hs.78748	KIAA0237 gene product	

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424945	A1221919		hypothetical protein FLJ10582	13.6
426344	H41821	Hs.322469	transcriptional activator of the c-fos p	13.4
446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	13.3
429946	RK9390	Hs.254125	KIAA1678	13.3
444119	RA1231	Hs.184261	ESTs, Weakly similar to T26685 hypothetical	13.3
438390	T06430	Hs.6194	chondroin sulfate proteoglycan BEHAVAB	13.2
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	13.2
412266	N95006	Hs.26133	ESTs	13.2
438078	BE455204	Hs.47448	ESTs	13.1
429538	A1143139	Hs.2288	vonin-like 1	13.1
425649	U30930	Hs.158540	UDP glucosyltransferase 8 (UDP-galactose	13.1
428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.0
437948	AA772920	Hs.303527	ESTs	13.0
444124	RA2097	Hs.6816	ESTs	12.6
428342	A1739168		Homo sapiens cDNA FLJ13456 fis, clone PL	12.7
419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	12.7
412959	D87458	Hs.75090	KIAA0287 protein	12.6
419863	AW952691	Hs.53045	Homo sapiens mRNA; cDNA DKFZp761D191 (f	12.6
431467	N71831	Hs.255398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	12.6
431019	NM_005249	Hs.2714	forkhead box G1B	12.4
420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA he	12.4
430091	AB032858	Hs.232032	KIAA1132 protein	12.4
445955	AB014544	Hs.21572	KIAA2644 gene product	12.2
447342	A1192268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA2010	12.2
420849	AI423132	Hs.146343	ESTs	12.0
421284	AL039123	Hs.103042	microtubule-associated protein 1B	11.9
431982	AL120173	Hs.201603	ESTs	11.9
411305	BE241596	Hs.89547	myelin basic protein	11.8
433551	A1985544	Hs.12450	protocadherin 9	11.6
431998	AC002302	Hs.77202	protein kinase C, beta 1	11.6
415170	RA4385	Hs.164578	ESTs	11.5
408552	AI435323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	11.4
435501	AW051819	Hs.122908	KIAA0591 protein	11.4
479556	X05608	Hs.211594	neurofilament, light polypeptide (8-kD)	11.1
423419	R55335	Hs.23339	ESTs	11.1
424432	AB037821	Hs.146888	protocadherin 10	10.9
433895	AW294729	Hs.274461	ESTs	10.9
415283	R49482	Hs.106541	ESTs	10.9
447101	N72185	Hs.44189	ESTs	10.9
440105	AA954010	Hs.5932	Homo sapiens clone 23809 mRNA sequence	10.9
438054	AA775626	Hs.193309	ESTs	10.8
433597	AA708205	Hs.100343	ESTs	10.7
421659	NM_014459	Hs.106511	protocadherin 17	10.6
445102	AW204610	Hs.22270	ESTs	10.6
428164	NM_001851	Hs.154850	collagen, type IX, alpha 1	10.6
451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 24	10.6
435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	10.6
480154	R13891	Hs.281587	Human (clone CTG-A4) mRNA sequence	10.5
407896	AW965688	Hs.100026	ESTs	10.4
420345	AW285230	Hs.25231	ESTs	10.4
428728	NM_016625	Hs.191381	hypothetical protein	10.3
424987	AL138167	Hs.96920	ESTs	10.3
440184	AB002257	Hs.7022	dedicator of cyto-kinesis 3	10.2
419078	M93119	Hs.85584	insulinoma-associated 1	10.2
445495	BE022841	Hs.38489	ESTs, Weakly similar to 130022 hypothi	10.1
416857	AA188775	Hs.292453	ESTs	10.0
445441	T64163	Hs.257882	adult carrier	10.0
419271	N45901	Hs.236332	ESTs	9.7
446711	AF169692	Hs.12450	protocadherin 9	9.8
426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	9.7
427204	AA701526	Hs.163953	ESTs	9.7
418087	RA5137	Hs.21868	ESTs	9.7
449300	AB656959	Hs.348514	ESTs	9.7
419985	H66373	Hs.5855	ESTs, Highly similar to BA293J16.3 (k.s.a	9.7
443785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	9.5
415486	RI1214	Hs.12384	ESTs, Weakly similar to 2109250A B cell	9.5
453720	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	9.4
439209	AL120659	Hs.6111	arylhydrocarbon receptor nuclear trans	9.4
424028	AF055084	Hs.135992	Homo sapiens cDNA FLJ11434 fis, clone Y7	9.4
419893	AA248897	Hs.48784	ESTs	9.2
414175	A308875	Hs.103849	hypothetical protein DKFZp761D112	9.2
400292	AA250737	Hs.72472	BMP-R1B	9.2
408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	9.2
454048	H05626	Hs.6521	ESTs	9.2
454037	RA01192	Hs.215377	Human DNA sequence from clone GS1-115M3	9.1
441016	AW135653	Hs.25845	ESTs	9.0
425187	AW014486	Hs.22509	ESTs	8.9
445568	H00918	Hs.268744	KIAA1795 protein	8.9
453941	U39817	Hs.36520	Bloom syndrome	8.9
422411	AW174843	Hs.22511	ESTs	8.8
447250	A1375572	Hs.172634	ESTs	8.8
424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	8.7
448902	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp7611912 (f	8.7

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	44886	H42169	Hs.347310	hypothetical protein FLJ14627	8.6	
	423135	N67655	Hs.26411	ESTs	8.5	
	418030	BE207573	Hs.83321	neuromedin B	8.4	
	448769	N66037	Hs.38173	ESTs	8.4	
5	407748	AL079409	Hs.38176	KIAA0606 protein, SCN Circadian Oscillator	8.3	
	400293	NS1002	Hs.306480	Homo sapiens mRNA; cDNA DKF761E212 (f	8.3	
	415279	F04237	Hs.1447	glial fibrillary acidic protein	8.2	
	451516	AB005115	Hs.12024	ESTs	8.2	
	419629	AB020595	Hs.91662	KIAA6989 protein	8.2	
10	437034	AA742643	gb:Y14C01.s1 NC1_CGAP_CGB1	Homo sapiens	8.2	
	456965	AW131888	Hs.127292	ESTs, Weakly similar to hypothetical pr	8.1	
	417417	F05745	Hs.69512	ATPase, Ca transporting, plasma membrane	8.1	
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	8.1	
	422664	AA315323	Hs.12807	gb:EST20390 Ratina II	Homo sapiens cDNA	8.1
15	452526	W38537	Hs.280740	hypothetical protein MGC3040	8.0	
	435793	AB037734	Hs.4993	KIAA1313 protein	7.9	
	415669	NM_050025	Hs.17859	serine (or cysteine) proteinase inhibito	7.9	
	407168	RA51175	Hs.117193	ESTs	7.9	
	447414	DE2343	Hs.74376	neuroblastoma (nerve tissue) protein	7.8	
20	427710	AI015631	Hs.23210	ESTs	7.8	
	410336	D54745	Hs.80247	cholecystokinin	7.8	
	415721	NM_001650	Hs.288550	sequestrin 4	7.7	
	438000	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_HUMAN III	7.7	
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	7.7	
25	428845	AL157579	Hs.153610	KIAA0751 gene product	7.7	
	443321	NM_005883	Hs.20912	adenomatous polyposis coli like	7.7	
	410305	AF020409	Hs.52185	solute carrier family 3 (sodium/hydrogen	7.6	
	443392	AI055821	Hs.293420	ESTs	7.6	
	429038	AL022513	Hs.194766	seizure related gene 6 (mouse)-like	7.5	
30	418738	AW388633	Hs.6682	solute carrier family 7 (cationic amino	7.5	
	422381	AW170565	Hs.47628	ESTs	7.5	
	447198	D61523	Hs.283435	ESTs	7.5	
	446555	AI536697	Hs.159863	ESTs	7.5	
35	453332	AI000341	Hs.220491	ESTs	7.4	
	407034	UB4540	gb:Human dystrobrevin isoform DTN-3 (DTN		7.4	
	425354	UE0207	Hs.155835	complement component 3a receptor 1	7.4	
	426814	AF036943	Hs.172619	myelin transcription factor 1-like	7.4	
	448507	AL133109	Hs.21333	Homo sapiens mRNA, cDNA DKF7566N1047 (f	7.4	
40	438845	AL355143	Hs.55663	Homo sapiens EST from clone 41214, full	7.4	
	445078	AK001256	Hs.22075	KIAA1576 protein	7.3	
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi]	7.2	
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	7.2	
	440210	AW674362	Hs.125236	ESTs	7.2	
45	413651	A207162	Hs.3815	statimycin-like-protein RB3	7.2	
	428409	AW117207	Hs.98523	ESTs	7.1	
	413409	AI638416	Hs.1440	DEAD(H) (Asp-Gln-Ala-Asp(His)) box polypep	7.1	
	443992	AW022228	Hs.322922	ESTs	7.1	
	435601	A36580	Hs.816	SRY (sex determining region Y)-box 2	7.1	
50	427840	R12014	Hs.20976	ESTs	7.0	
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	7.0	
	424893	AW295112	Hs.153848	Homo sapiens cDNA FLJ133033 lit, clone CV	7.0	
	452355	NS4926	Hs.29202	G protein-coupled receptor 34	7.0	
	414696	AF003020	Hs.75918	Hemann-Pick disease, type C1	7.0	
55	440152	AB002376	Hs.7006	KIAA0378 protein	7.0	
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	7.0	
	425782	U66468	Hs.158525	cell growth regulatory with EF-hand doma	7.0	
	416805	F13271	Hs.19981	Human clone 23560 mRNA sequence	7.0	
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	7.0	
60	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	6.9	
	403639	R38438	Hs.182575	solute carrier family 15 (H777) transport	6.9	
	443605	AI113581	Hs.198416	ESTs	6.9	
	444396	TS6213	Hs.4257	ESTs	6.9	
	444165	AL137443	Hs.10441	hypothetical protein FLJ11236	6.9	
	414245	BE148072	Hs.75850	WAS protein family, member 1	6.9	
65	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.9	
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	6.9	
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.9	
	411379	AI816344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	6.9	
	446782	AI653048	Hs.144006	ESTs	6.8	
70	426919	AL041228	Hs.127416	ELAV (embryonic lethal, abnormal vision,	6.8	
	423346	AI261677	Hs.10941	synaptonemin 1	6.8	
	436843	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	6.8	
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	6.8	
	410337	AB020725	Hs.58309	KIAA0518 protein	6.8	
75	422613	A034032	Hs.130322	Kv channel-interacting protein 1	6.8	
	413589	AW452631	Hs.313803	ESTs, Highly similar to AF15/833 1 noncl	6.8	
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypothesi	6.8	
	421141	AW117261	Hs.123914	ESTs	6.7	
	453786	RS1362	Hs.106642	ESTs, Weakly similar to T09052 hypothesi	6.7	
80	441916	AA993571	Hs.129075	ESTs	6.7	
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	6.7	
	428037	N47474	Hs.89230	potassium intermediate/small conductance	6.7	
	423343	AA324643	Hs.246106	ESTs	6.7	

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	456723	Z43902	Ha.4748	adenylate cyclase activating polypeptide	6.7
	414214	D49958	Ha.75819	glycoprotein M5A	6.7
	434811	AW671205	Ha.114280	ESTs	6.7
	424922	DE308547	Ha.271112	hypothetical protein MGC10825	6.7
5	449128	A952493	Ha.345303	ESTs	6.6
	431553	X76075	Ha.2799	cartilage linking protein 1	6.6
	420156	AW449258	Ha.6187	ESTs	6.6
	431117	AF003522	Ha.255000	delta (Drosophila)-like 1	6.6
	422960	AW694987	Ha.63864	cathenin 13, H-cathenin (heart)	6.6
10	429233	AA448419	Ha.45209	ESTs	6.5
	453924	RA9295	Ha.24865	ESTs	6.5
	433929	AJ375499	Ha.27379	ESTs	6.5
	426529	AF190100	Ha.170241	Homo sapiens clone IMAGE 23915	6.5
	414683	S78295	Ha.75888	hypothetical protein FLJ12702	6.4
15	409746	NM_004734	Ha.56294	RAE33A, human RAS oncogene family	6.4
	419169	AW851980	Ha.262346	ESTs, Weakly similar to ST2482 hypotheti	6.4
	453530	AF150278	Ha.33578	KIAA0820 protein	6.4
	422263	AA307628	Ha.129908	KIAA0591 protein	6.4
20	421568	AK000307	Ha.106825	hypothetical protein FLJ20300	6.4
	447197	R36075	Ha.106825	gby88801.s1 Soares placenta Nb2HP Homo	6.3
	426588	F07396	Ha.46627	ESTs	6.3
	410366	A267389	Ha.302659	hypothetical protein	6.3
	419498	AL036591	Ha.20887	hypothetical protein FLJ10392	6.3
25	446997	AA383439	Ha.16758	Solr-1 protein	6.3
	427958	AA418000	Ha.98280	potassium intermediate/small conductance	6.3
	445908	R13580	Ha.13436	Homo sapiens clone 24425 mRNA sequence	6.3
	412968	S72043	Ha.75133	metallothionein 3 (growth-inhibitory fac	6.3
	452834	A638627	Ha.105085	KAA1688 protein	6.3
30	408790	AW580227	Ha.47860	neurotrophic tyrosine kinase, receptor,	6.3
	418512	AW48674	Ha.10460	diacylglycerol kinase, zeta (10460)	6.2
	410299	AA160130	Ha.104006	gene product	6.2
	452744	A267652	Ha.246107	Homo sapiens mRNA: cDNA DKFZp434E082 (H	6.2
	427897	NM_017413	Ha.303084	apelin; peptide ligand for APJ receptor	6.2
35	416427	BE244050	Ha.79307	Rac/Cdc42 guanine exchange factor (GEF)	6.2
	430274	AF086592	Ha.46372	ESTs	6.2
	431552	A1815863	Ha.259873	saxonal transport of synaptic vesicles	6.2
	439807	BE540565	Ha.159460	ESTs	6.2
40	408950	AA707814	Ha.14945	long fatty acyl-CoA synthetase 2 gene	6.2
	412709	AL022337	Ha.74518	KAA0027 protein	6.2
	435624	AF214942	Ha.24489	formin 2	6.1
	425977	R15138	Ha.165570	Homo sapiens clone 25052 mRNA sequence	6.1
	420077	AW512260	Ha.87767	ESTs	6.1
	457005	AJ007421	Ha.172597	sal (Drosophila)-like 3	6.1
45	449471	AA386146	Ha.307594	ESTs	6.1
	423770	AW976796	Ha.132775	Homo sapiens cDNA FLJ10077 fs, clone HE	6.1
	438624	AA889055	Ha.123468	ESTs	6.1
	452752	AW044058	Ha.33578	KIAA0820 protein	6.1
	438208	AL041228	Ha.65379	ESTs	6.1
50	418972	AL110370	Ha.79500	growth-associated protein 43	6.1
	407808	AA663659	Ha.278769	histone deacetylase 3	6.1
	433701	AW445023	Ha.15155	ESTs	6.1
	418704	AA429104	Ha.45067	ESTs	6.1
	425250	H56895	Ha.198309	histogran rich basic protein	6.1
55	433244	AB040543	Ha.271285	KAA1510 protein	6.0
	422644	AB018259	Ha.118140	KAA0715 gene product	6.0
	420133	AA428117	Ha.155543	ESTs	6.0
	440491	R35252	Ha.130558	ESTs, Weakly similar to 2090260A D cell	6.0
	422728	AW937826	Ha.103062	ESTs, Weakly similar to ZNF1_HUMAN ZINC	6.0
60	415257	F03016	Ha.27513	ESTs	5.9
	417160	N76497	Ha.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.9
	430188	AL048242	Ha.234794	Homo sapiens mRNA, cDNA DKFZp5649083 (H	5.9
	427372	A4323668	Ha.280631	hypothetical protein DKFZp451C183	5.9
	430471	AF064845	Ha.241523	hypothetical protein FLJ10142	5.9
	433523	H29882	Ha.10142	ESTs	5.9
65	408926	AF217525	Ha.49002	Down syndrome cell adhesion molecule	5.9
	427317	AB028555	Ha.178780	KAA1032 protein	5.9
	426140	AF131798	Ha.343768	Homo sapiens clone 25119 mRNA sequence	5.9
	409892	AW956113	Ha.7149	gb:EST358183 MAGE resequences, MAGO Homo	5.9
	459516	A1045662	Ha.246858	EST	5.8
70	442910	A1365130	Ha.113307	ESTs, Weakly similar to T19326 hypotheti	5.8
	414737	A1160386	Ha.129687	ESTs	5.8
	424332	AA338919	Ha.101515	ESTs	5.8
	403142			NM_002706-Homo sapiens protein phosphat	5.8
75	420111	AA255652		gbc252h11.1 r1 NC_0GAP_GCB1 Homo sapiens	5.8
	450813	A1739525	Ha.203376	ESTs	5.8
	402145			Target Exon	5.8
	434792	AA649253	Ha.132458	ESTs	5.8
	427421	AA325138	Ha.235873	hypothetical protein FLJ22672	5.8
80	445745	AB007924	Ha.13245	KIAA0555 gene product	5.8
	420668	BE548277	Ha.102104	ESTs	5.8
	451407	AA131376	Ha.343809	fibroblast growth factor 120	5.7
	441102	AA973905		intermediate filament protein syncollin	5.7
	424560	AA158727	Ha.159555	protein predicted by clone 23733	5.7

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430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.7
405238			Target Exon	5.7
430890	NM_014442	Hs.279751	sialic acid binding to like lectin 6	5.7
440439	R319127	Hs.21433	hypothetical protein DKFZp5647J036	5.7
413492	D61470	Hs.15400	HSA0280 protein	5.7
427624	AA06245	Hs.24295	ESTs	5.7
418079	R40058	Hs.6911	ESTs	5.6
424458	M29773	Hs.1780	myelin associated glycoprotein	5.6
446299	AA497044	Hs.20887	hypothetical protein FLJ10352	5.6
429693	AF0906	Hs.26339	ESTs, Weakly similar to S21348 probable	5.6
430228	AW950639	Hs.6382	ESTs, Highly similar to T00391 hypothei	5.6
445255	NM_014941	Hs.12477	synaptosomal-associated protein, 91 kDa	5.6
436887	AW955157	Hs.19325	hypothetical protein DKFZp5470155	5.6
452898	AA814491	Hs.78792	ESTs	5.6
435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.6
436035	AA703679	Hs.106999	ESTs, Weakly similar to SYT5_HUMAN SYNAP	5.5
412190	R16180	Hs.27461	ESTs	5.5
459778	AW294059	Hs.34054	Homo sapiens cDNA: FLJ22409 fs, clone H	5.5
416490	AF090116	Hs.79346	regulator of G-protein signalling 7	5.5
423449	A149700	Hs.33057	ESTs	5.5
440966	A1703103	Hs.271350	hypothetical protein MGC16275	5.5
431914	A1701523	Hs.112577	ESTs	5.4
423476	AL338533		Human DNA sequence from clone RPS-1046G1	5.4
428588	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	5.4
447773	AI423330	Hs.36790	ESTs, Weakly similar to putative p150 (H	5.4
436936	AL134481	Hs.197476	ESTs	5.4
427260	R25941	Hs.25418	ESTs	5.4
427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fs, clone HE	5.4
452856	AF034799	Hs.30681	protein tyrosine phosphatase, receptor I	5.4
428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl	5.4
447385	AA610150	Hs.272072	ESTs, Weakly similar to D30222 hypothei	5.4
463348			C700166A1(12698061)db[BA021845.1](A8	5.4
438330	AW450572	Hs.257316	ESTs	5.3
428503	AA380153	Hs.20859	gbr:EST193093 Skin tumor 1 Homo sapiens cd	5.3
448148	NM_016578	Hs.20859	HDV pX associated protein-6	5.3
413866	W62187	Hs.33397	Homo sapiens cDNA: FLJ22219 fs, clone H	5.3
445225	A1215555	Hs.202398	ESTs	5.3
428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	5.3
418759	AA227879	Hs.187621	ESTs	5.3
422655			Target Exon	5.3
412046	Y07847	Hs.73088	PAS-related on chromosome 22	5.3
423869	BE409301	Hs.134012	Ctq-related factor	5.2
430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
453096	AW284631	Hs.11325	ESTs	5.2
450475	AW656634	Hs.200615	ESTs	5.2
429139	F09092	Hs.66087	ESTs	5.2
451783	R42554	Hs.210562	T-box, brain, 1	5.2
436556	H12043	Hs.91564	ESTs	5.2
424330	AW072953	Hs.333396	Homo sapiens cDNA FLJ13596 fs, clone PL	5.2
408453	AJ063838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	5.2
441499	AW262580	Hs.147574	protocadherin beta 16	5.2
427885			NM_001839^Homo sapiens calponin 3, acid	5.2
420865	L10333	Hs.99947	reticulon 1	5.2
426457	AW894667	Hs.165965	chimerin (chimeraxin) 1	5.2
417355	D13168	Hs.82002	endothelin receptor type B	5.1
429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	5.1
450639	A1703165	Hs.277174	ESTs	5.1
412811	H65382		ESTs	5.1
403379	NM_018432		Homo sapiens ovarian cancer related prot	5.1
441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	5.1
442832	AW205560	Hs.253569	ESTs	5.1
422709	AA315331	Hs.153465	ESTs	5.1
411555	AF113537	Hs.70669	HMP19 protein	5.1
419043	T19167	Hs.85666	ets variant gene 1	5.0
430979	AA479755	Hs.129010	ESTs	5.0
451390	AW118072		diacylglycerol kinase, zeta (104kD)	5.0
423676	AW563357	Hs.7847	ESTs	5.0
429918	AW873986	Hs.119383	ESTs	5.0
452785	AL359942	Hs.296434	erythroid differentiation and dendroclasi	5.0
453128	AW626516	Hs.31719	acylphosphatase 2, muscle type	5.0
428001	H97149	Hs.219507	ESTs, Moderately similar to Translating	5.0
430183	BE010038		gbr:PM3-EN0176-1004000-01-g04 EN0176 Homo	5.0
449969	AW285142	Hs.180187	Homo sapiens cDNA FLJ14337 fs, clone PL	5.0
439108	AW163034	Hs.6467	synaptotagmin 3	5.0
452671	AF020547	Hs.159147	chondroitin sulfate proteoglycan 3 (neur	5.0
451752	AF032957	Hs.26366	KIXA1171 protein	5.0
420578	AA813546	Hs.99034	GTP-binding protein Rho7	4.9
427415	AA175949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (r	4.9
428186	AW534300	Hs.255605	mannosidase, alpha, class 2A, member 2	4.9
445133	AW157646	Hs.198589	ESTs	4.9
410359	R38624	Hs.106313	ESTs	4.9
427144	X36097	Hs.2126	vasoactive intestinal peptide receptor 2	4.9
448548	R13209	Hs.21413	solute carrier family 12, (potassium-chi	4.9

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457561	AA331517	Hs.286055	chirwin (chirwin) 2	4.9
409100	H98216	Hs.42261	ESTs, Moderately similar to 138022 hypot	4.9
437117	AL049256	Hs.122593	ESTs	4.9
415101	R45331	Hs.144534	ESTs	4.9
439458	AW975186	gb:EST387294	MAGE resequences, MAGN Homo	4.9
442026	AI243749	Hs.8074	brain-specific angiogenesis inhibitor 3	4.9
438283	AI459331	Hs.37282	ESTs	4.9
449714	AB030315	Hs.23941	KIAA1189 protein	4.9
420871	AA702872	Hs.65300	ESTs	4.9
422266	EC267511	Hs.155392	collagen response mediator protein 1	4.9
426001	W57683	Hs.137476	paternally expressed 10	4.9
419103	Z40229	Hs.95423	hypothetical protein FLJ23033	4.8
446727	AB011035	Hs.16032	KIAA523 protein	4.8
409670	AF160367	Hs.46784	potassium large conductance calcium-acti	4.8
428189	AA424030	Hs.46627	ESTs	4.8
420092	AA814043	Hs.88045	ESTs	4.8
410631	AA086469	Hs.47171	ESTs	4.8
449277	AA001064	Hs.43670	ESTs	4.8
436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.8
414706	AW340125	Hs.76989	KIAA0057 gene product	4.8
439703	AI803373	Hs.31999	ESTs	4.8
439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	4.8
445290	AF059019	Hs.21956	Homo sapiens clone 24670 mRNA sequence	4.7
436734	AI937612	Hs.273758	hypothetical protein FLJ23112	4.7
408177	AI241733	Hs.43871	ESTs	4.7
445740	T78287	Hs.13226	Homo sapiens clone 25181 mRNA sequence	4.7
409527	AW977556	Hs.251735	ESTs, Weakly similar to 178855 sunneth	4.7
445523	Z30118	Hs.293789	ESTs, Moderately similar to unnamed prot	4.7
409172	Z99399	Hs.122593	ESTs	4.7
437748	AF234982	Hs.5814	suppression of tumorigenicity 7	4.7
421637	AF035290	Hs.106300	Homo sapiens clone Z5556 mRNA sequence	4.7
448244	AI458682	gb:U13611	x1 NCI_CGAP_Lu24 Homo sapiens	4.7
459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.7
447891	R41754	Hs.6496	ESTs	4.7
428968	U07616	Hs.173034	amphiphysin (SH-Mana syndrome with br	4.7
440819			NM_002587) Homo sapiens pearal (Drosophi	4.7
409125	R17268	Hs.343507	axonal transport of synaptic vesicles	4.7
437762	T78028	Hs.154679	synaptotagmin I	4.7
441668	AI811973	Hs.136313	ESTs	4.7
444190	AI878918	Hs.10526	crystallin and glycine-rich protein 2	4.6
429269	AA443013	Hs.99203	ESTs	4.6
433009	AA761568	gb:nc24c08.s1	NCI_CGAP_GCB1 Homo sapiens	4.6
416586	D44643	Hs.14144	secreted modular calcium-binding protein	4.6
427701	AA111101	Hs.243885	nuclear autoantigenic sperm protein (ris	4.6
429525	NM_001196	Hs.315899	Homo sapiens cDNA FLJ22373 fs, clone H	4.6
410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fs, clone PL	4.6
437698	R61837	Hs.7990	ESTs, Moderately similar to I84505 calci	4.6
448813	Z42023	Hs.106576	alanine-glyoxylate aminotransferase 2B	4.6
424264	D80400	Hs.22938	Human DNA sequence from clone RPT-304B14	4.6
448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZ547D086 (fr	4.6
419723	AL120193	Hs.339810	longevity assurance (LAG1; S. cerevisiae	4.6
424282	R76421	Hs.135694	ESTs	4.6
429401	AW296102	Hs.99272	ESTs, Weakly similar to S32567 AA prot	4.6
426413	AA377820	gb:EST90805	Synovial sarcoma Homo sapien	4.5
407896	D75435	Hs.41154	Zic family member 1 (odd-paired Drosophi	4.5
413248	T64858	Hs.21433	hypothetical protein DKFZ547A036	4.5
443731	AI083528	Hs.145418	ESTs	4.5
449539	W80363	Hs.58446	ESTs	4.5
420362	U79734	Hs.97206	huntingtin interacting protein 1	4.5
443301	AI733614	Hs.220587	ESTs, Moderately similar to ALUS_HUMAN A	4.5
423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZ564C142 (fr	4.5
437933	AI276132	Hs.146155	ESTs	4.5
446544	AI831932	Hs.7047	ESTs, Weakly similar to Unknown [H sapie	4.5
411642	NM_014932	Hs.71132	neurofilin 1	4.5
428282	N34905	Hs.44453	Homo sapiens cDNA: FLJ22559 fs, clone H	4.5
411498	NM_014210	Hs.70499	ectopic viral integration site 2A	4.4
408622	AA55060	Hs.202577	Homo sapiens cDNA FLJ12155 fs, clone MA	4.5
436637	AI783629	Hs.26766	ESTs	4.5
438456	AA913381	Hs.20994	ESTs	4.4
404533			ENSP00000009376+PREDI65 protein (Fragmen	4.4
413951	AW051200	Hs.75640	matutinin profile precursor A	4.4
417632	R20655	Hs.5422	glycoprotein MGB	4.4
425138	H08849	Hs.167484	glutamate receptor, ionotropic, N-methyl	4.4
457211	AW972665	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.4
413812	AA186687	Hs.44748	ESTs	4.4
448451	AW015994	Hs.345433	gb:U1-H-B0p-abt-g-09.6.U1.s1 NCI_CGAP_S	4.4
432281	AK001239	Hs.274263	hypothetical protein FLJ110377	4.4
458760	AI498631	Hs.111334	kerilin, light polypeptide	4.4
405919			NM_002578) Homo sapiens p21 (CDKN1A)-acti	4.4
447877	AI435184	Hs.164252	ESTs	4.4
431342	AW971018	Hs.21659	ESTs	4.4
408577	H50572	Hs.19315	ESTs, Highly similar to NR3C3_HUMAN PRO-N	4.4
445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	4.4

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422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	4.4
419088	A538323	Hs.52620	integrin, beta 8	4.4
428305	AA446628	Hs.2799	cartilage linking protein 1	4.4
410768	AF038185	Hs.66187	Homo sapiens clone Z3F00 mRNA sequence	4.4
427222	U75456	Hs.190787	issue inhibitor of metalloproteinase 4	4.4
451621	A8879148	Hs.26770	fatty acid binding protein 7, brain	4.4
424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	4.3
433932	AW954599	Hs.169330	neuronal protein	4.3
439335	S75106	Hs.8359	glutamate receptor, ionotropic, kainate	4.3
436039	AW023323	Hs.121070	ESTs	4.3
416220	N49776	Hs.170994	hypothetical protein MGC10946	4.3
409593	AA322277	Hs.57691	catherin 18, type 2	4.3
456497	AW967965	Hs.123648	ESTs, Weakly similar to AF108460.1 ubiru	4.3
420352	BE268835	gb.601117374F1	NIH_MGC_16 Homo sapiens c	4.3
454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	4.3
421790	AW896201	Hs.22654	sodium channel, voltage-gated, type 1, a	4.3
444216	AF070541	Hs.10584	Homo sapiens clone 24421 mRNA sequence	4.3
436391	AJ227092	Hs.146274	ESTs	4.3
452106	A1141031	Hs.21342	ESTs	4.3
422465	AF073710	Hs.117149	regulator of G-protein signalling 9	4.3
432885	AL133916	Hs.21963	hypothetical protein FLJ20063	4.3
404541			HM_030795 Homo sapiens stathmin-like 4 (4.3
424572	M19550		2',3'-cyclic nucleotide 3' phosphodiester	4.3
449048	Z45051	Hs.22920	similar to S58401 (cattle) glucose induc	4.3
409182	AA054970	Hs.122593	ESTs	4.3
444600	R41386	Hs.5995	ESTs	4.3
409838	AW65535	Hs.40389	ESTs	4.3
410592	R94088	Hs.43569	ESTs	4.3
440158	AA868507	Hs.125141	ESTs	4.2
445078	AB699975	Hs.4775	phallophilin 3	4.2
420570	AA515822	Hs.134832	ESTs	4.2
411555	AF106554	Hs.71345	neurofilament 3 (150kD medium)	4.2
412505	AA974449	Hs.21794	ESTs	4.2
418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.2
411707	R42637	Hs.21963	hypothetical protein DKF_Zp718D0514	4.2
449433	A1672095	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	4.2
441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	4.2
448243	AW369771	Hs.52620	integrin, beta 8	4.2
429149	AW193350	Hs.179922	ESTs, Weakly similar to U30222 hypothe	4.2
432676	AF084865		glt-Homo sapiens envelope protein RIC-3 (4.2
404584			Target Exon	4.2
422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
451254	A571016	Hs.172957	ESTs	4.2
423585	A0007863	Hs.185140	K/A-0403 protein	4.2
439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKF_Zp434N079 (fr	4.2
425287	R88249	Hs.155524	peanut (Drosophila)-like 2	4.2
425790	AW136286	Hs.288446	ESTs	4.2
450407	NM_000810	Hs.24959	gamma-aminobutyric acid (GABA) A recepto	4.2
425201	A3204621	Hs.155247	adipocyte C, fructose-bisphosphate	4.2
445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fs, clone NT	4.1
400777			NM_007322-Homo sapiens glutamate recept	4.1
422170	A791949	Hs.112432	ank-Müllerian hormone	4.1
410765	A594972	Hs.66180	nucleosome assembly protein 1-like 2	4.1
425402	A215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bind	4.1
438461	AW075485	Hs.285049	phosphoserine aminotransferase	4.1
421288	A1126821	Hs.30514	ESTs	4.1
416439	AA180363	Hs.118769	ESTs	4.1
419587	A638859	Hs.227599	ESTs, Weakly similar to T2D3_HUMAN TRANS	4.1
435040	AH932350	Hs.152825	ESTs	4.1
439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDN	4.1
458435	AA187118	Hs.144121	ESTs, Weakly similar to T45915 hypothetical	4.1
413320	AA084071	Hs.53815	Homo sapiens mRNA; cDNA DKF_Zp547N093 (fr	4.1
436899	AA764852	Hs.291567	ESTs	4.1
454171	AW854832		gb-QVZ CT0261-20 099-011-805 CT0261 Homo	4.1
453118	AW195849	Hs.252757	ESTs	4.1
428771	A0208952	Hs.183143	K/A-1039 protein	4.1
444185	AW298350	Hs.66020	ESTs	4.1
422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
430147	R60704	Hs.224434	hairy/enhancer-of-split related with YRP	4.1
456060	C14594	Hs.45184	Homo sapiens cDNA FLJ12784 fs, clone MA	4.1
438119	AW511097	Hs.112765	ESTs	4.1
415827	H11462	Hs.23079	ESTs	4.1
437397	AA349847	Hs.4221	hypothetical protein DKF_Zp718H039	4.1
441330	AH92560	Hs.131175	ESTs	4.1
404063	A0203836	Hs.140386	ESTs	4.0
435294	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fs, clone HE	4.0
447397	BE247676	Hs.18442	E-1 enzyme	4.0
425360	A092634	Hs.156114	protein tyrosine phosphatase, non-recept	4.0
432022	AL112042	Hs.272346	Homo sapiens mRNA; cDNA DKF_Zp761L1212 (f	4.0
420602	AF060877	Hs.95236	regulator of G-protein signalling 20	4.0
408081	AW451597	Hs.167409	ESTs	4.0
453113	BE005771	Hs.153746	hypothetical protein FLJ22490	4.0
436511	AA721252	Hs.291502	ESTs	4.0

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	448944	AD014605	Hs.22599	atrophin-1 interacting protein 1; activi	4.0
	419412	AW161058	Hs.50297	synuclein, beta	4.0
	490901	AW970386	Hs.269423	ESTs	4.0
5	453438	AA469535	Hs.22752	ESTs	4.0
	455822	AC339132		C-rich RNA sequence binding factor 1	4.0
	416553	AA89416	Hs.344043	Homo sapiens cDNA FLJ11469 fs, clone HE	4.0
	437449	AL390153	Hs.208339	Homo sapiens mRNA; cDNA DKF Zp7626113 (f	4.0
	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	4.0
	439450	HS1613	Hs.125304	ESTs	4.0
10	453752	AL134539	Hs.254129	KIAA1678	4.0
	459080	AW192083	Hs.290855	ESTs	4.0
	438810	AW897846	Hs.6421	hypothetical protein DKF Zp761009121	4.0
	446233	AJ282028	Hs.25205	ESTs	4.0
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like protein	4.0
15	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.0
	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.0
	423279	AW959861	Hs.290943	ESTs	4.0
	418340	N31772	Hs.79326	fasciculation and elongation protein zeta	3.9
	410126	BE165274		KIAA0036 gene product	3.9
20	431173	AW971198	Hs.294068	ESTs	3.9
	446936	H10207	Hs.47314	ESTs	3.9
	424899	AL119387	Hs.115802	ESTs	3.9
	419638	AW134924	Hs.190325	ESTs	3.9
	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	3.9
25	438142	T90309	Hs.295951	ESTs	3.9
	412659	AW753865	Hs.74376	oligomycin related ER localized prot	3.9
	412788	AA120960	Hs.198416	ESTs	3.9
	410909	AW988161	Hs.53112	ESTs, Moderately similar to ALU8_HUMANA	3.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.9
30	432809	AA656509	Hs.131703	ESTs	3.9
	424186	AF536021	Hs.288070	Homo sapiens cDNA FLJ10281 fs, clone HE	3.9
	425400	AB023198	Hs.158135	KIAA0581 protein	3.9
	449932	AI675444	Hs.263024	ESTs	3.9
	434072	H70654	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.9
35	450590	AF701507	Hs.273740	ESTs	3.9
	415946	AB384465	Hs.144769	ESTs, Weakly similar to 138022 hypotheti	3.9
	414040	NS8513	Hs.321711	ESTs	3.9
	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.9
40	443210	AF552949	Hs.9451	hypothetical protein MGCL3168	3.9
	448448	NM_014954	Hs.212239	KIAA0955 protein	3.9
	447067	R42098	Hs.21964	ESTs	3.9
	413199	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.9
	429421	AL031658		Human DNA sequence from clone RP1-310013	3.9
45	415736	R87548	Hs.78854	ATPase, Na ⁺ transporting, beta 2 polypep	3.8
	417333	AL157455	Hs.173179	bromodomain and PHD finger containing, 3	3.8
	418771	AA807881	Hs.25329	ESTs	3.8
	417565	A1203405	Hs.47831	ESTs	3.8
	412420	AL035669	Hs.73853	bone morphogenetic protein 2	3.8
50	420002	AW969736	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	3.8
	435312	AJ243396	Hs.4865	voltage-gated sodium channel beta-3 subu	3.8
	435832	AA425588	Hs.41841	Bruno (Drosophila)-like 4, RNA binding	3.8
	435654	AJ278120	Hs.4596	putative serpin-repeat containing prote	3.8
	453079	AB211222	Hs.110165	glucosyl[10]yls NCI, CGAP, P-33 Homo sapi	3.8
55	425905	AB032959	Hs.318584	novel C2HC4 type Zinc finger (zinc finger	3.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	3.8
	437756	AA767537	Hs.157096	ESTs	3.8
	453633	AA325869	Hs.31463	C4001107:g[585234]g[14054015.1] (AF0	3.8
60	441732	AW298818	Hs.127341	KIAA0281 gene product	3.8
	415884	H22966	Hs.13471	ESTs	3.8
	432646	AW753310		gb RC3-CT0254-031099-012-c05 CT0254 Homo	3.8
	451099	AW227465	Hs.267159	KIAA1409 protein	3.8
	447057	AI423407	Hs.157697	ESTs	3.8
	418915	AJ474778	Hs.118977	ESTs	3.8
65	441111	AA308867	Hs.126594	ESTs	3.8
	447818	AF799498	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.8
	457183	H91882	Hs.118559	Dvl-binding protein IDAX (inhibition of	3.8
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	3.8
70	410711	AB002316	Hs.65746	KIAA0318 protein	3.8
	428878	AA435884	Hs.48526	ESTs	3.8
	438944	AA302517	Hs.50222	KIAA1444 protein	3.8
	420398	AB002379	Hs.100113	KIAA0381 protein	3.8
	418325	AW247430	Hs.84152	cystathionine-beta synthase	3.8
75	427209	H05909	Hs.52423	KIAA1565 protein	3.7
	445319	AF952708	Hs.12513	Homo sapiens clone 23687 mRNA sequence	3.7
	428841	AI419430	Hs.104535	ESTs	3.7
	414821	M63035	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.7
	443310	BE552018	Hs.133152	ESTs	3.7
80	407728	AW071502	Hs.175931	ESTs	3.7
	429643	AA455880	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.7
	444127	N63620	Hs.13281	ESTs	3.7
	425652	AB021742	Hs.322431	neurogenic differentiation 2	3.7
	458072	AB890347	Hs.271523	Homo sapiens cDNA: FLJ22785 fs, clone K	3.7

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	459660	M79082	Hs.2928	ESTs	3.7
	432188	A1362952	Hs.257837	solute carrier family 7 (cationic amino	3.7
	437627	AW469925	Hs.257837	ESTs	3.7
5	408508	A1806109	Hs.135736	KIAA1580 protein	3.7
	440999	AF119214	Hs.22791	transmembrane protein with EGF-like and	3.7
	410623	AW958932	Hs.293833	ESTs	3.7
	430744	AA485229	Hs.105649	ESTs	3.7
	454392	BE260893	Hs.236311	homodomain-interacting protein kinase 2	3.7
	453739	AL130266	Hs.236311	ESTs	3.7
10	407195	H91679	gb:U0407.1	Soares fetal liver cyp19	3.7
	405239	U93281	gb:U0407.1	Soares 3 alpha hydroxysteroid dehydro	3.7
	433615	AA732682	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	424900	AL135588	Hs.153203	MyoD family inhibitor	3.7
	451027	AW519204	Hs.40868	ESTs	3.7
15	415131	D61119	gb:HUM158C11B	Clontech human fetal brain	3.7
	443454	A1057494	Hs.133421	ESTs	3.7
	423779	AW071837	Hs.57971	ESTs	3.7
	452092	BE245374	Hs.27942	hypothetical protein FLJ11210	3.6
	435910	AK084152	Hs.21782	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
20	447028	A1973128	Hs.167257	brain link protein-1	3.6
	452997	N64777	Hs.44656	ESTs	3.6
	408601	U47928	Hs.86122	protein A	3.6
	407332	A1801565	Hs.200113	Homo sapiens cDNA FLJ11379 fl, clone HE	3.6
	455646	BE054420	gb:RC4-6T0311-241199-012-c08	6T0311 Homo	3.6
25	433657	A124356	Hs.8124	Phi domain containing protein in retina 1	3.6
	421679	AA751110	Hs.203933	ESTs	3.6
	445985	AA324885	Hs.22777	carbonic anhydrase XI	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	411775	H08342	gb:U0407.1	Soares infant brain TNE H	3.6
30	439099	AB037900	Hs.5462	protein kinase C and casein kinase subst	3.6
	433615	BE330513	Hs.27936	hypothetical protein MGCA537	3.6
	423611	AB011163	Hs.125908	KIAA0591 protein	3.6
	453169	AB037815	Hs.32156	KIAA1394 protein	3.6
	436954	AA740151	Hs.130425	ESTs	3.6
35	435249	AF098263	Hs.170053	G-protein coupled receptor 88	3.6
	432058	AW655996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	419390	A1701162	Hs.90207	hypothetical protein MGCI1138	3.6
	428483	A1908539	Hs.184592	KIAA0344 gene product	3.6
	409557	BE182895	Hs.21193	ESTs	3.6
40	418049	AA211467	Hs.190498	Homo sapiens, Similar to nuclear localiz	3.6
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.6
	425331	AW962128	gb:EST374201	MAGE resequences, MAGG Homo	3.6
	445105	AF238969	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	3.6
	421051	AL119203	Hs.138411	Homo sapiens mRNA, cDNA DKFZP568J1922 (I	3.6
45	446420	AW015693	Hs.135614	ESTs	3.6
	428138	AA773842	Hs.293799	ESTs	3.6
	404185			Target Exon	3.6
	427517	AA644142	Hs.7107	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	443150	A034467	Hs.34650	ESTs	3.6
50	408065	AW954272	gb:EST366342	MAGE resequences, MAGC Homo	3.6
	435092	AL137310	Hs.4749	Homo sapiens mRNA, cDNA DKFZp761E13121 (3.6
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	3.6
	423560	A0251195	Hs.132891	hypothetical protein MGCA4400	3.6
55	432892	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	3.6
	412350	AW659306	Hs.73826	protein tyrosine phosphatase, non-recept	3.6
	438753	BE282233	Hs.7423	hypothetical protein from EUPROMAGE 2168	3.6
	451734	NM_005176	Hs.26944	neurogranin (protein kinase C substrate,	3.6
	437056	A147061	gb:ok33a1.1	Soares_NSF_F8_9W_OT_PA_P_S	3.6
	438328	A1492261	Hs.32450	ESTs	3.6
60	451499	NM_005503	Hs.26468	amyloid beta (A4) precursor protein bind	3.6
	423641	AL137295	Hs.130489	ATPase, amorphospholipid transporter II	3.6
	434784	AA649051	Hs.164007	ESTs	3.5
	441834	AL138034	Hs.7979	KIAA0736 gene product	3.5
	421183	AL135740	Hs.102447	TSC-22-like	3.5
65	452108	AW125982	Hs.203013	hypothetical protein FLJ12748	3.5
	425970	RI13406	Hs.56782	ESTs	3.5
	425115	RI4664	Hs.123956	ESTs	3.5
	444471	AB020684	Hs.11217	KIAA0877 protein	3.5
	419929	U90265	Hs.93810	cerebral cavernous malformations 1	3.5
70	407782	A077715	Hs.38384	putative secreted signal homodimeric to I	3.5
	422584	A148006	Hs.222120	ESTs	3.5
	433323	AA805132	Hs.159142	ESTs	3.5
	435743	T66861	Hs.12962	ESTs	3.5
	450287	AW901347	Hs.35592	hypothetical protein FLJ23342	3.5
	403341			Target Exon	3.5
75	443761	A1525743	Hs.345187	ESTs	3.5
	458743	R53169	Hs.80712	KIAA0202 protein	3.5
	447925	AW232271	Hs.250718	ESTs	3.5
	445424	AB028945	Hs.12616	corticin SH domain-binding protein	3.5
	416874	H98752	Hs.42568	ESTs	3.5
80	430456	AA314998	Hs.241503	hypothetical protein	3.5
	419647	AA348947	Hs.91816	hypothetical protein	3.5
	412707	AW206373	Hs.16443	Homo sapiens cDNA FLJ21721 fl, clone C	3.5

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444458	BE041526	Hs.31746	hypothetical protein DKFZ547F072	3.5
451066	A1758650	Hs.205132	ESTs	3.5
452334	AW152225	Hs.165909	ESTs, Weakly similar to C86022 hypothet	3.5
452071	AB028985	Hs.94805	ATP-binding cassette, sub-family A (ABC)	3.5
432525	A1543595	Hs.94830	ESTs, Moderately similar to T30394 A kn	3.5
442118	AA976718	Hs.202242	ESTs	3.5
421686	AB011156	Hs.106794	KIAA0584 protein	3.5
428955	AF059214	Hs.194587	cholesterol 25-hydroxylase	3.5
444326	AF033517	Hs.270710	ESTs	3.5
443361	A1752626	Hs.133273	ESTs	3.5
427527	R87582	Hs.179915	guanine nucleotide binding protein (G pr	3.4
434542	AA765510	Hs.51250	hypothetical protein FLJ13164	3.4
415235	AW470411	Hs.268433	neurabinin	3.4
407000	AW952281	Hs.295184	guanine nucleotide binding protein (G pr	3.4
417084	H08370	Hs.33067	ESTs	3.4
432925	AA878324	Hs.268433	ESTs	3.4
439520	H05430	Hs.268433	neurabinin	3.4
453710	AL119136	Hs.235131	homodomain-interacting protein kinase 2	3.4
412783	BE275738	Hs.74578	DEAD/DH (Asp-Glu-Ala-Asp)-like box polytyp	3.4
435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.4
437125	XG5724	Hs.2839	Morrie disease (pseudoglioma)	3.4
449511	A1970264	Hs.197075	ESTs	3.4
448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZ506P1124 (f	3.4
430968	AW972830	Hs.2381425	MAGE resequences, MAGL, Homo	3.4
413530	AA130156	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	3.4
412043	BE158622	Hs.333371	Homo sapiens clone TA-40 untranslated mRN	3.4
445656	RS9860	Hs.262306	ESTs	3.4
412820	BE001236	gb:CM3-BN0075-240200-101-d11 (BN0075	Homo	3.4
458912	AR11055	Hs.20943	ESTs	3.4
452449	AW068558	Hs.20943	ESTs	3.4
427085	AA743935	Hs.202325	ESTs	3.4
419852	AW503756	Hs.285164	hypothetical protein cJ551D2.5	3.4
448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.4
437411	A240668	Hs.113099	ESTs	3.4
445828	F05602	Hs.81907	ESTs	3.4
415347	C15944	Hs.90005	superior cervical ganglia, neural specifi	3.4
431733	AW298410	Hs.21475	ESTs	3.4
415549	H10562	Hs.21691	ESTs	3.4
400205			NM_006255/Homo sapiens RAD21 (S. pombe)	3.4
437528	NS5946	Hs.169745	crumb2 (Drosophila) homolog 1	3.4
442593	R39804	Hs.31961	ESTs	3.4
442927	A1024347	Hs.131519	ESTs	3.4
429528	A1985303	Hs.99361	ESTs	3.4
450765	A1733488	Hs.144082	ESTs	3.4
437387	A1198874	Hs.28347	AQO25 protein	3.4
430347	NM_002039	Hs.239706	GRB2 associated binding protein 1	3.4
404283			ENSP00000244751; Copine-like protein KIA	3.4
433229	AB040925	Hs.91625	KIAA1452 protein	3.4
440274	R24595	Hs.7122	scrapie responsive protein 1	3.4
436114	AA778232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.4
439690	AA843868	Hs.190557	ESTs	3.4
450784	AW245803	Hs.47289	ESTs	3.3
417868	A078454	Hs.122592	ESTs	3.3
437973	AA018825	Hs.7934	Kruppel-like factor 4 (gnt)	3.3
456209	W06533	Hs.297972	ESTs	3.3
421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gcl-B) sul	3.3
438201	AA780243	Hs.54547	ESTs	3.3
400302	N48056	Hs.1915	isolate hydrolase (picostate-specific memb	3.3
425897	AA936315	Hs.48965	Homo sapiens cDNA; FLJ21693 fls, clone C	3.3
423169	BE047009	Hs.21837	ESTs, Weakly similar to KIAA0927 protein	3.3
415539	A1733881	Hs.72472	BNP-R1B	3.3
430337	AB931255	Hs.202427	ESTs	3.3
408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fls, clone PL	3.3
423420	A1571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp7611224 (f	3.3
429084	AJ001442	Hs.195614	splicing factor 3b, subunit 3, 130KD	3.3
440435	AL042201	Hs.21273	transcription factor MYD-spl10	3.3
453785	A1368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.3
448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cl	3.3
435207	AA334774	Hs.12845	hypothetical protein MGCI3159	3.3
424632			NM_02490/Homo sapiens hypothetical prot	3.3
411565	AW851728	Hs.102490	gbrMF2-CT10222-011199-007-406 CT10222	3.3
415845	H95279	Hs.293788	gbr-yu2002-s1 Soares fetal liver spleen	3.3
432627	AW450938	Hs.180115	ESTs	3.3
426525	T78300	Hs.300642	serologically defined colon cancer anti	3.3
401272			CS900559-g112314159emoyCA899338.11(A	3.3
435071	D60683	Hs.35495	ESTs	3.3
433128	AB021923	Hs.23367	EST-YD1 protein	3.3
426920	AA393535	Hs.132121	ESTs	3.3
423668	Y10148	Hs.131138	neurokinin receptor 2	3.3
435056	AW023337	Hs.5422	glycoprotein M6B	3.3
445534	AL039823	Hs.12840	Homo sapiens gemline mRNA sequence	3.3
425010	T16837	Hs.4241	ESTs	3.3
445250	A1218133	Hs.147617	ESTs	3.3

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5	421394	AW578202	Hs.289364	hypothetical protein FLJ22251	3.3
	450358	AB010098	Hs.24937	coorin, actin-binding protein, 2b	3.3
	411048	AK001742	Hs.67991	hypothetical protein DKFp434G052	3.3
	432488	AA51010	Hs.216540	ESTs	3.2
	443672	AA323582	Hs.39617	histybetaine (gamma), 2-oxoglutarate di	3.3
	412719	AW016610	Hs.816	ESTs	3.3
	420050	AL118615	Hs.94653	neurochondin	3.3
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.3
10	405454	AA636381	Hs.315111	nuclear receptor co-repressorHDAC3 comp	3.3
	411482	AA553672	Hs.266311	granin-like neuroendocrine peptide precu	3.2
	434574	AI424458	Hs.33470	ESTs	3.2
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.2
	426757	AW005640	Hs.136206	ESTs	3.2
	428167	AA170021	Hs.16382	ESTs	3.2
15	415597	AW952520	Hs.207536	ESTs	3.2
	400362	AF068294	Hs.272414	Homo sapiens HDCA645P mRNA, partial cds	3.2
	417675	AB03607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	425550	AW253055	Hs.119357	ESTs	3.2
	404120			CS000537-g[3298555]gAAC41376.1(AF0	3.2
20	417123	BE326521	Hs.159450	ESTs	3.2
	450313	AK038989	Hs.332633	Bardet-Biedl syndrome 2	3.2
	426999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	3.2
	435236	AF181982	Hs.242407	G-protein-coupled receptor, family C, gr	3.2
25	452519	AW295597	Hs.61884	Homo sapiens, clone IMAGE.4290026, mRNA,	3.2
	415558	AA851543	Hs.125719	ESTs	3.2
	451996	AW514021	Hs.245510	ESTs	3.2
	425560	AW207748	Hs.59115	ESTs	3.2
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	3.2
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	3.2
30	414300	AJ304870	Hs.189680	ESTs	3.2
	437634	AA769254	Hs.233554	glnu3603.1 NCL CGAP, CG81 Homo sapiens	3.2
	430634	AA810624	Hs.38936	ESTs, Weakly similar to H2BHLHUMAN HISTO	3.2
	447714	AW296313	Hs.255537	ESTs	3.2
	412021	AW885592		gltRC4-OT0071-090300-011-g11 OT0071 Homo	3.2
35	443431	AK056847	Hs.20654	ESTs	3.2
	445774	AJ254165	Hs.339863	ESTs	3.2
	431327	AW572220	Hs.105426	ESTs	3.2
	413335	AK613318	Hs.48442	ESTs	3.2
40	430809	AJ791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	3.2
	446859	AL133311	Hs.3781	solute carrier family 1, ligal high affi	3.2
	450682	HS0603	Hs.94037	hypothetical protein FLJ23053	3.2
	439039	AI656707	Hs.49713	ESTs	3.2
	401720			NM_014587?Homo sapiens SRY (sex determi	3.2
45	453740	AL120265	Hs.311809	ESTs, Moderately similar to POU2F9 fami	3.2
	451032	W03652	Hs.332879	Homo sapiens mRNA, cDNA DKFp454P116 (f	3.2
	413834	BE296896	Hs.224179	ESTs, Weakly similar to I38022 hypotheti	3.2
	438138	R98299	Hs.177502	ESTs	3.2
	436336	W82147	Hs.113594	ESTs	3.2
	417189	R13550	Hs.246773	ESTs	3.2
50	424066	Z96348	Hs.112461	ESTs, Weakly similar to I38022 hypotheti	3.2
	435767	H73505	Hs.117874	ESTs	3.2
	415314	N88802	Hs.5422	glycoprotein M58	3.2
	446475	BE615134	Hs.247474	hypothetical protein FLJ21032	3.2
55	414699	AB15523	Hs.76330	synectin, alpha (non A4 component of am	3.2
	438549	BE386801	Hs.21858	trinuucleotide repeat containing 3	3.2
	463896	AW293483	Hs.252005	KIAA1853 protein	3.2
	415639	AF070390	Hs.30689	Homo sapiens clones 24622 and 24623 mRNA	3.1
	428832	AA578329	Hs.324239	ESTs, Moderately similar to ZNF7_HUMAN 2	3.1
60	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonine	3.1
	429046	XS7436	Hs.194772	oligodendrocyte myelin glycoprotein	3.1
	421896	N82233	Hs.45107	ESTs	3.1
	413985	BE048146	Hs.75873	synaptin 1A (brain)	3.1
	414734	AA151712	Hs.82572	ESTs	3.1
65	446147	AL133064	Hs.14051	Homo sapiens mRNA, cDNA DKFp434A2417 (f	3.1
	427712	AI368024	Hs.283696	ESTs	3.1
	406481			Target Exon	3.1
	453204	R10739	Hs.191990	ESTs	3.1
	422890	Z43784	Hs.48965	ankyrin 3, node of Ranvier (ankyrin G)	3.1
70	422981	HI0540	Hs.48965	Homo sapiens cDNA, FLJ21693 fts, clone C	3.1
	421030	AW151357	Hs.129883	microtubule-associated protein tau	3.1
	423503	AB007880	Hs.129883	Homo sapiens KIAA0420 mRNA, complete cds	3.1
	413985	AI018666	Hs.75667	synaptophysin	3.1
	431721	AB032996	Hs.269044	KIAA1170 protein	3.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
75	428076	AB028977	Hs.123574	KIAA1054 protein	3.1
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	3.1
	412799	AJ267508		glt.acq1N03.1 Stanley Frontal SB pool 1	3.1
	459318	NM_000038		glt.Homo sapiens adenomatous polyposis c	3.1
80	453324	W03652	Hs.232099	ESTs	3.1
	424009	F11696		glt.HSC20D041 normalized infant brain CD	3.1
	426222	AJ208737	Hs.122810	Homo sapiens cDNA FLJ11489 fts, clone HE	3.1
	414684	RS4418	Hs.153745	hypothetical protein FLJ13456	3.1
	445852	AV660697	Hs.282700	ESTs	3.1

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427241	AA399988	Hs.112087	Human DNA sequence from clone RP11-530N1	3	1
455388	AW936234		gb:QV0-DT0020-090200-105-p05 DT0020 Homo	3	1
415838	RA4336	Hs.7093	ESTs	3	1
451692	AL137422	Hs.28549	Homo sapiens mRNA; cDNA DKFp761A1623 (f	3	1
454294	Z55978		Human clone Z3826 mRNA sequence	3	1
434460	AA474486	Hs.3852	KIAA0368 protein	3	1
449919	AI674485	Hs.200141	ESTs	3	1
440688	AW404591	Hs.147440	ESTs, Weakly similar to Z192_HUMAN ZINC	3	1
416801	X9834	Hs.75911	sal (Drosophila) hie-2	3	1
428060	AA420616	Hs.254483	ESTs	3	1
423597	AL043117	Hs.129672	sperm associated antigen 9	3	1
452454	AW620480		gb:QV2-ST0298-140200-042-F10 ST0298 Homo	3	1
445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3	1
413974	BE206336	Hs.27788	ESTs	3	1
422772	AL119585	Hs.120228	KIAA0749 protein	3	1
423672	AB020316	Hs.134015	uronyl 2-sulfotransferase	3	1
435375	AT33610	Hs.167832	ESTs	3	1
450561	AW552160	Hs.53640	ESTs	3	1
428647	AA830050	Hs.124344	ESTs	3	1
400658			ENSP000002370811:KIAA1217 PROTEIN (FRAGM	3	0
443945	AI950064	Hs.148485	ESTs, Weakly similar to AA7161 Mac-2-in	3	0
446519	AJ076543	Hs.313	secreted phosphoprotein 1 [proteinin,	3	0
433980	AA137152	Hs.295049	phosphosulfate aminotransferase	3	0
437738	AA766914	Hs.203475	ESTs, Weakly similar to ALUT_HUMAN ALU S	3	0
444772	AW450900	Hs.178859	ESTs	3	0
435325	AL15475	Hs.35453	Homo sapiens mRNA; cDNA DKFp761G151 (fr	3	0
439971	WJ32474	Hs.301746	RAP2A, member of RAS oncogene family	3	0
408449	NM_004408	Hs.166151	dynamitin 1	3	0
432821	BE170702	Hs.279005	solute carrier family 21 (organic anion	3	0
453657	WJ3237	Hs.296162	AD303 protein	3	0
407235	D05669	Hs.169407	SAC2 (suppressor of actin mutations 2, ca	3	0
428862	NM_000346	Hs.2316	SRV (sex determining region Y)-box 9 (y	3	0
424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fs, clone HE	3	0
454253	AV690717	Hs.47144	DKFZP580H0619 protein	3	0
405650	T65617	Hs.101257	hypothetical protein MGC3295	3	0
418211	BE244745	Hs.247474	hypothetical protein FLJ21032	3	0
440461	RS2728	Hs.7193	KIAA1183 protein	3	0
452630	H23230	Hs.22481	ESTs, Moderately similar to AA6010 X-in	3	0
431431	AL69711	Hs.252953	Human DNA sequence from clone RP3-403A15	3	0
447881	BE620686	Hs.75354	GCH1 (general control of amino-acid synt	3	0
454042	H22570		hypothetical protein FLJ20093	3	0
429168	AA384682	Hs.146589	ESTs, Weakly similar to JCS238 galactosyl	3	0
451331	AA017410	Hs.40568	ESTs	3	0
446377	AW014022	Hs.170053	ESTs	3	0
430251	AA609246	Hs.181451	ESTs	3	0
420558	AW965215	Hs.130707	ESTs	3	0
454119	BE549773	Hs.40510	uncoupling protein 4	3	0
451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	3	0
435321	R16814	Hs.112062	ESTs	3	0
412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3	0
423858	AL137328	Hs.133483	Homo sapiens mRNA; cDNA DKFp43490550 (f	3	0
431242	AA967742	Hs.347534	KIAA1201 protein	3	0
403922			C21K000178-01[341207]hAF61215.1JAF22	3	0
445899	AI263736	Hs.145626	ESTs	3	0
440261	M81886	Hs.71717	glutamate receptor, ionotropic, AMPA 1	3	0
444580	AW930171	Hs.104143	ESTs	3	0
434269	AK001169	Hs.3781	similar to murine leucine-rich repeat pr	3	0
419551	F07809	Hs.85506	paired box gene 6 (aniridia, keratitis)	3	0
448439	BE613280	Hs.77550	hypothetical protein MGC1780	3	0
432229	AW290976	Hs.143587	ESTs	3	0
443726	AI963625	Hs.148362	ESTs	3	0

TABLE 138:

65	Phy: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers
70	Play 408065 410099	CAT Number 103646_1 117647_1 Accession AW954272 AI003154 AA059300 AA046911 AA061638 TB0671 AIT14254 D03374 AW998843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW501977 AW501980 W52882 T07735 AA484549 W60590 D52685 T38111 BE327043 AW901768 BE551237 AA917004 AA716027 AA439568 AA823724 AB055952 AA517096 AA084516 BE467736 AI092635 AB87863 AB97593 AA336618 A167419 A118634 T31586 AA436630 AA706191 AA041169 AA422304 T03534 AA211402 AIZ04899 AJ364472 AW827081 AA788593 T32736 AT067935 AA167791 AA747914 AA636370 AB85504 BE198274 AB853209 AA210908 H24222 AA081774 BE000035 BE000034 AA334969
75	410126 411565 411775 412021 412799	117765_1 129256_1 125757_1 127156_1 123217_1 123943_1 Accession AW851726 AW851907 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628 H08342 RS2430 Z42067 AA059285 AW885592 AW885594 AW885579 AW885551 AG7506 AA121045 AA1136521 H08362 AW067730 AA335014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AA424991 AB593507 AB63108 AA599060 AD01148 AA586699
80	412811 412820 415131	1330039_1 1523680_1 Accession R99887 AA813482 AW016452 H05363 R41807 AB364258 AA620526 A214940 AW081419 AW090733 AW068875 Z38240 AA121027 R1734 BE001236 BE001177 BE001180 BE001234 D61119 D81508 D81734

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NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
5	406533	Minus	277132-277595
	420659	Minus	73525-73564
	400777	Plus	70745-71121
	401272	Minus	98374-98509
	401720	Plus	7783-8468
	402145	Plus	113096-114600
10	402604	Plus	20353-20767
	402605	Minus	47680-47993
	402855	Minus	59763-59909
	403022	Plus	50769-50864
	403142	Plus	85285-90131
15	403341	Plus	30699-30910
	403696	Minus	143467-143634
	404120	Plus	135775-136000
	404185	Minus	129171-129327
	404283	Minus	99460-99564
20	404541	Plus	103455-103664
	404684	Plus	138651-139153
	404632	Plus	45095-45225
	404819	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	405238	Minus	51728-51836
25	405239	Plus	144345-144664,144690-144836,151750-151883,152407-152484
	405346	Minus	43390-43462
	405519	Plus	2630-2967
	405681	Minus	91439-91579
30			

TABLE 14A: ABOUT 1111 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 14A lists about 1111 genes up-regulated in glioblastoma compared to normal central nervous system (CNS). These were selected from 59880 probesets on the Affymetrix/Exon Hu3.0 GeneChip array such that the ratio of "average" glioblastoma to "average" CNS tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 85th percentile amongst various brain tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Exon probeSet identifier number
 ExAcon: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of GLIOBLASTOMA to CNS

Pkey	ExAcon	UnigeneID	Unigene Title	R1
45	422737	U05939	Hs.115571 collagen, type III, alpha 1 (Ehlers-Danlos)	32.8
	423961	D13666	Hs.136348 perlecan (OSF-Jos)	28.0
	433001	AF217513	Hs.279905 clone HQ0310 PRO0310p1	25.3
	414555	N93669	Hs.76422 phospholipase A2, group IIA (platelets)	24.3
	424800	U035588	Hs.153203 myoD family inhibitor	22.6
50	417309	H80720	Hs.81592 KIAA0101 gene product	22.2
	449539	W80363	Hs.58446 ESTs	20.7
	453392	U23752	Hs.32964 SRY (sex determining region Y)-box 11	18.7
	414625	X06370	Hs.77432 epidermal growth factor receptor (avian)	15.6
	441490	A057819	Hs.10526 cysteine and glycine-rich protein 2	17.2
	412420	U035588	Hs.73853 bone morphogenetic protein 2	16.7
55	417130	AW276958	Hs.81256 S100 calcium-binding protein A4 (calcium)	16.7
	414217	U039289	Hs.279398 Homo sapiens cDNA FLJ23165 f6, clone L	14.3
	431941	AK002016	Hs.272227 Homo sapiens cDNA FLJ10399 f6, clone CO	14.3
	424397	J04086	Hs.155346 lipopolysaccharide (LPS) II alpha (170kD)	14.1
60	446584	U53445	Hs.15432 downregulated in ovarian cancer 1	13.9
	427672	X12784	Hs.119129 collagen, type IV, alpha 1	13.6
	427604		Target Exon	13.6
	424635	AA420687	Hs.115455 Homo sapiens cDNA FLJ14259 f6, clone PL	13.0
	428330	L22524	Hs.2256 matrix metalloproteinase 7 (matrilysin)	12.9
65	434078	AW880709	Hs.283683 chromosome 8 open reading frame 4	12.5
	414761	AU077228	Hs.77256 enhancer of zeste (Drosophila) homolog 2	12.4
	424322	BE953869	Hs.381878 hypothetical protein FLJ23468	12.2
	456759	BE299150	Hs.127792 delta (Drosophila)-like 3	12.1
	409638	AW450420	Hs.21335 ESTs	11.5
70	441269	AW012006	Hs.187884 ESTs	10.5
	436020	AW505076	Hs.301865 Dicerase syndrome critical region gene 8	10.5
	422163	AF027208	Hs.112380 ptenin (mouse)-like 1	10.1
	444969	AW023334	Hs.160628 ESTs	10.1
	430132	AA204686	Hs.234149 hypothetical protein FLJ20547	9.9
75	433437	U20536	Hs.3290 caspase 6, apoptosis-related cysteine pr	9.4
	445101	T75322	Hs.12314 Homo sapiens mRNA, cDNA DN57258C109 (11)	9.2
	413929	BE501689	Hs.75617 collagen, type IV, alpha 2	9.1
	425187	AW014486	Hs.22509 ESTs	9.1
	449722	BE780074	Hs.23960 cyclin B1	8.9
	449611	AW97394	Hs.187035 ESTs	8.9
80	428242	H55709	Hs.22250 leukemia inhibitory factor (cholestergic	8.9
	419239	AA468183	Hs.184588 Homo sapiens cDNA FLJ23241 f6, clone C	8.9
	443731	AW083928	Hs.145418 ESTs	8.8
	402855		NM_001833*:Homo sapiens calpain 3, acid	8.7

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447342	AI199258	His.19322	Homo sapiens. Similar to RIKEN cDNA 2010	8.6
410102	AW248508	Es.279727	ESTs; homologue of PEM-3 [Dros savignyi]	8.5
420602	AF060877	His.99236	regulator of G-protein signalling 20	8.4
417426	NM_002291	His.82124	laminin, beta 1	8.4
433800	AB34361	His.138150	long type I cell membrane-associated gly	8.3
417051	AI575944	His.188691	Homo sapiens cDNA FLJ12033 fs, clone HE	8.1
409461	AA382169	His.54483	N-myc (and STAT) interactor	8.1
414622	AF752866	His.76669	nicotinamide N-methyltransferase	8.1
433691	CI4187	His.103538	ESTs	8.0
447726	AI.137638	His.15368	matrin 2	8.0
417043	NM_004369	His.80968	collagen, type VI, alpha 3	7.9
447004	AW299568	His.157539	ESTs	7.9
409799	D1.1928	His.76845	phosphoserine phosphatase-like	7.8
425075	AW513621	His.270149	ESTs, Weakly similar to 2109260A B cell	7.8
419938	AU076772	His.1279	complement component 1, r subcomponent	7.7
419508	AW997938	His.90786	ATP-binding cassette, sub-family C (CFTR	7.7
411411	AA345241	His.55950	ESTs, Weakly similar to KIAA1330 protein	7.5
435291	BE584522	His.344037	protein regulator of cytokinesis 1	7.5
422048	NM_012445	His.288126	spondin 2, extracellular matrix protein	7.5
406972	MG2053		gb:human H19 RNA gene, complete cds.	7.4
442802	AL133035	His.8728	hypothetical protein D0FZp434G171	7.4
427501	NM_014788	His.179703	KIAA0129 gene product	7.3
409142	AL138177	His.50758	SMC4 (structural maintenance of chromoso	7.3
409602	AC33769	His.156351	ESTs	7.3
418113	AI272141	His.83484	SRV (sex determining region Y)-box 4	7.2
449961	AW265634	His.133700	ESTs	7.2
413203	XS4942	His.83758	CDC28 protein kinase 2	7.2
424840	D79987	His.153479	extra spindle poles, S. cerevisiae, homo	7.2
428728	NM_018625	His.191381	hypothetical protein	7.1
429183	AB014604	His.197555	KIAA0704 protein	7.1
435451	AF055270	His.278554	heterochromatin protein 1	7.1
422106	D84239	His.111732	Fc fragment of IgG binding protein	7.0
406850	AI624300	His.172528	collagen, type I, alpha 1	7.0
453941	XJ3917	His.36520	Bloom syndrome	6.9
425234	AW152225	His.105909	ESTs, Weakly similar to D8022 hypoteth	6.9
421977	WB4107	His.110165	ribosomal protein L28 homolog	6.8
411078	AI222020	His.152364	CocooCrisp	6.7
427019	AA001732	His.173233	hypothetical protein FLJ10970	6.7
448789	N86037	His.381173	ESTs	6.7
418400	BC243025	His.301089	KIAA0246 protein	6.6
408161	AW952912	His.300283	hypothetical protein MGC3032	6.6
440210	AW674562	His.125296	ESTs	6.6
437036	AI571514	His.133022	ESTs	6.5
411988	AZ07410	His.65260	Homo sapiens, clone IMAGE3636299, mRNA,	6.5
416659	UO3272	His.75432	fortilin 2 (congenital contractural ara	6.6
449300	AI669595	His.346514	ESTs	6.5
440052	AI633744	His.195548	ESTs, Weakly similar to I38022 hypoteth	6.5
412326	RD7586	His.73817	small inducible cytokine A3 (homologous	6.5
434808	AF155108	His.258108	Homo sapiens, Similar to RIKEN cDNA 2810	6.5
452461	N78223	His.108108	transcription factor	6.5
408243	Y00787	His.624	interleukin 8	6.5
424954	NM_005446	His.1846	tumor protein p53 (Li-Fraumeni syndrome)	6.4
453375	AA099947		a disintegrin and metalloproteinase doma	6.4
406478			Target Exon	6.4
427528	AU077143	His.179565	minichromosome maintenance deficient (S	6.4
439710	AF086543		gb:Homo sapiens full length insert cDNA	6.4
458614	AI489557	His.170661	ESTs, Weakly similar to Z195_HUMAN ZINC	6.4
410275	AI554545	His.68301	angiotensin-2	6.4
425289	AW139342	His.155530	interferon, gamma-inducible protein 16	6.3
427871	AW992405	His.59622	Homo sapiens, clone IMAGE3507281, mRNA,	6.3
436895	AF037335	His.5338	carbonic anhydrase XII	6.3
447458	AI741082	His.155661	ESTs	6.3
447439	AA313565	His.145620	ESTs, Weakly similar to KIAA1205 protein	6.3
413719	BC49580	His.75498	small inducible cytokine subfamily A (Cy	6.2
449598	AW295142	His.180187	Homo sapiens cDNA FLJ14337 fs, clone PL	6.2
440704	MG5241	His.162	insulin-like growth factor binding prot	6.2
400419	AF084545		Target	6.2
412140	AA219691	His.73625	RAB8 interacting, kinesin-like (rablins	6.2
409731	AA125985	His.56145	thymosin, beta, identified in neuroblast	6.2
424085	NM_002914	His.139228	apoptosis factor C (picalator 1) 2 (40	6.2
429469	MG4590	His.27	glycine dioxygenase (decarboxylating,	6.1
430630	AW269920	His.2621	cystatin A (protein A)	6.0
410054	XS3415	His.195464	I-lamin A, alpha (actin-binding protein-	6.0
432281	AK001239	His.774263	hypothetical protein FLJ10377	6.0
413527	BE182052	His.246973	ESTs	6.0
413053	AL036737	His.75194	chitinase 3-like 1 (cartilage glycoprote	5.9
421899	AJ011895	His.109281	Netl-associated factor 1	5.9
407182	AA312651	His.230157	ESTs	5.9
410286	AI739159	His.51898	DZF2556A2124 protein	5.9
409529	M33552	His.56729	lymphocyte-specific protein 1	5.9
446557	AI335191	His.260702	ESTs, Weakly similar to 2109260A B cell	5.8
418097	RA5137	His.21968	ESTs	5.8
428450	NM_014791	His.184339	KIAA0175 gene product	5.8

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419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	5.7
421988	AW450481	Hs.161333	ESTs	5.7
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, <i>S.cerevisiae</i>)	5.7
416111	AA033813	Hs.179018	chromatin assembly factor 1, subunit A (5.7
434846	AW255369	Hs.119168	ESTs	5.7
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	5.7
445272	AB85742	Hs.28474	ESTs	5.6
443247	BE614387	Hs.33393	c-Myc target JPO1	5.6
423198	AB11933	Hs.16284	cell division cycle 25A	5.6
445673	AA250970	Hs.251946	poly(A) binding protein, cytoplasmic 1-1	5.6
437034	AA742643		gb.ny11c1.1 NCL_CGAP_GCB1 Homo sapiens	5.6
429447	AW812452	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	5.6
424687	JO5070	Hs.151736	matrix metalloproteinase 9 (gelatinase B	5.6
437056	AA765202	Hs.102142	ESTs	5.6
426935	NM_000088	Hs.172928	collagen, type I, alpha 1	5.6
453361	AA035197	Hs.107375	ESTs	5.5
418293	A1224483	Hs.16063	hypothetical protein FLJ21877	5.5
425348			C7001664.g112658001hgAB21849.11 (AB	5.5
458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
452799	AI948829	Hs.213786	ESTs	5.4
448935	AI078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
422869	AK001375	Hs.121628	hypothetical protein FLJ13548	5.4
442547	AA308397	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.4
424009	F11590		gb.HSC30041 normalized infant brain cDN	5.4
440332	A1218517	Hs.188051	ESTs	5.4
422694	AF129535	Hs.272027	F-box only protein 5	5.4
443684	Q02617	Hs.194397	epirin receptor	5.4
422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
432731	R31178	Hs.287820	fibronectin 1	5.4
426108	AA622637	Hs.165468	programmed cell death 5	5.3
407624	AW157431	Hs.248941	ESTs	5.3
411048	AK001742	Hs.67951	hypothetical protein DKFp334G0522	5.3
412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	5.3
414020	NM_007294	Hs.75703	small inducible cytokine A1 (homologous	5.2
414774	XQ2410	Hs.77274	plasmaingogen activator, urokinase	5.2
413786	AW613780	Hs.13500	ESTs	5.2
454860	AW835757		gb.CV4.LT0015-24200-110-b08.LT0016 Homo	5.2
428037	N47474	Hs.89230	potassium intermediate/small conductance	5.2
420311	AW445044	Hs.38207	Human DNA sequence from clone RP4-S3015	5.1
410737	AF154335	Hs.78891	LHM domain protein	5.1
445637	A1261700	Hs.145544	ESTs	5.1
425882	U83115	Hs.161002	absent in melanoma 1	5.1
415682	A3474726	Hs.191870	ESTs	5.1
414053	BE391635	Hs.15725	transgelin 2	5.1
445884	AA355925	Hs.36232	KIAA0186 gene product	5.1
431512	BE270734	Hs.2795	lactate dehydrogenase A	5.1
432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	5.0
433323	AA805132	Hs.159142	ESTs	5.0
443744	AB94326	Hs.271540	ESTs, Weakly similar to 178865 serine/th	5.0
410434	AF051152	Hs.63068	tol-like receptor 2	5.0
420018	U56387	Hs.94376	proprotein convertase subtilisin/kexin 1	4.9
419485	AA485223	Hs.59807	ESTs, Weakly similar to unnamed protein	4.9
445131	NM_000929	Hs.290	phospholipase A2, group V	4.9
412777	A1335773	Hs.270123	ESTs	4.9
449246	AW411209	Hs.23363	hypothetical protein FLJ10983	4.9
433244	AB040943	Hs.271285	KIAA1510 protein	4.9
407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.9
445118	A1208762	Hs.345672	ESTs	4.9
417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	4.9
420092	AA814043	Hs.88045	ESTs	4.9
412811	H05362		ESTs	4.9
436607	AW617283	Hs.211061	ESTs	4.9
438456	AA913381	Hs.20594	ESTs	4.9
443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibitor	4.9
431553	X78075	Hs.2799	cartilage linking protein 1	4.9
439999	AA115811	Hs.68138	zinc homeobox gene family, member E	4.9
411252	AB018549	Hs.69328	MD-2 protein	4.9
444381	BE367335	Hs.283713	ESTs, Weakly similar to S64054 hypothesi	4.8
429433	AA452899	Hs.213508	ESTs, Weakly similar to KIAA1353 protein	4.8
403349	NM_001406		cytokerin-B3	4.8
402274			C19004458-9g14567179[gb]AA023607.1AC00	4.8
426044	AA502490	Hs.170290	ESTs	4.8
423600	AB633559	Hs.310359	ESTs	4.8
425905	AB032959	Hs.318584	novel C2HC4 type Zinc finger (zinc finger	4.8
431117	AF033522	Hs.250509	delta (Drosophila)-like 1	4.8
418054	NM_002318	Hs.83354	lysyl oxidase-like 2	4.7
441703	AW390054	Hs.192843	leucine zipper protein FKSG14	4.7
439627	BE621702	Hs.29076	hypothetical protein FLJ21841	4.7
445900	AF070526	Hs.126036	Homo sapiens clone 24787 mRNA sequence	4.7
435937	AA830893	Hs.119769	ESTs	4.7
403961			Target Exon	4.7
407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10534 f5, clone OV	4.6
408523	AW833259	Hs.314287	ESTs	4.6

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5	432058	AW65996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	444609	AW571659	Hs.279081	ESTs	4.0
	445666	S59960	Hs.282386	ESTs	4.0
	437814	AD88152	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP D	4.0
	414948	C15240	Hs.182155	ESTs	4.0
10	435542	AA687376	Hs.222120	ESTs	4.0
	422564	A1148006	Hs.222120	ESTs	4.0
	446571	AW016812	Hs.200266	ESTs	4.0
	433558	W55321	Hs.111460	cyclic/calmodulin-dependent protein kin	4.0
	458946	AA009716	Hs.42311	ESTs	4.0
15	449655	A1021987	Hs.59970	ESTs	4.0
	426449	A1914536	Hs.97152	ESTs	4.0
	457292	A1521270	Hs.261462	hypothetical protein FLJ14251	4.0
	444735	AL042201	Hs.21273	transcription factor NYD ap10	4.0
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	4.0
20	420649	A1866964	Hs.124704	ESTs, Moderately similar to S55657 alpha	4.0
	116406	D89961	Hs.75259	isoprene HMGC fusion partner-like 2	3.9
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.9
	449256	AA059050	Hs.59847	ESTs	3.9
	421637	AF035290	Hs.105300	Homo sapiens clone 23556 mRNA sequence	3.9
25	456306	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.9
	438372	A1140189	Hs.129191	ESTs	3.9
	427375	AL035480	Hs.177536	metallocarboxypeptidase CPX-1	3.9
	415131	D61119	Hs.141460	gb:HM150C118 Clontech human fetal brain	3.9
	439231	AW581935	Hs.154138	Homo sapiens mRNA: cDNA DKFZp434B079 (tr	3.9
30	424998	U55515	Hs.154138	chitinase 3-like 2	3.9
	433376	AC093361	Hs.74122	caseinase 4, apoptosis-related cysteine pr	3.9
	455104	BE064863	Hs.3329	chr:RC1:BT0313:110000-015-06 BT0313 Homo	3.9
	443426	AF098158	Hs.9329	open reading frame 1	3.9
	119594	AA013051	Hs.91417	spicosomerase (H) binding protein	3.9
35	417576	AA339449	Hs.82265	phosphoribosylglycamide formyltransfer	3.9
	116857	AA188775	Hs.252453	ESTs	3.9
	434784	AA549051	Hs.164007	ESTs	3.8
	438898	A1819863	Hs.106243	ESTs	3.8
	405102	U45351	Hs.621	ectin, galactoside-binding, soluble, 3	3.8
40	422081	AW136820	Hs.196011	ESTs	3.8
	411688	AW553440	Hs.236994	gb:EST355510 MAGE resequences, MAGB Homo	3.8
	447343	AA255641	Hs.236994	ESTs, Highly similar to S02392 alpha-2-m	3.8
	406395			Target Exon	3.8
	433875	AW977653	Hs.75319	nucleoside nucleotidase M2 polypeptide	3.8
45	403696			CA001100?gb:R552342gb:AA054015.1 (AF0	3.8
	443740	R56434	Hs.21062	ESTs	3.8
	413076	U10694	Hs.75188	weel (S. pombe) homolog	3.8
	409189	AA125694	Hs.13436	gb:27905-r1 Stratagene neuroepithelium	3.8
	444326	AB939357	Hs.270710	ESTs	3.8
50	436899	AA764852	Hs.291567	ESTs	3.8
	445075	AG51827	Hs.344677	ESTs	3.8
	415852	L24496	Hs.80409	growth arrest and DNA-damage-inducible,	3.8
	429163	AA984765	Hs.183688	gb:am02a10.S1 Searns_NFL_T_GBC_S1 Homo s	3.8
	416114	A1695549	Hs.183688	glucuronidase, beta	3.8
55	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	3.8
	446839	BE091926	Hs.18244	mitotic spindle coiled-coil related prot	3.8
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.8
	416664	H72780	Hs.20289	ESTs	3.8
	449444	AW818436	Hs.23590	souise carrier family 16 (monocarboxylic	3.8
60	419735	AW750056	Hs.189577	Homo sapiens cDNA FLJ14743 fs, clone NT	3.8
	448275	BE514434	Hs.20530	kinesin-like 2	3.7
	425141	Y14443		zinc finger protein 200	3.7
	411537	BE073260		gb:MR0-BT0551-000300-102-e05 BT0551 Homo	3.7
	422648	D86983	Hs.118993	Metabona associated gene	3.7
65	449145	AB321212	Hs.156408	ESTs	3.7
	428860	AA429616	Hs.249483	ESTs	3.7
	404584			Target Exon	3.7
	418596	AW976721	Hs.253327	ESTs	3.7
	458072	AB993047	Hs.271923	Homo sapiens cDNA: FLJ22785 fs, clone K	3.7
70	445908	RT13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	3.7
	439979	AW600291	Hs.5823	hypothetical protein FLJ10430	3.7
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	3.7
	427809	M26380	Hs.180878	lipoprotein lipase	3.7
	436674	AA725002	Hs.272018	low molecular mass ubiquitinone-binding pr	3.7
75	413450	Z99716	Hs.78372	N-acetylglucosaminidase, alpha-	3.7
	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fs, clone PL	3.7
	448048	BE281291	Hs.170408	ESTs, Moderately similar to AAT5582 B-est	3.7
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420892			C180074?gb:R552342gb:R552342	3.7
80	448019	AW947164	Hs.195641	ESTs, Moderately similar to 138022 hypot	3.7
	428873	A701609	Hs.98908	ESTs	3.7
	437323	AA371145	Hs.194397	legfin receptor	3.7
	413895	AA484359	Hs.30715	potassium voltage-gated channel, Isk-lik	3.7
	425139	AW630488	Hs.25338	protease, serine, 23	3.7
	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	3.7
	439574	AA469788	Hs.165190	ESTs	3.7
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfat	3.7

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407838	BE146411	Ha.0342	putative nuclear protein	3.7
437748	AF234882	Ha.5814	suppression of tumorigenicity 7	3.6
437470	AL390147	Ha.134742	hypothetical protein DKFp547D065	3.6
400288	X06256	Ha.149809	integrin, alpha 5 (fibronectin receptor,	3.6
453438	AA699035	Ha.22792	ESTs	3.6
415024	AA83981	Ha.189114	ESTs	3.6
419713	AW968058	Ha.92381	nucleic acid diphosphate linked mol	3.6
441523	AW514263	Ha.301771	ESTs, Weakly similar to ALUUF_HUMAN !!!	3.6
416427	BE244050	Ha.70387	Rac2Gels2 guanine exchange factor (GEF)	3.6
440002	Y15227	Ha.20149	deleted in lymphocytic leukemia 1	3.6
441362	BE514410	Ha.23044	RAD51 (S. cerevisiae) homolog (E. coli Rec	3.6
456534	X91195	Ha.100623	phospholipase C, beta 3, neighbor pseudo	3.6
402739			Target Exon	3.6
450297	AW901347	Ha.38592	hypothetical protein FLJ23342	3.6
443715	A1583187	Ha.9700	cyclin E1	3.6
403011			ENSP00000215330? Probable stannocalc	3.6
428403	A1363048	Ha.326159	leucine rich repeat (in FLJ) interaction	3.6
425202	AW952882	Ha.152049	ESTs, Weakly similar to I38022 hypothetical	3.6
408557	BE182696	Ha.211193	ESTs	3.6
453948	A1970797	Ha.64859	ESTs	3.6
440226	BE295782	Ha.159	tumor necrosis factor receptor superfamily	3.6
425331	AW967128		gb. EST374201 MAGGE resequences, MAGG Homo	3.6
442385	H92862	Ha.124813	hypothetical protein MGC14817	3.6
437640	AA764893	Ha.272155	ESTs, Weakly similar to I38022 hypothetical	3.6
424051	AL110203	Ha.138411	Homo sapiens mRNA, cDNA DKFZ586J1922 (f	3.6
405481			Target Exon	3.6
433835	A1806185		gb-wf06a10.v1 Source_NFL_T_CRC_S1 Homo s	3.6
456052	BE311901	Ha.28935	gb-S0114201.4F1 NH1_MGC_141 Homo sapiens c	3.6
453857	AL080235	Ha.35861	DKFZP586E1621 protein	3.5
439726	AW440893	Ha.293707	ESTs, Weakly similar to I38598 zinc finger	3.5
416913	AW934714	Ha.934714	gb-TC1-070201-53129-011-aa11 DT0001 Homo	3.5
413402	Z68155	Ha.50291	laminin, beta 2 (laminin 5)	3.5
403108			ENSP00000241415? Hypothetical 67.7 kDa p	3.5
426509	M31166	Ha.2050	pentoxin-related gene, rapidly induced b	3.5
418883	BE387036	Ha.1211	acid phosphatase 5, tartrate resistant	3.5
432186	AL029352	Ha.2628	solute carrier family 7 (cationic amino	3.5
448789	BE539108	Ha.22051	hypothetical protein MGC15548	3.5
427239	AA830210	Ha.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.5
425212	AW962253	Ha.171616	ESTs	3.5
422936	NM_001809	Ha.1594	centromere protein A (170)	3.5
442254	A1278777	Ha.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
407253	AA411175	Ha.141939	ESTs, Moderately similar to S65657 alpha	3.5
457211	AW972565	Ha.32369	ESTs, Weakly similar to S51797 vasodil	3.5
452682	AA458183	Ha.5071	proteoglycan membrane binding protein	3.5
421247	BE391727	Ha.102319	general transcription factor IIR, polyg	3.5
418049	AA211457	Ha.190489	Homo sapiens, Similar to nuclear localiz	3.5
453952	AL134539	Ha.254129	KIAA1678	3.5
418426	AA180256	Ha.210473	Homo sapiens cDNA FLJ14872 lis. clone PL	3.5
412014	A1830850	Ha.430161	ESTs, Weakly similar to A66101 X-linked	3.5
440370	AA884000	Ha.8173	hypothetical protein FLJ10803	3.5
407729	T4707	Ha.270862	ESTs	3.5
436527	A1869251	Ha.115325	RAB7, member RAS oncogene family-like 1	3.5
455846	BE094420		gb-PCA-670311-241199-012-c06 E10311 Homo	3.5
418630	A1851311	Ha.251946	poly(A)-binding protein, cytoplasmic 14	3.5
432242	AW022715	Ha.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
424503	NM_002205	Ha.149609	integrin, alpha 5 (fibronectin receptor,	3.4
449532	A675444	Ha.263024	ESTs	3.4
427700	AA262294	Ha.180353	fluid specificity phosphatase 5	3.4
403849			Target Exon	3.4
429747	M87507	Ha.2490	caspace 1, apoptosis-related cysteine pr	3.4
451446	A1826288	Ha.171637	hypothetical protein MGC2028	3.4
434589	AF141363		gbltomo sapiens full length insert cDNA	3.4
403381			NM_002210? Homo sapiens integrin, alpha	3.4
420841	A1825251	Ha.94037	hypothetical protein FLJ23053	3.4
433606	AA780385	Ha.187885	ESTs	3.4
452655	AA431395	Ha.37251	ESTs	3.4
411789	AF245605	Ha.721627	Adican	3.4
440948	AW188311	Ha.128619	ESTs	3.4
438516	W76326	Ha.128619	gb-z690404.1 Source_beta_hort_NbH119W	3.4
418821	AA430002	Ha.183161	ESTs	3.4
459660	W93082		ESTs	3.4
404209			Target Exon	3.4
443850	NM_001425	Ha.9999	epithelial membrane protein 3	3.4
430684	AA810624	Ha.30936	ESTs, Weakly similar to H2H8_HUMAN HISTO	3.4
425300	AA901773	Ha.270259	ESTs	3.4
403300	AA258245	Ha.127573	Homo sapiens FKBP4 (FKBP4) mRNA, compl	3.4
458438	AI141520	Ha.151464	ESTs, Weakly similar to ALUC_HUMAN !!!	3.4
444911	U06117	Ha.250	xanthine dehydrogenase	3.4
421084	A1345432	Ha.101382	tumor necrosis factor, alpha-induced pro	3.4
441287	AW293132	Ha.131373	ESTs	3.4
449650	AW294936	Ha.156762	ESTs	3.4
405605			C2001342.g1127814.p26434NAH4_RAT SO	3.4
433791	AA719352	Ha.112718	ESTs	3.4

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	405238		Target Exon	34
	417986	X81120	Hs.75110 cannabinoid receptor 1 (brain)	34
	414372	AA143854	gb2055402.1 Stratagene pancreas (83/20	34
	435523	T63949	Hs.11090 membrane-spanning 4-domains, subfamily A	34
5	405739	A566709	Hs.180426 ribosomal protein S2	34
	442710	A015631	Hs.23210 ESTs	34
	452526	W36537	Hs.280740 hypothetical protein MGC3040	34
	450600	C14904	Hs.45184 Homo sapiens cDNA FLJ12284 fs, clone MA	34
	435805	U80743	Hs.306034 intrucleotide repeat containing 12	34
10	421674	T10707	Hs.295355 hypothetical protein FLJ23135	34
	425242	D13635	Hs.155287 KIAA0010 gene product	34
	436805	AA731533	Hs.270751 ESTs	34
	418641	BE243136	Hs.80597 a disintegrin and metalloprotease doma	34
	430669	AT91150	Hs.262068 ESTs, weakly similar to I38022 hypot	34
15	428878	AA436884	Hs.48526 ESTs	33
	413774	AA131782	Hs.182314 ESTs	33
	406533		ENSF00000203376-FRED65 protein (Fragmen	33
	422448	AW372922	Hs.116774 integrin, alpha 1	33
20	423905	AW575960	Hs.135150 lung type-I cell membrane-associated gly	33
	430637	BE160081	Hs.256290 S100 calcium-binding protein A11 (calgiz	33
	427899	AA252926	Hs.332053 serum amyloid A1	33
	434206	AW135973	Hs.185479 ESTs, weakly similar to S65890 mitogen i	33
	435387	AB90741	Hs.232809 ESTs	33
	436265	AA731331	Hs.190668 ESTs	33
25	412971	AA889628	Hs.35125 ESTs	33
	441701	AW339828	Hs.127497 ESTs	33
	416967	NM_001725	Hs.89555 bactericidal/permeability-increasing pro	33
	434577	R37316	Hs.179769 Homo sapiens cDNA, FLJ22487 fs, clone H	33
	418216	AA662240	Hs.263099 AF15q14 protein	33
30	436137	A056769	Hs.133512 ESTs	33
	428715	AW257116	Hs.53126 ESTs	33
	449249	TS2285	Hs.193115 Homo sapiens mRNA for KIAA1764 protein,	33
	440074	AA863045	Hs.10669 ESTs, weakly similar to T00050 hypothet	33
	405046		C3009978:gb280045cdg(BA01578.1) (ABO	33
35	437816	AI823445	Hs.280699 ESTs	33
	401272		C30005569:gb12314195jamb(CA989338.1) (A	33
	408696	AE10447	Hs.48778 niban protein	33
	432343	NM_002960	Hs.2961 S100 calcium-binding protein A3	33
40	407881	AW072003	Hs.40968 heparan sulfate (glucosamine) 3-O-sulfat	33
	439978	BE13540	Hs.124673 Homo sapiens cDNA FLJ11477 fs, clone HE	33
	421094	AW978202	Hs.289064 hypothetical protein FLJ22251	33
	428722	U78456	Hs.190787 issue inhibitor of metalloproteinase 4	33
	446134	AW161234	Hs.13393 TBP-like 1	33
	412281	AB10654	Hs.14119 ESTs	33
45	436282	R91513	Hs.272104 ESTs, Moderately similar to ALU1_HUMAN A	33
	452203	X57522	Hs.103305 transporter 1, ATP-binding cassette, sub	33
	421307	BE539976	Hs.103305 Homo sapiens mRNA, cDNA DKFpZ434B0425 (f	33
	409463	AA58165	Hs.17796 hypothetical protein MGC2376	33
	411555	AW851728	gb:LRZ-CT0222-011195:orf-406 CT0222 Homo	33
50	410422	AL042014	Hs.63348 Homo sapiens, clone MGC:15203, mRNA, com	33
	450506	NM_004460	Hs.172987 fibroblast activation protein, alpha	33
	451264	AS71016	Hs.172987 ESTs	33
	423784	AC030039	Hs.132826 Homo sapiens cDNA FLJ14913 fs, clone PL	33
55	433325	AW206986	Hs.143905 ESTs	33
	419886	Z99362	gb:HSZ99362 DKFZpharmy1 Homo sapiens cDNA	33
	420552	AK000492	Hs.98806 hypothetical protein	33
	451778	AE26131	Hs.62554 ESTs, weakly similar to zinc finger prot	32
	427594	BE410293	Hs.179718 v-mpl-exon myeloblastosis viral oncogen	32
60	433607	AE17336	Hs.191791 ESTs	32
	418661	NM_001949	Hs.1189 E2F transcription factor 3	32
	440533	AT208217	Hs.142879 ESTs	32
	426746	J33626	Hs.20537 uridine monophosphate synthetase (protot	32
	404120		C5000537:gb13298595(gb)AAC41376.1) (AF0	32
	453920	AI133148	Hs.36602 I factor (complement)	32
65	437014	AA808757	Hs.222531 ESTs, weakly similar to S59501 interloer	32
	424479	AF064228	Hs.149098 sarcosine	32
	413278	BE563085	Hs.833 interferon-stimulated protein, 15 kDa	32
	425922	AL157466	Hs.162751 Homo sapiens mRNA, cDNA DKFpZ671E2423 (f	32
	407304	AA565832	Hs.271649 g1:n32b03.s.1 NCL CGAP_AA1 Homo sapiens	32
70	411571	BE040604	gb:R01111737AF1 NIH_MGC_16 Homo sapiens c	32
	420352	BE254883	gb:RCS-ST0293-140200-014-H05 ST0293 Homo	32
	454765	AW819629	Hs.63287 carbonic anhydrase IX	32
	410407	X66839	Hs.286950 Homo sapiens cDNA, FLJ22528 fs, clone H	32
75	412490	AW801564	Hs.9469 plectudin homology domain-containing, 1	32
	434563	AF063994	Hs.25338 ESTs	32
	417124	BE122762	Hs.57776 ESTs, Moderately similar to I38022 hypot	32
	407378	AA292624	Hs.57776 hypothetical protein FLJ22329	32
	439764	T26536	Hs.61418 hypothetical protein FLJ22329	32
	415536	BE543594	Hs.334629 Target Exon	32
80	440523	NM_003063	Hs.274170 Opa-interacting protein 2	32
	406060		Hs.149420 ESTs	32
	432250	AA452088	Hs.274170	32
	437269	AA433484	Hs.149420	32

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5	449115	AW559652	Hs.37528	ESTs, Weakly similar to AF090944.1 PRO06	3.2
	425146	AW554627		gb:EST386657 MAGE resequences, MAGC Homo	3.2
	436210	A825420	Hs.197824	ESTs	3.2
	437698	R61837	Hs.7990	ESTs, Moderately similar to B94565 calci	3.2
	444371	BE540274	Hs.229	forkhead box M1	3.2
10	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.2
	445828	F05802	Hs.61907	ESTs	3.2
	450810	BE207588	Hs.334360	transforming growth factor beta 1 induce	3.2
	439533	W76021		gbr25464C4.r1 Soares_fetal_heart_NH9H19M	3.2
	418079	R40058	Hs.6911	ESTs	3.2
15	418781	T41160	Hs.8404	ESTs	3.2
	427265	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	3.2
	431319	AA873350	Hs.302322	ESTs	3.2
	445413	AA151342	Hs.12677	CCF-147 protein	3.2
	424947	R77952		ESTs, Weakly similar to alternatively sp	3.2
20	429490	A971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.2
	426765	AA743603	Hs.172708	nucleoprotein 58kD	3.2
	419726	US3330	Hs.1274	bone morphogenetic protein 1	3.1
	425849	AJ000512	Hs.295323	serum/glucocorticoid regulated kinase	3.1
	439566	AF086387		gbr: Homo sapiens full length insert cDNA	3.1
25	425274	AF127481	Hs.301945	lymphoid blast crisis oncogene	3.1
	433753	BE262233	Hs.7423	hypothetical protein from EUROIMAGE 2168	3.1
	432565	AF193766	Hs.13872	cysteine-like protein C17	3.1
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	443431	A056847	Hs.20654	ESTs	3.1
30	428289	MX301	Hs.2253	complement component 2	3.1
	415843	R20529	Hs.8806	ESTs	3.1
	419652	AL157485	Hs.31973	hypothetical protein	3.1
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytostatin)	3.1
	457579	ABJ30816	Hs.36761	HRAS-like suppressor	3.1
35	425579	AA278449	Hs.137429	ESTs	3.1
	408115	AA251393	Hs.280502	Homo sapiens, Similar to RIKEN cDNA 5430	3.1
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.1
	405183			NM_016358?Homo sapiens requiois homeob	3.1
	426765	AA34780	Hs.4248	var 2 oncogene	3.1
40	440286	U28598	Hs.7138	cholinergic receptor, muscarinic 3	3.1
	431176	A026984	Hs.293662	ESTs	3.1
	417918	AA209205	Hs.153754	hypothetical protein FLJ112606	3.1
	437945	T78519		gbr:yf06036.r1 Soares fetal liver spleen	3.1
	404632			NM_024950?Homo sapiens hypothetical prot	3.1
45	428917	AA437337	Hs.15669	ESTs	3.1
	429940	W25215		gbr:zb07a09.r1 Soares_senescent_fibroblas	3.1
	444016	AA448154		gbr:zw0209.r1 Soares_testis_NHT Homo sap	3.1
	430701	AF750833	Hs.233971	ESTs	3.1
	402229	BE292804		mitochondrial ribosomal protein S2	3.1
50	454177	AW807321		gbr:MR4-ST0062-240300-003-g05 ST0062 Homo	3.1
	400090			Evo Control	3.1
	419325	W84915	Hs.42419	ESTs	3.1
	435844	AA700867	Hs.269859	ESTs	3.1
	423042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.1
55	458810	BE407125	Hs.231510	ESTs	3.1
	414403	AW969551	Hs.76064	abdominal protein L27a	3.1
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434k2172 if	3.1
	432888			C1001173? g[751120]br[727904] hypothe	3.1
	430335	AW968485		gbr:EST380561 MAGE resequences, MAGJ Homo	3.1
60	455899	BE155112		gbr:PM1-HT0350-151299-003-a03 HT0350 Homo	3.1
	432044	AW972727		gbr:EST384618 MAGE resequences, MAGL Homo	3.1
	443105	X97613	Hs.9004	chondrin sulfate proteoglycan 4 (neta	3.1
	423789	AKQ02084	Hs.132851	hypothetical protein FLJ11222	3.1
	439538	AA837323	Hs.56407	ESTs	3.1
65	437681	A2107938	Hs.186556	Homo sapiens, Similar to TEA domain fami	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	443021	AA368546	Hs.8904	lg superfamily protein	3.1
	433894	A907682	Hs.243253	ESTs	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13495	3.1
70	403996	A979168	Hs.344096	glycoprotein (transmembrane) hmb	3.1
	449162	A632740	Hs.10476	ESTs	3.1
	417893	AA290605	Hs.190002	ESTs	3.1
	433578	BE336886	Hs.3416	adipose differentiation-related protein	3.0
	438380	T06430	Hs.61394	chondrin sulfate proteoglycan BEHA6b	3.0
75	457556	AT334488	Hs.144082	ESTs	3.0
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.0
	414733	BE514535	Hs.77717	minichromosome maintenance deficient (S	3.0
	431019	NM_005249	Hs.2714	forkhead box G18	3.0
	434583	T96231	Hs.17762	ESTs	3.0
80	455481	AW948317		gbr:RCB-MT0015-280300-021-a09 MT0015 Homo	3.0
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	3.0
	414396	BE548266	Hs.78057	galactose-4-epimerase, UDP-	3.0
	458760	AA498531		fertilin, light polypeptide	3.0
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.0
	411543	AW851248		gbr:IL3-CT0220-160200-056-F01 CT0220 Homo	3.0
	435375	AT733610	Hs.187832	ESTs	3.0
	407047	X65965		gbr:H.sapiens SOD 2 gene for manganese su	3.0

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	432065	AA01039	Hs.2903	protein phosphatase 4 (formerly X), cata	3.0
	443338	R9575	Hs.302808	ESTs	3.0
	433062	AK001757	Hs.281348	hypothetical protein FLJ10895	3.0
5	412135	AW955309	gb:U4-NN0338.300300.155-e07 NN0038 Homo	3.0	
	418669	L85992	Hs.87197	Human clone IMAGE35527 unknown protein	3.0
	449385	AI65047.1	Hs.347290	ESTs	3.0
	426384	AA72078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3.0
	436267	AW459338	Hs.100115	ESTs	3.0
10	440348	AB935320	Hs.223090	ESTs	3.0
	427235	AI126288	Hs.192232	ESTs	3.0
	420116	NM_013241	Hs.95231	FH1FH2 domain-containing protein	3.0
	419764	BE62524	Hs.93183	vasodilator-stimulated phosphoprotein	3.0
	406713	XM4596	Hs.198253	major histocompatibility complex, class	3.0
15	448921	AW015211	Hs.146181	ESTs	3.0
	427695	R88483	Hs.172662	ESTs	3.0
	453324	W26592	Hs.232089	ESTs	3.0
	404722			Target Exon	3.0
	426536	AA46440	Hs.98643	ESTs	3.0
20	442786	HS0733	Hs.295261	ESTs, Moderately similar to ALLUB_HUMAN A	3.0
	444396	T65213	Hs.4257	ESTs	3.0
	440483	A1200836	Hs.190396	ESTs	3.0
	429973	AK43317	Hs.164680	ESTs	3.0
	450125	AA005418	Hs.158196	ESTs	3.0
25	417409	BE272506	Hs.82109	syndecan 1	3.0
	429559	AA454993	Hs.138343	ESTs, Weakly similar to I78865 serine/th	3.0
	455776	BE008746	gb:CM2-070693-210300-123-009 ET0693 Homo	3.0	
	427954	J03060	Hs.247551	measles 1	3.0
	422418	AK001383	Hs.116386	hypothetical protein FLJ10521	3.0
30	427527	AI809057	Hs.203441	immunoglobulin heavy constant mu	3.0
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78865 serin	3.0
	451130	A0752260	Hs.345554	ESTs	3.0
	431431	AL096711	Hs.252853	Human DNA sequence from clone RP3-403A15	3.0
	425248	AW957442	Hs.252766	ESTs	3.0
35	427257	AB059935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.0
	431636	AF178152	Hs.271411	beta-site APP-cleaving enzyme 2	3.0
	416355	LA8075	Hs.269006	ESTs	3.0
	406406	AI742501	Hs.169756	complement component 1, s subcomponent	3.0
40	419829	AI524228	Hs.115185	ESTs, Moderately similar to PC4259 lent	3.0
	412646	NM_005825	Hs.74359	transmembrane protein (63KD), endoplasm	2.9
	423869	BE40531	Hs.134012	CtF-related factor	2.9
	422710	AW936566	Hs.201876	ESTs	2.9
	445906	N28939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.9
	428751	M55210	Hs.214962	laminin, gamma 1 (formerly LAMB2)	2.9
45	430413	AW642182	Hs.241352	small inducible cytokine A5 (RANTES)	2.9
	443433	R44743	Hs.301667	ESTs	2.9
	444145	BE153823	Hs.262385	ESTs, Weakly similar to 200439A chromos	2.9
	425262	DE7119	Hs.155418	GS3955 protein	2.9
	442476	AF969475	gb:AF069475 Homo sapiens astrocytoma lb	2.9	
50	443361	A1792626	Hs.133273	ESTs	2.9
	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.9
	415709	AA649850	Hs.278558	ESTs	2.9
	453385	AW286101	Hs.252906	ESTs	2.9
	422609	AL222996	Hs.6518	serine protease N	2.9
	443378	AW392550	Hs.5280	proteasome (prosome, macropain) subunit,	2.9
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.9
	443502	A074528	Hs.133949	ESTs	2.9
	441143	AW747996	Hs.160999	ESTs, Moderately similar to A58194 throm	2.9
	416300	AW291942	Hs.23628	3 beta-hydroxy-delta 5-C27-steroid oxid	2.9
60	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.9
	408989	AW361666	Hs.49500	KIAA0746 protein	2.9
	427418	AA402507	Hs.325520	LAT1-3TM protein	2.9
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.9
	428827	AW067805	Hs.172665	methylcrotonylhydroxylase dehydrogenase	2.9
65	403290			C100010111-gt4758212[re]NP_004411.1]d	2.9
	403890	X54232	Hs.2699	glycogen 1	2.9
	441217	AF92163	Hs.213246	ESTs	2.9
	416287	AI672319	Hs.76935	methionine aminopeptidase; eIF-2 associa	2.9
	443836	BE221613	Hs.140553	ESTs	2.9
	451527	AF022813	Hs.26518	transmembrane 4 superfamily member 7	2.9
70	411110	RA3523	Hs.217754	hypothetical protein FLJ22202	2.9
	420886	AA805453	Hs.100396	ESTs, Weakly similar to T29012 hypothel	2.9
	493979	AA835002	Hs.125611	ESTs	2.9
	426197	AA004410	Hs.100009	acyl Coenzyme A oxidase 1, palmityl	2.9
75	409679	AA070786	Hs.279888	gb:zm68007.1 Stralagen neuroepithelium	2.9
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	2.9
	457244	AA581385	Hs.162473	ESTs, Weakly similar to 138022 hypothel	2.9
	432036	AF224266	Hs.272373	interleukin 20	2.9
	457364	AW971037	Hs.272373	gb:ES1381323 MAGE mRNAs, MAGE Homo	2.9
80	437860	AA333063	Hs.279888	Homo sapiens cDNA FLJ22165 fs, clone L	2.9
	463544	AA631785	Hs.171914	Homo sapiens cDNA FLJ14209 fs, clone NT	2.9
	454968	AW649046	Hs.171914	gb:IL3-CT0214-150000-085 H06 CT0214 Homo	2.9
	437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	2.9
	400890			Target Exon	2.9

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426895	AW251932	Hs.88936	ESTs	29
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	29
408872	AI476139	Hs.13291	ESTs	29
414799	AI524416	Hs.77326	insulin-like growth factor binding prote	29
406645	AC3860	Hs.308626	major histocompatibility complex, class	29
416569	HE4891		gbyr58h03.1 Soares fetal liver spleen	29
439130	AA306090	Hs.124707	ESTs	29
451433	AA021140	Hs.269265	ESTs, Weakly similar to A46010 X-linked	29
430314	AA364601	Hs.239136	pro-B-cell colony-environment factor	29
424306	AW075531	Hs.154443	musclechromosome maintenance deficient (S,	29
420172	AA601122	Hs.95655	secreted and transmembrane 1	29
424855	BE092285	Hs.29124	hypothetical protein FLJ13187	29
416505	HE6470	Hs.16504	ESTs	29
415195	AW005480	Hs.943	natural killer cell transcript 4	29
423674	NM_000055	Hs.1327	butyrylcholinesterase	29
452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fic, clone C	28
447499	AW262580	Hs.147674	procalcitonin beta 10	28
411373	BE326276	Hs.8861	ESTs	28
456816	AK001509	Hs.144391	hypothetical protein FLJ10567	28
414232	W86946	Hs.238246	hypothetical protein FLJ122479	28
416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	28
447133	AF157482	Hs.19400	MDM2 (p16) arrest deficient, yeast, h	28
439624	AA885255	Hs.123468	ESTs	28
452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	28
408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	28
424028	AF055084	Hs.153602	Homo sapiens cDNA FLJ14354 fic, clone Y7	28
421619	AA75110	Hs.203033	ESTs	28
459551	W79000	Hs.44545	ESTs, Weakly similar to B34087 hypotheti	28
452785	AL359942	Hs.296434	erythroid differentiation and nucleosid	28
432842	AW674093	Hs.334822	hypothetical protein MGC4485	28
433291			Target Exon	28
453096	AW294631	Hs.11325	ESTs	28
422545	X02761	Hs.287820	fibronectin 1	28
440296	D00829	Hs.180610	splicing factor proline/glutamine rich (28
427154	AL137262	Hs.325630	hypothetical protein MGC4289	28
422282	AF016226	Hs.114309	spolipon protein L	28
434868	RS0032	Hs.159263	collagen, type VI, alpha 2	28
414727	BE466904	Hs.191052	gbitz2803.1 NCIC_GAP_G06 Homo sapiens	28
437437	AA225869		hypothetical protein DKFZp76LJ0311	28
427722	AK000123	Hs.186479	hypothetical protein FLJ20116	28
434323	AA345519	Hs.9541	complement component 1, q subcomponent,	28
444006	BE336085	Hs.10085	type I transmembrane protein Fcrl4	28
448432	AI783586	Hs.206575	ESTs	28
453682	T79703		gbitz71e08.1 Soares fetal liver spleen	28
447627	AW020886	Hs.42091	ESTs	28
418657	BE140602	Hs.246645	ESTs	28
409157	AA064631		gbitz27c03.1 Soares_pineal_gland_N3HPG	28
457653	AI820719	Hs.154662	DnaI (Hsp40) homolog, subfamily A, membe	28
456908	AO53971	Hs.220954	hypothetical protein FLJ14129	28
439220	AW296340	Hs.130417	ESTs, Weakly similar to Z195_HUMAN ZINC	28
418312	AW937468	Hs.170307	Rai guanine nucleotide exchange factor R	28
454581	AW805189		gbitzVRA-ST0118-26 1099-012-e10 ST0118 Homo	28
419169	AI851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	28
400645			Target Exon	28
413951	AW051200	Hs.75640	nativelic peptide precursor A	28
441360	AW091713	Hs.106597	Homo sapiens, Similar to RIKEN cDNA 1110	28
404150			Target Exon	28
420336			ENSPFO0000217246*DJ803K15.1 (novel prote	28
454457	AW753456		gbitzQV2-C10261-26 1099-011-d11 C10261 Homo	28
439544	W26354	Hs.28891	hypothetical protein FLJ11360, atensis p	28
430363			ENSPFO000004665:Zinc finger protein 131	28
447183	AI554723	Hs.173182	ESTs	28
446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	28
426141	CO5886	Hs.293972	ESTs	28
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fic, clone K	28
430335	CR0007	Hs.239499	KIAA0185 protein	28
447071	AW026667	Hs.244376	ESTs	28
428899	AAJ44610	Hs.194431	palladin	28
409558			ENSPFO0000237108*1HAA1217 PROTEIN (FRAGM	28
433942			Target Exon	28
420665	AI006770	Hs.30258	ESTs	28
409734	BE161664	Hs.56155	hypothetical protein	28
456645	AF227156	Hs.110103	RNA polymerase I transcription factor RR	28
401841			NM_015113.Homo sapiens KIAA0399 protein	28
447247	AA389351	Hs.237955	Homo sapiens cDNA: FLJ13090 fic, clone NT	28
450150	AI754391	Hs.23510	Kruppel-like factor 12	28
409154	U72882	Hs.50842	interferon-induced protein 35	28
410257	AW918005	Hs.12600	N-ethylmaleimide-sensitive factor attach	28
448224	R48700	Hs.20733	Homo sapiens cDNA: FLJ22266 fic, clone H	28
410269	AA316181	Hs.61635	an transmembrane epithelial antigen of	28
447512	AW958148	Hs.129454	ESTs	28
417749	OU9196	Hs.82520	polymerase (DNA-directed), delta 4	28
415293	RA9462	Hs.106541	ESTs	28

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	429335	Y13187	Hs.748368	Homo sapiens dmef gene, intron 11	2.7
	435065	BE064391		gb RCA-810310-110000-015-b08-B10310 Homo	2.7
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.7
5	406785	AA58061		gb rik10i03 v1 NCL_CGAP_Oo2 Homo sapiens	2.7
	433036	BE347358	Hs.190273	ESTs, Moderately similar to T79285 hypot	2.7
	428630	AS94480	Hs.98765	ESTs	2.7
	423692	AW974944	Hs.200577	ESTs	2.7
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	452811	AA337079	Hs.118593	hypothetical protein FLJ17150	2.6
10	457035	AA336074	Hs.119143	ESTs, Moderately similar to RAA51513 pro	2.6
	427725	Y66839	Hs.192533	mitogen-activated protein kinase kinase	2.6
	433681	A004377	Hs.200360	Homo sapiens cDNA FLJ130277, clone NT	2.6
	423748	A114908	Hs.30211	hypothetical protein FLJ2313	2.6
	427684	A076727	Hs.47522	ESTs	2.6
15	403431			Target Exon	2.6
	439332	AW842747	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (H	2.6
	412749	AA378417	Hs.74564	signal sequence receptor, beta (barostat)	2.6
	409703	NM_006187	Hs.56009	Z'-3-oligoadenylate synthetase 3 (100 k	2.6
	405717			CD000318;gb10052653;swtHP_055314.1) pu	2.6
20	426503	AA380153		gb EST93093 Skin tumor 1 Homo sapiens cD	2.6
	414039	M83221	Hs.858	v-rel avian reticuloendotheliosis virus	2.6
	452663	A089575	Hs.9071	progesterone membrane binding protein	2.6
	447567	AW292139	Hs.115789	ESTs	2.6
	408005	AF025374	Hs.46465	T-cell, immune regulator 1	2.6
25	407103	AA424881	Hs.255301	hypothetical protein MGC13170	2.6
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I30022 hypot	2.6
	435113	AA655469	Hs.117735	ESTs	2.6
	419015	T79282	Hs.14463	ESTs	2.6
	427648	A1376722	Hs.180062	proteasome (prosome, macropain) subunit,	2.6
30	453707	AW003879	Hs.126522	Homo sapiens, clone MGC; 16722, mRNA, com	2.6
	419227	BE274009	Hs.772	glycogen synthase 1 (muscle)	2.6
	404053			Target Exon	2.6
	415069	AA159831	Hs.29286	ESTs, Weakly similar to I49636 DNA-bind	2.6
	449625	NM_014253		odx [odd/Oxt/en-m, Drosophila) homolog 1	2.6
35	438033	T25483	Hs.6059	EGF-containing fibulin-like extracellular	2.6
	451593	AF161879	Hs.26708	CD121 protein	2.6
	435820	AA700705	Hs.13852	ESTs	2.6
	443753	AW367578	Hs.134749	ESTs	2.6
	416097	BE367371	Hs.118564	hypothetical protein FLJ20085	2.6
40	415986	Z43567		gb HSC-1F2C21 normalized infant brain cDN	2.6
	439755	AW748482	Hs.77873	B7 homolog 3	2.6
	408371	AF161545	Hs.44439	hypothetical protein	2.6
	445658	A169002	Hs.127650	ESTs	2.6
	438186	N30158	Hs.122645	ESTs	2.6
45	449426	T92251	Hs.198882	ESTs	2.6
	422605	H16646	Hs.118666	hypothetical protein PP591	2.6
	415788	AW628686	Hs.78851	KIAA0217 protein	2.6
	448596	AW372914	Hs.86149	phosphoinositid 3-phosphate-binding prot	2.6
50	402326	W72838		A1025687;L-870395-150199-019-B7085 Homo	2.6
	441128	AA570265		ESTs, Weakly similar to T23273 hypotelli	2.6
	402372	AW960049	Hs.293660	Homo sapiens, clone IMAGE3535475, mRNA,	2.6
	428977	AK001404	Hs.194698	cyclin B2	2.6
	424278	AK003723	Hs.144517	hypothetical protein FLJ20716	2.6
55	445211	BE345601	Hs.118249	ESTs, Weakly similar to YC18_HUMAN HYPOT	2.6
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	2.6
	417838	R24713	Hs.22514	ESTs	2.6
	402670	AW973577		ESTs	2.6
	423267			Target Exon	2.6
60	454354	AW389896		gb RCA-ST0173-191099-032-e12 ST0173 Homo	2.6
	452903	A1953425	Hs.345291	ESTs, Weakly similar to I38022 hypotelli	2.6
	427830	AA416598	Hs.98233	ESTs	2.6
	435953	A0767097	Hs.114142	ESTs	2.6
	430744	AA465229	Hs.105649	ESTs	2.6
65	413335	A613318	Hs.48442	ESTs	2.6
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotelli	2.6
	431865	AA521106	Hs.136375	ESTs, Weakly similar to S65824 reverse 1	2.6
	424274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	447854	AW138454	Hs.115594	ESTs	2.6
	412799	A1267606		gb xq91h03.x1 Stanley Frontal S8 pool 1	2.6
70	455409	AW596932		gb PM2-DT0023-050400-003-h03 DT0023 Homo	2.6
	426212	A-297567	Hs.43278	hypothetical protein	2.6
	433055	AW021436	Hs.31917	Homo sapiens, clone MGC-9568, mRNA, comp	2.6
	434339	A1076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	2.6
	434898	AW500458	Hs.29556	KIAA0460 protein	2.6
75	438118	AW753311	Hs.346690	ESTs	2.6
	431786	AW452784	Hs.220719	ESTs	2.6
	421689	NE7820	Hs.105626	KIAA1696 protein	2.6
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.6
	424684	AW752714	Hs.5174	ribosomal protein S17	2.6
80	439823	AW655657		ESTs	2.6
	411962	A0499050		gb x85d12.r1 Soares_pregnant_ukerus_NH	2.6
	445774	A1254165	Hs.339968	ESTs	2.6
	403492			C10001573-3-gl7302749gbAAAF57877.1 (AE	2.6

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5	450625	AW970107	Hs.2076	gb:EST382188 IMAGE; reassessment, MAGK Homo	2.6
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOK 4, clone HF.1	2.6
	440131	A023425	Hs.222225	ESTs	2.6
	438525	AW368528	Hs.100885	ESTs	2.6
	412947	AF022375	Hs.73753	vascular endothelial growth factor	2.6
	406662	X62006	Hs.172550	poly(pyrimidine tract binding protein (the	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	402260			NM_014367 Homo sapiens fibrinogen (FBL	2.6
	429599	AA806106	Hs.123694	ESTs	2.6
10	429562	A1732767	Hs.158101	Homo sapiens cDNA FLJ14673 fs, clone NT	2.6
	432527	AW975028	Hs.102754	ESTs	2.6
	434420	AA688278	Hs.19484	hypothetical protein FLJ22578	2.6
	457732	BE330078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.6
	424408	A1754813	Hs.146428	collagen, type V, alpha 1	2.6
15	413151	H47969	Hs.141971	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	416244	N39535	Hs.32748	ESTs	2.6
	403104			C800005-4-gal10432393(wm)NCAC10263.11(A	2.6
	402780			NM_007302? Homo sapiens gbl/lonale rocap	2.6
20	433009	AA761666	Hs.139262	gb.nu24c28.s1 NCL_CGAP_GCB1 Homo sapiens	2.6
	424090	X99699	Hs.139262	XIAP associated factor-1	2.6
	432212			NM_019595 Homo sapiens intercedin 2 (IT	2.6
	407055	RS4126	Hs.40500	similar to S. cerevisiae RER1	2.6
	436849	AA454809	Hs.172928	collagen, type I, alpha 1	2.6
	443462	A064680	Hs.171176	ESTs	2.6
25	439593	AW247529	Hs.6793	platelet-activating factor acetylhydrolase	2.6
	450269	A1631883	Hs.239545	ESTs, Weakly similar to 2109260A.B cell	2.6
	419571	AW674962	Hs.91146	protein kinase D2	2.6
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.6
	444881	A1623268	Hs.192805	ESTs	2.6
30	420658	AW965215	Hs.130070	ESTs	2.6
	437634	AW263046	Hs.265158	ESTs	2.6
	426894	A1204209	Hs.143911	ESTs	2.6
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.6
	434171	BE274568	Hs.347349	KIAA0548 protein	2.6
35	410174	AA306027	Hs.59461	DMF2P43425 protein	2.6
	427245	AA421022	Hs.97739	ESTs	2.5
	437085	AA743935	Hs.202029	ESTs	2.5
	400362	AF068264	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	2.5
40	452221	C21322	Hs.206057	hypothetical protein FLJ22442	2.5
	436079	AF085837	Hs.38348	ESTs	2.5
	437267	AA748180	Hs.159346	hypothetical protein FLJ21369	2.5
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	2.5
	427624	AA406245	Hs.24895	ESTs	2.5
45	435177	A018174	Hs.42936	ESTs	2.5
	449433	A1672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bindi	2.5
	447853	A1434204	Hs.164285	ESTs, Weakly similar to AFG1_YEAST AFG1	2.5
	416704	H77795	Hs.39785	ESTs	2.5
	401686			Target Exon	2.5
50	445677	H96577	Hs.6838	rat homolog gene family, member E	2.5
	413840	A1301558	Hs.146381	RNA binding motif protein, X chromosome	2.5
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	2.5
	420289	NS5354	Hs.96358	8-oxoguanine nucleic acid glycosylase	2.5
	421848	X15800	Hs.108886	collagen, type VI, alpha 1	2.5
55	421234	AA907153	Hs.190000	ESTs	2.5
	414598	A1094221	Hs.135150	lung type I cell membrane-associated gly	2.5
	420162	BE378432	Hs.95577	cyclin-dependent kinase 4	2.5
	451599	AW135417		hypothetical protein FLJ14464	2.5
	433523	H25882		ESTs	2.5
60	429125	AA446854	Hs.271004	ESTs, Weakly similar to 138022 hypother	2.5
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	2.5
	404748			ENSRP0000338177? Similar to kynurenic 3	2.5
	413507	BE145360	Hs.190064	ESTs, Weakly similar to 138022 hypother	2.5
	418886	AA993982	Hs.130658	ESTs	2.5
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	2.5
65	452367	U71207	Hs.22079	eyes absent (Drosophila) homolog 2	2.5
	436268	AW867451	Hs.107125	platelet-derived vesicle associated protein	2.5
	459527	AW977556	Hs.291735	ESTs, Weakly similar to 178885 serinotri	2.5
	450543	A1394037	Hs.170296	Homo sapiens cDNA: FLJ22090 fs, clone H	2.5
70	434818	AA605097	Hs.5396	ESTs	2.5
	444534	AW271626	Hs.42294	ESTs	2.5
	452113	A1853393		gb.wml1a02.x1 NCL_CGAP_1M4 Homo sapiens	2.5
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fs, clone MA	2.5
	434012	AA621425	Hs.186256	ESTs	2.5
75	447143	AW292408	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv	2.5
	445955	AHS3006	Hs.155374	ESTs	2.5
	419817	AA743434	Hs.193778	ESTs	2.5
	457886	AA781745	Hs.126820	Homo sapiens, clone IMAGE:4299555, mRNA,	2.5
	431454	AW975080	Hs.229218	ESTs	2.5
80	425016	BE245272	Hs.154198	E4F transcription factor 1	2.5
	427513	A1476318	Hs.192490	ESTs	2.5
	441318	A1078234	Hs.176130	ESTs	2.5
	424830	AW270580	Hs.189511	ESTs, Weakly similar to putative p150 (H	2.5
	414271	AK909275	Hs.73871	protein kinase C binding protein 1	2.5

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5	445089	A1860021	Hs.345028	ESTs. Moderately similar to A47582 B-cell	2.5
	411983	A436798	Hs.117078	Homo sapiens cDNA: FLJ23028 fs, clone L	2.5
	408292	AW178383	Hs.282700	gb.RC3-HT0105-010999-002-H08 HT0105 Homo	2.5
	445862	A1860097	Hs.282700	ESTs	2.5
	448970	AW138892	Hs.30148	gb.UA-H.D1-acc-a-06-0.U1.s1 NC1_CGAP_Su	2.5
10	459200	Y09305	Hs.30148	homeodomain-interacting protein kinase 3	2.5
	422527	BE336857	Hs.119787	transforming growth factor, beta-induced	2.5
	433388	A142672	Hs.295539	hypothetical protein FLJ22191	2.5
	430222	A1067737	Hs.122810	Homo sapiens cDNA FLJ11489 fs, clone HE	2.5
	441265	R05350	Hs.171535	ESTs	2.5
15	441627	AA547552	Hs.58086	branched chain aminotransferase 1, cytos	2.5
	438714	AA814859	Hs.294112	ESTs	2.5
	441020	W75233	Hs.35962	ESTs	2.5
	418291	BE303489	Hs.265036	hypothetical protein MGC4126	2.5
	434267	A1205589	Hs.116243	ESTs	2.5
20	466821	W03766	Hs.116243	tropomodulin 3 (ubiquitous)	2.5
	402615			CI003844*gyf912550[ref](NP_036483.1) of	2.5
	416545	H95279	Hs.293788	gb.yc070022.s1 Soares fetal liver spleen	2.5
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.5
	444884	A1201094	Hs.148540	ESTs	2.5
25	440826	AW083618	Hs.344256	ESTs. Moderately similar to ALU2_HUMAN A	2.5
	431374	BE256532	Hs.251871	CTP synthase	2.5
	468993	A1007798	Hs.343628	acylfurantransferase 4B (beta-galactosidase	2.5
	422484	AA568770	Hs.123158	Homo sapiens cDNA FLJ12630 fs, clone NT	2.5
	442604	AW000118	Hs.131257	ESTs	2.5
30	402945	AA304053	Hs.13836	ESTs. Weakly similar to 138022 hypothet	2.5
	451530	A1731447	Hs.13836	gb.n13a15.gy NC1_CGAP_Cot Homo sapiens	2.5
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.5
	430426	AA478807	Hs.125173	ESTs	2.5
	418526	BE019020	Hs.65838	solute carrier family 16 (monocarboxylic	2.5
35	402590			Target Exon	2.5
	442085	AA975688	Hs.159965	ESTs	2.5
	448148	NM_016578	Hs.20509	HBV pX associated protein 8	2.5
	432888	T86823		gb.yd81a08.s1 Soares fetal liver spleen	2.5
	424126	AA335835	Hs.96917	ESTs	2.5
40	458727	A1064494	Hs.96917	gb.RC-BT113-060495-024 BT113 Homo sapien	2.5
	407989	AW135208	Hs.256092	ESTs	2.5
	404571	F98092	Hs.66087	NM_015902* Homo sapiens progesterin induce	2.5
	432222	NM_001262	Hs.4584	ESTs	2.5
	420608	BE548277	Hs.103104	cyclin-dependent kinase inhibitor 2C (p1	2.5
45	432688	AA586001	Hs.43296	ESTs	2.5
	406871	AA893857	Hs.180842	ribosomal protein L13	2.5
	443516	AA325621	Hs.9527	apoptosis related protein APP-3	2.5
	446895	BE621800	Hs.79444	putative small membrane protein NID67	2.5
	426514	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.5
50	437267	AW511443	Hs.258110	ESTs	2.5
	405251	AL040927	Hs.210422	ESTs	2.5
	431198	AL047634	Hs.221913	ESTs	2.5
	413944	AW001579	Hs.9545	Homo sapiens mRNA for KIAA1741 protein,	2.5
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-ase	2.5
55	428032	AW997704	Hs.11493	Homo sapiens cDNA FLJ13536 fs, clone PL	2.5
	422017	NM_003807	Hs.110776	STAT induced STAT inhibitor-2	2.5
	424662	NM_002670	Hs.151536	RAB13, member RAS oncogene family	2.5
	423779	AW071837	Hs.57971	ESTs	2.5
	402863			Target Exon	2.5
60	465421	A1279978	Hs.22547	ESTs	2.5
	439019	AF085902	Hs.271737	ESTs	2.5
	412577	222968	Hs.74076	CD163 antigen	2.5
	404891			Target Exon	2.5
	418043	T18167	Hs.83666	ets variant gene 1	2.5
65	449482	AW294078	Hs.171992	ESTs	2.5
	429300	BE243933	Hs.108642	zinc finger protein 22 (KIX 15)	2.5
	429109	AL008537	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.5
	460587	A101635	Hs.207077	ESTs	2.5
	414385	X00442	Hs.75990	haptoglobin	2.5
70	440473	BE562314	Hs.58111	Homo sapiens, clone IMAGE-3677165, mRNA,	2.5
	406851	AA608784		major histocompatibility complex, class	2.5
	414821	M03335	Hs.77424	Fc fragment of IgG, high affinity Ia, re	2.5
	417663	R01743	Hs.180451	ESTs	2.5
	425341	X72874	Hs.2293	phosphorylase kinase, alpha 1 (muscle)	2.5
75	450953	H43540	Hs.25292	ribonuclease H1, large subunit	2.5
	407198	H91679		gb.yv0407.s1 Soares fetal liver spleen	2.5
	411742	AW247593	Hs.71819	eukaryotic translation initiation factor	2.5
	409449	H11341	Hs.13366	Homo sapiens cDNA: FLJ23557 fs, clone L	2.5

TABLE 14B:

Phy	Unique Exon prohesat identifier number
CAT number	Cone cluster number
Accession	Corbank accession numbers

80	Phy	CAT number	Accession
	408292	1050507_1	AW178363 AW346011 AW845964 AW845988 AW845977 AW846002

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	409157	110863_1	AA064631 AA722000 AA064793
	409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA0100017 AA079891 AA113255 AA075168 AA062764 AA083380 N04829 AA084752 AA076512 AA085119 AA085206 AA085045
5	410888	122582_2	AAW09324 BE144877 BE144956
	411537	124898_1	BE073250 BE073378 BE073379 AAW050533 AAW050529
	411543	124917_1	AAW051248 AAW0511425 AAW0508095 AAW051021 AAW050905
	411565	1249756_1	AAW051728 AAW051607 AAW051821 AAW051702 AAW051547 AAW051727 AAW051658 AAW051617 AAW051628
	411671	125369_1	BE049094 AA0700765 H06770 AA094646 R02483 C03868 N56170
10	411688	125407_1	AAW053440 T08109 AAW057085
	411962	126744_1	AAW09050 AA070525 W47733
	412021	1272156_1	AAW085592 AAW086594 AAW085579 AAW085651
	412135	1272145_1	AAW085309 AAW085290 AAW085307 AAW085397 AAW085378 AAW085402 AAW085403 AAW085311 AAW085298 AAW085390 AAW085488 AAW085468 AAW085481 AAW085288
15	412799	132817_1	A267606 AA121045 AA126521
	412811	132943_1	H03632 AAW097370 AA252014 R13591 AA121201 D060420 BE263263 BE047862 Z41952 AA424991 AA093507 AA053108 AA599000 AA091148 AA598689 R33887 AA13482 AAW016452 H06383 R41807 A0364268 AA0620528 A241940 AAW089149 AAW090733 AAW088875 Z38240 AA121202 R17734
20	413866	140720_1	Z43567 H24119 AA134240
	414372	142309_1	AA143654 AAW753140 AA233770 AAW970865 AA596075 AA492132
	414686	1511318_1	C17535 D59244 D58878 D70990
	415131	1523680_1	D61119 D81506 D81734
	416422	1938311_1	H60457 H68709 H73526 H54335 R87154
	416569	1601567_1	H64691 R03444 R03458 R05590
	416971	162676_1	H69714 R05975 W04283
	416913	163001_1	AAW534714 BE161007 BE162500 AAW749902 AA768064 BE162458 BE161005 AA159049 AAW513465 BE161006 BE162459
25	419896	1888662_1	Z99362 Z99363
	420332	192079_1	BE238633 AAW098316 A259818 AAW043305 R14744 AA580388 BE071923 R36280
	420670	195442_1	AAW97277 AA533021 AA275187
	420886	197344_1	AAW05453 AA281379
	422551	217767_1	AAW967284 AA312192 AA3112203
30	422713	231290_1	AAW54182 AAW54188 AA323993
	424029	234177_1	F11690 AAW095370 AA333636 D06330
	424200	236595_1	AA337221 AA336756 AAW096196
	424686	242486_1	AA345504 AA345251 AAW063243
	424947	245247_1	R17952 AA348059 AAW095960 AAW095982 AA565552 AA070702 AA9479510 R05973
35	425146	247244_1	AAW954627 AA594529 AA351258 R25935
	425331	250195_1	AAW06128 AA355363 AA427363
	426503	261823_1	AA380153 AA380233 AAW095329
	429163	300543_1	AA084766 AAW974271 AA592975 AA447312
40	429640	310884_1	W025215 AA461078 AA461391
	430635	319641_1	AAW095445 AAW096870 AA430922 BE350425
	430968	326269_1	AAW972830 AA527647 AA489320 AA507382
	432044	340773_1	AAW972727 AA524825 AAW972733
	432363	345489_1	AA534489 AAW970240 AAW570233
45	432886	355780_1	H06623 AA521425 AA732332 AA595680 AA570737
	433009	357371_1	AA476168 AA573621 H02014 R06670
	433523	368873_1	H25882 AAW65533 AAW149901 AA572917 AA088500 AA06466 AA336390 AAW084390 AAW084320
	433835	374758_1	AAW06185 AA610063 AA693069 AA693075
	434589	38925_1	AF147363 T47219 T47218
50	435065	395325_1	BE064051 BE064305 AA483613 H99644
	435542	407744_1	AA687376 H74234 AAW975503
	436608	42361_3	AA628930 AA126603 BE504035
	437034	431713_1	AA42643 AA080875 AAW97668
	437437	43709_1	AA422683 AA296516 AAW097533 AA1186390 AA1356195 AA148427 R22748 A033624 AA63853 H05327 AAW075751 BE561645 AA375533 BE017136 AA236444 T09346 AA247450 N65777 W38725 AA143846 AA084048 AA092229 AA051464 W04713 R11251 W13656 AA042319 AA482976 A1224533 H
55	437945	44580_1	T78519 H58988 U72516
	438458	457837_1	AAW97516 AA080807 D25648
	439518	47334_1	W07632 AF086341 W77230
	439533	47345_1	W76021 AF088052 W72465
60	439566	47387_1	AF086387 W77884 W72711
	439710	47550_1	AF086543 W96291 W96225
	441121	51021_1	AAW07526 AA0914761 AA473721 AA473237 AA022165 AA554007 AA127551 N90525 AAW973623 AA447991 AA243852 BE328550 AA148171 AA359627 AA015068 AA335657 AA232991 AAW016855 AA096902 AA233101 AA127550 BE512923
	442476	543547_1	AF069475 AF069477 AF069476
65	444016	58989_1	AA4448154 AF647571
	444168	593829_1	AA739078 AA126285 H2814
	446821	69435_1	W03766 AA337775 AAW06500 AAW60726
	448970	791254_1	AAW135852 AA038298 AA613164 AA63668 AA611082
70	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AAW063569 BE161640 AA039600 BE165542 AAW296554 AA323193 AA235370 AAW75770 AA06714 AA725977 RA4332 D03044 A203107 F07491 R03360 R25094 AA913631 AA984062 BE1382 AA016320 AA5526 T61415 AA331486
	450166	8267_1	AA429504 RA1304 AA729467 H06041 AA007226
	450375	83327_1	AA009647 AA313254 AA374293 AAW05405 H04410 AAW060284 AA151166 BE157467 BE157601 H04384 AA44291 AAW563674 H04021 H01532 AA190993 H02313 H09905 H01642 AA852876 AA113758 AA628915 AA746952 AA161014 AA099554 H69067
	450906	836_1	NM_004460 I095778 U76833 AAW03005 AAW471133 C02434 W45237 AAW793518 BE070112 AA587479 AA584429 AA190535 AA446661 AA478772 AAW022661 AA582535 AA599775 AAW613870 AA435793 AAW094230 AA051766 AA200109 AA080296 AA439511 AAW09728 W42634 AA052504 AA402569 AA695653 AWO
75	450625	84032_1	AAW970187 AA513951 AA010406
	451129	859870_1	BE072881 BE072946 A7672181
	451230	868645_1	A7914747 A791327 AAW086089
	452113	898654_1	AAW08531 BE177422
80	452503	903_2	X57522 AAW29647 A346197 AA304683 L12005 L12006 L12017 L12008 L12013 NM_000950 F05770 F07620 X57521 R12624 T4482 AA346259 AAW062508 AA080476 F08426 H23432 AA313737 AA383782 H78052 AA847441 AA487637 AA315770 AA353161 AA819778 AA054458 AA346733 AA381447 A04

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453331 96214_1 A120065 123681 N77468 H51833 AA14727 R75732 C18450 R72999 A056755 T49904 H03868 AA41158 R33395 AA410596 T48869 D63292
R31961 H12498 H02666 AA035018 R75957 AB03329 R27526 C36203 AB009932 A1808765 R78948 AA41149 AA376929 A378760 A378620 T48870
R7390

5 453682 977454_1 T75703 T96307 ALD793725
454177 1049393_1 AW087321 AW087352 AW177104 AW087319 AW087115 AW087344 AW1807324 AW17816 BE141575 AW045849 AW087105 AW045866 BE140942
AW087178 AW087167 AW087396 AW087320 AW087306 AW045866

10 454354 1129589_1 AW389896 AW389896 AW389906 AW09203 AW389873
454457 1207214_1 AW753456 AW753036 AW054868 AW054862
454765 122507_1 AW087189 AW087201 AW1813574
454765 122506_1 AW081920 AW045420
454860 1237372_1 AW083567 AW053537 BE160187
454968 1247029_1 AW049045 AW047956 AW049039 AW047957 AW048279 AW048998 AW048034 AW048033
455104 1253737_1 BE054863 BE153688 AW056751 BE153820 BE064737 BE153674 BE064130 BE065062 BE153536 AW058622 BE155079 BE084651 BE153665
BE046560 BE064601

15 455409 1283355_1 AW053632 AW053609 AW036657 AW036611 AW036739 AW036734 AW036779 AW036688 AW036659 AW036738 AW036827 AW036737 AW036736
AW036740 AW036733 AW036777 AW036830 AW036834 AW036829 AW036772 AW036638 AW036658 AW036636 AW036774 AW036778 AW036766
AW036776 AW036831 AW9

20 455481 1293182_1 AW0494317 AW049322 AW049329 AW048316 AW048298 AW048330 AW048325 AW048324
455646 1348557_1 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
455778 1364506_1 BE068746 BE068802 BE068755 BE068876 BE068947 BE068881 BE068892
455899 1381547_1 BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452
456304 176820_1 A0520973 A173407 A0520884 AA225796 AA225060 AA225101
457354 328154_1 AW071037 A4558019 AA452245

25 457876 42814_2 A0521940 N67106 A744264 AA080846 AAG43417 AAG43416 Z70715
458199 504866_1 AW136417 A114106 A034990 A091670 A523802 AW0572908 A0458690 A024374 A0305972 A400702 A1337535 A0568111 A0521308 A0492336
A150775 A072904 A0665077 A0371810 A0509139 AW082128 A0335251 A087192 AW051174 A023232 A053689 A0207791 A070910 A032047
A04

TABLE 14C:

Ref: Unique number corresponding to an Ecos protease
 Pept: Sequence: The 7 digit numbers in this column are GenBank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 N1_positon: Indicates nucleotide positions of predicted exons.

	Pept	Ref	Strand	N1_positon
35	400492	9213749	Minus	123881-124090
	400533	6981826	Minus	277132-277595
	400645	8117663	Minus	58471-58716
40	400658	8118459	Minus	73325-73644
	400780	8131663	Minus	118372-118619
	400850	1927150	Minus	4506-4601
	400924	7107613	Minus	30309-30498
	401272	9797373	Minus	98374-98509
45	401454	5186023	Minus	114659-114832
	401696	3417290	Minus	46209-46401
	401702	1871197	Minus	68182-68325
	401841	7864537	Plus	80988-80006,51920-92085
	402032	7636761	Plus	62253-62475
50	402082	8117478	Minus	190046-190183
	402229	9965022	Minus	15739-15951,16166-16779
	402239	7690131	Plus	38175-38304,42133-42266
	402260	3399865	Minus	113765-113791,115653-115765,116808-116940
	402274	2035596	Plus	5604-6527
55	402604	9906420	Plus	20393-20767
	402615	9926801	Plus	131590-132157
	402799	3355547	Plus	35716-36899
	402855	9662653	Minus	50763-50909
	402936	8894303	Plus	51625-51771
60	403011	6693597	Minus	3468-3623
	403104	7331404	Minus	41800-41973
	403108	8880935	Plus	83253-83667
	403212	7630897	Minus	156037-156210
	403267	7887182	Plus	116078-121885
65	403288	8081479	Plus	133763-133899,135813-135958
	403290	8883176	Plus	19286-20076
	403291	7238870	Plus	59177-95435
	403349	8569773	Minus	167815-168374
	403361	8570313	Minus	112496-112687
70	403431	7139839	Plus	96509-96690
	403481	9965004	Plus	33406-33633
	403696	3135242	Minus	143467-143634
	403790	8084957	Minus	87826-87947,89835-90002
	403849	7708855	Plus	35043-95519
75	403942	7111825	Minus	99806-99757
	403961	7596876	Minus	110393-110603
	403969	8569909	Plus	31237-31375,32405-32505
	404053	3548785	Plus	61797-64205
80	404120	7342152	Plus	133775-136000
	404150	7534086	Plus	162811-162943
	404170	9930793	Plus	168838-169248
	404209	5006246	Minus	11247-11514
	404272	9885189	Plus	83207-83355,84358-84496,90519-90720,91371-91447

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5	404407	7329316	Minus	48154-48499
	404571	7249169	Minus	112450-112648
	404584	9857511	Plus	138651-139153
	404592	9943965	Minus	39067-39275
10	404632	9796668	Plus	45296-45329
	404748	7263437	Plus	11446-11591
	404891	7329392	Plus	84974-85125
	405046	7596829	Minus	4373-4528
15	405141	8980911	Plus	93861-10054
	405183	7209040	Plus	12335-12553
	405238	7249119	Minus	51728-51836
	405348	2914717	Minus	43310-43462
20	405516	9454624	Plus	112707-112876,113676-113854
	405558	1621110	Plus	4502-4641,5553-6083
	405605	5836195	Minus	117070-117270
	405717	9588573	Plus	11275-11973
25	405760	6066938	Minus	37424-38045
	405863	7657610	Plus	49419-49620
	405941	6788796	Plus	2798-3444
	405950	6699623	Minus	20339-20746
30	406290	5686274	Plus	8711-9368
	406395	9256242	Minus	20825-20960
	406478	9857502	Plus	65144-65323,68553-68950
	406481	9854741	Minus	91439-91579

TABLE 15A: ABOUT 1033 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES
 Table 15A lists about 1033 genes up-regulated in glioblastoma compared to normal normal adult tissues. These were selected from 5960 probesets on the Affymetrix/HuEos H03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" glioblastoma level was set to the 85th percentile amongst various brain tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove genetic background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.
 Pkey: Unique Eos probe/identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 RI: Ratio of GLIOBLASTOMA TO NORMAL ADULT TISSUES

Pkey	ExAccon	UnigeneID	Unigene Title	RI
427343	A850044	Hs.178377	protein kinase C binding protein 2	60.5
431917	D16181	Hs.2868	peripheral myelin protein 2	54.9
418375	NM_003081	Hs.84399	synaptosomal-associated protein, 25kD	53.1
428321	A899994	Hs.2868	peripheral myelin protein 2	49.6
409389	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	45.4
425147	AL133751	Hs.4774	Homo sapiens mRNA; cDNA DKFZ761C1712 (f	43.9
413472	BE242870	Hs.75379	solute carrier family 1 (glut high affi	42.7
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	42.3
456759	BE259150	Hs.127792	delta (Drosophila)-like 3	39.1
428638	N46614	Hs.163095	hypothetical protein FLJ12015	37.9
417183	RS2089	Hs.172717	ESTs	37.6
426325	D28114	Hs.163309	myelin-associated oligodendrocyte basic	36.5
425088	A4663372	Hs.163955	hypothetical protein FLJ12015	34.3
429307	D60642	Hs.316369	g13HUA0252508 Human fetal brain (Tfujira	33.9
449494	AW227014	Hs.133315	Homo sapiens cDNA: FLJ23075; nt, clone L	33.9
423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZ761J1324 (f	32.7
429276	AF056085	Hs.198612	G protein-coupled receptor 51	32.3
413333	M74026	Hs.75297	fibroblast growth factor 1 (acidic)	27.9
420133	AK068769	Hs.105201	ESTs	27.2
412733	AA984472	Hs.74554	KIAA0080 protein	27.6
425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	27.3
416829	AB013805	Hs.80220	calnexin (calnexin-associated protein), d	27.1
421460	Z48051	Hs.141338	myelin oligodendrocyte glycoprotein	25.2
402604			Target Ecos	25.2
437204	AL110216	Hs.22826	ESTs, Weakly similar to I55214 salivary	24.3
422656	A870435	Hs.1569	LM homeobox protein 2	23.6
447359	NM_012093	Hs.18288	adenylyl kinase 5	23.3
426678	BE466204	Hs.47448	ESTs	22.9
435708	AI362949	Hs.75169	ESTs	22.9
429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	22.7
429229	AC015450	Hs.226331	ESTs	22.2
409395	U46145	Hs.339678	dystrobrevin, alpha	22.4
425799	T08133	Hs.182906	Homo sapiens mRNA for KIAA1872 protein,	21.9
425057	AA826434	Hs.1619	achoele scute complex (Drosophila) homol	21.3
444378	RI1329	Hs.47850	neurotrophic tyrosine kinase, receptor,	21.0
444513	AL132124	Hs.71717	glutamate receptor, ionotropic, AMPA-1	21.0
419078	M93119	Hs.85584	insulinoma-associated 1	21.0
425048	H05468	Hs.164502	ESTs	20.9
453392	U23752	Hs.32964	SRF (sex determining region Y)-box 11	19.3
422653	AB015337	Hs.133466	slit (Drosophila) homolog 1	19.3
418110	RI3323	Hs.217754	hypothetical protein FLJ22202	19.2
447004	AW26968	Hs.157539	ESTs	18.6
439415	F05538	Hs.4273	ESTs	18.6
441497	RS1064	Hs.23172	ESTs	18.5

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425523	AB0071	HL 15824	RIAA0479 protein
413597	AF004285	HL 117183	ESTs
433551	AY88544	HL 12450	proctoderm 9
426392	JI10233	HL 2285	secretory granule, neuroendocrine protein
435847	AD73006	HL 34714	ESTs
418338	NM_002522	HL 84154	neuronal pentonin 1
437268	AI754847	HL 227571	regulator of G-protein signaling 4
408064	D51408	HL 21825	ESTs
425817	MC2062	HL 158917	histone H4 (zodhiar-associated protein), a
422980	N45659	HL 76722	a CCAAT-henriched binding protein (CEBP),
448302	AI480208	HL 182906	Home sapiens mRNA for KIAA1872 protein,
429466	MB8355	HL 12827	ESTs
441350	AB202658	HL 7782	prostate/placental antigen MA2
448672	AF55511	HL 225106	ESTs
448743	AB032962	NL 21896	KAA1136 protein
415910	U02350	HL 78913	chemokine (C-X-C) receptor 1
441285	NM_002374	HL 167	microtubule-associated protein 2
431015	NM_005248	HL 2714	brainhead box G18
431941	AK000106	HL 272227	Home sapiens cDNA FLJ20099 (fr. clone CO
433800	U034361	HL 135150	lung type-II cell membrane-associated gly
416370	N50470	HL 203659	ESTs, Weakly similar to 130202 hyphoth
425979	AF050291	HL 5823	hyphothetical protein FLJ10493
440264	AB020694	HL 11217	KIAA0877 protein
444783	AK001468	HL 62180	anillin (Drosophila Scratch homolog), act
448595	AB014454	HL 21572	ESTs
441440	AB007891	HL 1495	protein 466 kDa gene product
424982	NM_003597	HL 194704	tetrachrinch, glioma inactivated 1
428780	AL119344	HL 13326	ESTs, Weakly similar to 2004395A chromos
429516	AI049662	HL 246858	ESTs
441264	AI139123	HL 103042	ribitolubule-associated protein 1B
425842	AI73881	HL 31358	Home sapiens cDNA FLJ13458 (fr. clone PL
405852	AI436323	HL 31141	Home sapiens mRNA for KIAA1568 protein,
412959	DB7458	HL 75090	KIAA0282 protein
439199	BA6073	HL 26299	ESTs
422419	FS3536	HL 25339	ESTs
445495	BE622641	HL 38489	ESTs, Weakly similar to 130202 hyphoth
415849	U02059	HL 6806	ESTs
425272	AB85742	HL 228474	ESTs
425744	AF265702	HL 246107	Home sapiens mRNA: cDNA DKFZ450430E2 (fr
426344	HA1821	HL 322459	transcriptional activator of the c-fos p
415734	NM_014747	HL 78748	KIAA0237 gene product
426269	FI15302	HL 168590	Home sapiens mRNA: cDNA DKFZ566A1046 (fr
444119	RI12131	HL 184251	ESTs, Weakly similar to T26586 homology
429849	AK42132	HL 14643	ESTs
434277	X77748	HL 3786	glutamate receptor, metabotropic 3
427897	NM_017413	HL 303084	apelin; peptide ligand for APJ receptor
435941	U39817	HL 36820	Brown lipodystrophy
424120	TB0579	HL 292070	ESTs
418738	AV338633	HL 6682	solute carrier family 7 (cationic amino
413905	BE241596	HL 69547	myelin basic protein
424484	U221919	HL 69547	Home sapiens protein FLJ10582
445939	W60063	HL 58446	ESTs
409638	AV450420	HL 21335	ESTs
441016	AV138653	HL 25845	ESTs
429037	X51895	HL 194705	H.sapiens GENX-5624 mRNA, 3' UTR
437034	UB5450	HL 194705	Home sapiens thymineless lethal DTN 3 (DTN
445372	AB020604	HL 14945	long allyl-acyl-CoA synthetase 2 gene
425984	AV836277	HL 165636	Home sapiens protein DKFZ2761C07121
424432	AB037821	HL 146958	proctoderm 10
424953	AV256112	HL 153548	Home sapiens cDNA FLJ13303 (fr. clone OV
425640	T03930	HL 158640	UDP-galactose-4-epimerase 2 (UDP-aldose
438380	T06430	HL 6194	chondroitin sulfate proteoglycan RHA48A
446658	AV863357	HL 7847	ESTs
425052	Z44514	HL 7847	Home sapiens mRNA for KIAA1753 protein,
409651	AI18187	HL 103538	ESTs
427978	NM_016625	HL 191381	Home sapiens protein
427701	AA411101	HL 243886	nuclear autoantigenic sperm protein (his
431968	AC023032	HL 77202	protein kinase C, beta 1
423896	AN254729	HL 274463	ESTs
414547	N71831	HL 256358	Home sapiens mRNA: cDNA DKFZ46450526 (fr
419249	X14767	HL 89768	gamma-aminobutyric acid (GABA) A recepto
445041	T64183	HL 252982	solute carrier
446782	AB53044	HL 144006	ESTs
4251552	AI122113	HL 311663	ESTs
447611	AF160692	HL 12450	proctoderm 9
447804	AA776654	HL 190309	ESTs
443795	AA446952	HL 190125	basic-helix-loop-helix-PAS protein
415109	FS2795	HL 25594	serpinlike 13 receptor, alpha 2
419683	AW52691	HL 93485	Home sapiens cDNA: cDNA DKFZ761D191 (fr
435191	RI5612	HL 4817	ESTs
419271	UA3401	HL 238532	Home sapiens clone 2464 mRNA sequence
429927	NM_001115	HL 25252	adenylate cyclase 8 (brain)

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415293	R49462	Hs.105541	ESTs	9.9
440184	A6002297	Hs.7022	dedicator of cyto-kinesis 3	9.8
452526	W38537	Hs.280740	hypothetical protein MGC3040	9.8
427304	AA61526	Hs.163863	ESTs	9.6
420547	AF151140	Hs.39736	gonadotropin-regulated testicular RNA he	9.6
421659	NM_014459	Hs.106511	protocadherin 17	9.6
426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	9.5
428656	X05608	Hs.211584	neurofilament, light polypeptide (8kD)	9.5
447101	N72185	Hs.441499	ESTs	9.5
442613	A004002	Hs.130622	Kv channel-interacting protein 1	9.5
454027	R40192	Hs.21527	Human DNA sequence from clone GSI-115M3	9.5
445102	AW204610	Hs.22270	ESTs	9.5
435793	AB037734	Hs.4953	KIAA1313 protein	9.5
437948	AA772820	Hs.303827	ESTs	9.5
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	9.4
415170	R44386	Hs.164578	ESTs	9.3
415486	H12214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	9.2
435501	AW051819	Hs.129508	KIAA0591 protein	9.2
416072	AL110370	Hs.79500	growth associated protein 43	9.2
442910	A1365130	Hs.11307	ESTs, Weakly similar to T19326 hypofethi	9.1
438090	AA777381	Hs.291530	ESTs, Weakly similar to ALLUC_HUMAN !!!	9.1
425187	AW014486	Hs.22509	ESTs	9.1
424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fis, clone Y7	9.0
430091	A8032958	Hs.233023	KIAA1132 protein	9.0
427540	R12014	Hs.20976	ESTs	9.0
447198	D61523	Hs.283435	ESTs	9.0
448611	A1870394	Hs.197075	ESTs	8.9
444124	R43097	Hs.6818	ESTs	8.9
451996	AW514021	Hs.245510	ESTs	8.8
454048	H05626	Hs.6921	ESTs	8.8
412285	N59006	Hs.261133	ESTs	8.8
433597	AA708205	Hs.100343	ESTs	8.7
447342	A1199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	8.6
450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	8.6
415102	AW245808	Hs.279727	ESTs; homologous of PEM-3 [Clona savignyi]	8.5
423135	N67655	Hs.26411	ESTs	8.5
418097	R45137	Hs.21868	ESTs	8.4
420602	AF060877	Hs.99236	regulator of G-protein signaling 20	8.4
419721	NM_001650	Hs.288650	acoupoint 4	8.4
448300	AW56289	Hs.346514	ESTs	8.4
436954	AA740151	Hs.130425	ESTs	8.3
425354	UG0207	Hs.155935	complement component 3a receptor 1	8.3
424997	AL138167	Hs.96920	ESTs	8.3
442710	A015581	Hs.23210	ESTs	8.2
448625	NM_014253	Hs.23210	odt (odd Olfen-m, Drosophila) homolog 1	8.2
451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2/6	8.2
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	8.0
449605	AW138281	Hs.198416	ESTs	8.0
407885	AW965888	Hs.100826	ESTs	8.0
414175	A1038876	Hs.103849	hypothetical protein DKFZp761D112	7.9
429946	R49390	Hs.254129	KIAA1678	7.9
402093	N51002	Hs.306480	Homo sapiens mRNA, cDNA DKFZp761E2112 f	7.9
455501	A0369580	Hs.316	SRY (sex determining region Y)-box 2	7.9
406799	D11928	Hs.76845	phosphoserine phosphatase-like	7.8
415279	F04237	Hs.1447	glial fibrillary acidic protein	7.8
429918	AW873986	Hs.119383	ESTs	7.8
449433	A672096	Hs.3012	ESTs, Weakly similar to S26650 DNA-bndi	7.8
422411	AW749443	Hs.22511	ESTs	7.7
448902	Z45998	Hs.22543	Homo sapiens mRNA, cDNA DKFZp761H1912 f	7.7
452355	N54926	Hs.29202	G-protein-coupled receptor 34	7.7
447414	D62343	Hs.74736	neuroblastoma (nerve tissue) protein	7.7
407168	R45175	Hs.117183	ESTs	7.6
448555	A1536697	Hs.159963	ESTs	7.6
428536	A143138	Hs.2298	vesinin-like 1	7.6
408947	AL080093	Hs.43117	Homo sapiens mRNA, cDNA DKFZp564N1602 f	7.6
423682	U73734	Hs.57206	huntingtin interacting protein 1	7.6
435624	AF218942	Hs.24889	formin 2	7.6
440105	AA694010	Hs.6932	Homo sapiens clone Z8809 mRNA sequence	7.6
412068	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	7.5
445588	H00918	Hs.265744	KIAA1796 protein	7.5
417160	N76497	Hs.1737	proteolipid protein 1 (Pelizaeus-Merzbac	7.5
423361	AW170055	Hs.47628	ESTs	7.5
456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	7.5
458332	A000341	Hs.222491	ESTs	7.4
409902	A337658	Hs.156351	ESTs	7.3
448321	NM_005883	Hs.20912	adenomatous polyposis coli like	7.3
420345	AW295230	Hs.25231	ESTs	7.2
402855		NM_001839	Homo sapiens calponin 3, acid	7.2
424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	7.2
426741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	7.2
448986	H42169	Hs.347310	hypothetical protein FLJ14627	7.2
415651	A1207162	Hs.3815	stathmin-like protein RB3	7.1
412709	AL023237	Hs.74518	KIAA0027 protein	7.1

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	451621	A1879148	Hs.26770	fatty acid binding protein 7, brain	7.1
	445745	A8007924	Hs.13245	KIAA0455 gene product	7.1
	439451	AF086270	Hs.27854	heterochromatin-like protein 1	7.1
	418030	BE205753	Hs.83321	neurorubin B	7.1
5	400922	AA250737	Hs.72472	GMP-R18	7.1
	407748	AL047909	Hs.38176	KIAA0606 protein, SCN Circadian Oscillator	7.0
	404035	AL042201	Hs.21273	transcription factor NYD-5p10	7.0
	414696	AF020020	Hs.76918	Niemann-Pick disease, type C1	7.0
10	417117	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	7.0
	400152	AB002376	Hs.7006	KIAA0378 protein	7.0
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	7.0
	454293	H49739	Hs.134013	ESTs, Moderately similar to HK65_L_HUMAN H	7.0
	447197	R35075	Hs.172619	glt-y88801.11 Soares placenta No.2HP Homo	7.0
15	428814	AF036943	Hs.172619	myelin transcription factor 1-like	6.9
	416836	D54745	Hs.80247	cholecystokinin	6.9
	447350	A1375572	Hs.172634	ESTs	6.9
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypothesis	6.9
20	430339	AW023323	Hs.121070	ESTs	6.9
	444396	T65213	Hs.4257	ESTs	6.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to T08022 hypothesis	6.9
	438330	AW450672	Hs.257316	ESTs	6.8
	410305	AF030409	Hs.62185	solute carrier family 9 (proton/hydrogen	6.8
	421141	AW117261	Hs.125914	ESTs	6.7
25	412788	AA120960	Hs.198416	ESTs	6.7
	411078	A1220020	Hs.182364	Coccolip	6.7
	443455	AB001025	Hs.5349	gamma-lin receptor 3	6.7
	440769	H65037	Hs.38173	ESTs	6.7
	441523	AW1514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN III	6.7
	414214	D49958	Hs.75819	glycoprotein M6A	6.6
30	439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	6.6
	437036	A571514	Hs.133922	ESTs	6.6
	429239	AA448419	Hs.45209	ESTs	6.6
	434164	AF0207019	Hs.148135	serine/threonine kinase 33	6.6
35	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	6.5
	452834	AA388827	Hs.109685	KIAA1688 protein	6.5
	441916	AA903571	Hs.129075	ESTs	6.5
	451516	A1800515	Hs.12024	ESTs	6.5
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.5
40	452461	N78223	Hs.108106	transcription factor	6.5
	453375	AA005447	Hs.114280	ESTs	6.4
	434811	AW971205	Hs.114280	ESTs	6.4
	424624	AB032947	Hs.151301	Ca2-dependent activator protein for sac	6.4
	429250	H6585	Hs.198308	tryptophan rich basic protein	6.3
45	414245	BE140072	Hs.75850	WAS protein family, member 1	6.3
	433447	L29195	Hs.3281	neuronal pentraxin II	6.3
	424922	BE386547	Hs.217112	hypothetical protein MGC10825	6.3
	426919	AL041228	Hs.148135	ELAV (embryonic lethal, abnormal vision,	6.3
	411411	AA345241	Hs.59860	ESTs, Weakly similar to KIAA1330 protein	6.3
50	415669	NM_026525	Hs.78649	serine (or cysteine) proteinase inhibitor	6.2
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.2
	433929	A1375499	Hs.27379	ESTs	6.2
	423346	A676877	Hs.127416	synaptotagmin 1	6.2
	448148	NM_016578	Hs.20029	HBV pX associated protein-8	6.2
55	412140	AA219691	Hs.73625	RA86 interacting, kinesin-like (tubulins	6.2
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.2
	420608	BE548277	Hs.103104	ESTs	6.2
	424085	NM_002914	Hs.135028	replication factor C (p130) 1 2 (40	6.2
	422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypothesis	6.2
60	428845	AL157579	Hs.153610	KIAA0751 gene product	6.1
	439274	AF086092	Hs.48372	ESTs	6.1
	447459	AW262580	Hs.147674	protocadherin beta 16	6.1
	425977	R15118	Hs.165570	Homo sapiens clone 25052 mRNA sequence	6.1
	453924	R49295	Hs.24880	ESTs	6.1
	449340	AW235786	Hs.195359	hypothetical protein MGC10564	6.1
65	420077	AW512260	Hs.87767	ESTs	6.1
	431721	AB032996	Hs.268004	KIAA1170 protein	6.1
	433701	AW445023	Hs.15155	ESTs	6.1
	430968	AW572830	Hs.15155	glt-EST1384525 MAGE resequences, MAGL Homo	6.1
70	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.1
	456723	Z43902	Hs.4748	adenylylate cyclase activating polypeptide	6.0
	448681	AL102781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.0
	429900	AA460421	Hs.30875	ESTs	6.0
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALLU_HUMAN A	6.0
	423281	AK001729	Hs.274263	hypothetical protein FLJ10377	6.0
75	448243	AK935771	Hs.52620	integrin, beta 8	6.0
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	6.0
	419704	AA428104	Hs.45057	ESTs	6.0
	430936	AL134451	Hs.197478	ESTs	6.0
	423409	AW117207	Hs.98523	ESTs	6.0
80	433244	AB040943	Hs.271285	KIAA1510 protein	6.0
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDN	6.0
	408096	BE750162	Hs.83765	dihydrofolate reductase	6.0
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	6.0

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422544	AB018259	Hs.118140	KIAA0176 gene product	6.0
413627	BE182082	Hs.246973	ESTs	6.0
419985	H66373	Hs.5856	ESTs, Highly similar to bA39316.3 (Hsa)	6.0
410386	AL267589	Hs.302689	hypothetical protein	5.9
429183	AB014604	Hs.197965	KIAA0704 protein	5.9
430188	AL040242	Hs.234794	Homo sapiens mRNA; cDNA DKFZ5648003 (H)	5.9
441102	AA973905	Hs.21365	intermediate filament protein syncoilin	5.9
448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
407182	AA312551	Hs.230157	ESTs	5.9
437372	AA323668	Hs.283631	hypothetical protein DKFZp547G183	5.9
433523	H29882	Hs.10441	ESTs	5.9
444165	AL137443	Hs.10441	hypothetical protein FLJ11236	5.9
424343	AW956360	Hs.4748	adenylate cyclase long polypeptide	5.9
420186	AW440228	Hs.61817	ESTs	5.7
422664	AA318323	Hs.12827	gb:EST20390 Ratna II Homo sapiens cDNA	5.8
446727	AB011095	Hs.16032	KIAA0523 protein	5.8
448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (I)	5.8
430132	AA204696	Hs.234149	hypothetical protein FLJ22047	5.8
425782	U66468	Hs.150525	cell growth regulatory with EF-hand doma	5.8
419629	AB020695	Hs.91662	KIAA0888 protein	5.8
452279	AA286844	Hs.61260	hypothetical protein FLJ13164	5.8
407806	AA663559	Hs.273789	histone deacetylase 3	5.8
414737	AI160396	Hs.125897	ESTs	5.8
432154	AI701523	Hs.112577	ESTs	5.8
410099	AA081630	Hs.12554	KIAA0036 gene product	5.8
411379	AB18344	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	5.8
404042	T89127	Hs.21433	hypothetical protein DKFZp47J036	5.7
424580	AA158727	Hs.150555	protein predicted by clone 23732	5.7
419498	AL036591	Hs.20887	hypothetical protein FLJ10392	5.7
436643	AA179526	Hs.10941	ESTs, Weakly similar to IPF1_HUMAN PROTE	5.7
416111	AA333813	Hs.79018	chromatin assembly factor 1, subunit A (5.7
419088	AI534323	Hs.52620	integrin, beta 8	5.7
435109	AA922153	Hs.132780	hypothetical protein MGC15729	5.7
428568	F12101	Hs.185701	Homo sapiens mRNA full length insert cDN	5.7
451752	AB022997	Hs.26966	KIAA1171 protein	5.7
413492	DT6470	Hs.76400	KIAA0280 protein	5.7
414683	S78296	Hs.76988	hypothetical protein MGC12702	5.6
418079	RA0958	Hs.6911	ESTs	5.6
445873	AA253970	Hs.251946	poly(A)-binding protein, cytoplasmic 1.1	5.6
437034	AA742843	Hs.251946	glyoxal oxidase 1 NC, GGAAP, GCB1 Homo sapiens	5.6
415944	AI909154	Hs.251946	gh:QV-87200-Q10499-007 B7300 Homo sapien	5.6
452785	AL359942	Hs.296434	erythroid differentiation and nucleosid	5.6
400801	AA451597	Hs.197409	ESTs	5.6
436867	AA953157	Hs.191235	hypothetical protein DKFZp47D155	5.6
413589	AA463631	Hs.313803	ESTs, Highly similar to AF157633.1 noncl	5.6
416506	AA084246	Hs.65339	G protein-coupled receptor 39	5.6
433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	5.5
448269	AA487044	Hs.70887	hypothetical protein FLJ10392	5.5
425154	NM_201851	Hs.154850	collagen, type IX, alpha 1	5.5
447773	AI423930	Hs.36790	ESTs, Weakly similar to putative p150 (H	5.5
422421	AA325138	Hs.235873	hypothetical protein FLJ22672	5.5
453128	AW026056	Hs.31791	adenylylase 2, muscle type	5.5
453220	AB033069	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	5.5
440866	AI703103	Hs.217180	hypothetical protein MGC16275	5.4
428976	AL037824	Hs.194695	ras homolog gene family, member 1	5.4
419723	AL120193	Hs.339810	longevity assurance (LAG-1, S. cerevisiae	5.4
452789	AB948629	Hs.213786	ESTs	5.4
426008	AL023513	Hs.194768	seizure related gene 6 (mouse) like	5.4
445265	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	5.4
424332	AA338919	Hs.101615	ESTs	5.4
440210	AW874562	Hs.125296	ESTs	5.4
414825	U66370	Hs.77452	epidermal growth factor receptor (avian	5.4
448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	5.4
452786	R81362	Hs.106642	ESTs, Weakly similar to T09052 hypothet	5.4
406790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	5.4
423476	AI535633	Hs.47860	Human DNA sequence from clone RP5-1046G1	5.4
446507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (I)	5.4
419683	AA248897	Hs.48784	ESTs	5.4
407728	AI0071502	Hs.175931	ESTs	5.4
453313	BE035711	Hs.153746	hypothetical protein FLJ22490	5.4
422804	AF129635	Hs.272027	F box only protein 5	5.4
452856	AF034799	Hs.30681	protein tyrosine phosphatase, receptor t	5.4
434792	AA649253	Hs.132458	ESTs	5.4
412180	R18180	Hs.274461	ESTs	5.3
425988	P07396	Hs.46637	ESTs	5.3
444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	5.3
429698	AB065068	Hs.26339	ESTs, Weakly similar to S21348 probable	5.3
424458	M29273	Hs.13780	myelin associated glycoprotein	5.3
446997	AA383139	Hs.161758	Spr-1 protein	5.3
427302	AA00540	Hs.135282	Homo sapiens cDNA FLJ11554 fs, clone HE	5.3
439607	BE540565	Hs.159400	ESTs	5.3
448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.3
410037	AB020725	Hs.58009	KIAA0918 protein	5.3

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451407	AA131376	Hs.343809	fibroblast growth factor 12B	5.3
430287	AW182459	Hs.125759	ESTs, Weakly similar to LEUS_HUMAN LEUK	5.3
428784	Y12851	Hs.193470	putative receptor P2X ₂ ligand-gated io	5.3
118512	AW498974		diacylglycerol kinase, zeta (10kD)	5.2
435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.3
420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN81_HUMAN Z	5.2
407896	D76435	Hs.411154	Zc family member 1 (odd-paired Drosophi	5.2
404819			NM_002658 Homo sapiens prenat (Drosophi	5.2
426503	AA80153		gb.E519303 Skin tumor 1 Homo sapiens cd	5.2
405348			C700164-p1125906 (p14b)GAC1046_11 (AB	5.2
431552	A818563	Hs.259873	axonal transport of synaptic vesicles	5.2
418677	S83308	Hs.87224	SRX (sex determining region Y)-box 5	5.2
427250	R39441	Hs.25418	ESTs	5.2
428337	V47474	Hs.89230	potassium intermediate/small conductance	5.2
445740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	5.2
430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFp761G02121 (5.2
432869	BE409301	Hs.134012	Clq-related factor	5.2
416220	N49776	Hs.170954	hypothetical protein MGC10945	5.2
457005	AJ307421	Hs.172597	sol (Drosophila)-like 3	5.1
447072	D61594	Hs.17279	lysyl/protein sulfotransferase 1	5.1
414372	AA143654		gb.za65a02.1 Stratagene pancreas (93720	5.1
410631	AA086469	Hs.47171	ESTs	5.1
414821	MC3335	Hs.77424	Fc fragment of IgG, high affinity Ia, re	5.1
420133	AA426117	Hs.155543	ESTs	5.1
453884	AA355925	Hs.35232	KIAA0186 gene product	5.1
414922	D00723	Hs.77631	glycine cleavage system protein H (amino	5.1
411727	BE499594	Hs.190162	gb.h2uc20803 + H2C_CCAP_GC36 Homo sapiens	5.1
441969	NM_003947	Hs.8004	huntingtin-associated protein interaction	5.1
437387	A1196874	Hs.28847	AD026 protein	5.0
400533			ENSP00000209376-PRED65 protein (Fragmen	5.0
430979	AA79755	Hs.125010	ESTs	5.0
445944	AB014605	Hs.22599	atrophin-1 interacting protein 1, activi	5.0
444600	R41398	Hs.6996	ESTs	5.0
453785	A1368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	5.0
428876	AA436384	Hs.46526	ESTs	5.0
444670	H53379	Hs.33256	hypothetical protein MGC5370	5.0
440471	AA885146	Hs.307944	ESTs	5.0
410434	AF051152	Hs.63668	tol-like receptor 2	5.0
441390	AH629560	Hs.131175	ESTs	4.9
448765	R15337	Hs.21568	Homo sapiens mRNA; cDNA DKFpZp547D086 (h	4.9
422263	AA307639	Hs.129608	KIAA0591 protein	4.9
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.9
407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.9
417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	4.9
448546	R13209	Hs.21413	actin carrier family 12, (potassium-chl	4.9
420092	AA814043	Hs.88045	ESTs	4.9
448571	AW016812	Hs.200266	ESTs	4.9
412811	H06382		ESTs	4.9
409100	H88216	Hs.42245	ESTs, Moderately similar to I38022 hypot	4.9
403142			NM_002708 Homo sapiens protein phosphat	4.9
414300	AJ040470	Hs.186660	ESTs	4.9
436607	AW661783	Hs.211061	ESTs	4.9
431553	X78075	Hs.2799	cardiac linking protein 1	4.9
448326	AH621483	Hs.344503	ESTs	4.9
420005	L10333	Hs.99947	reticulon 1	4.9
421688	AK000307	Hs.106825	hypothetical protein FLJ20300	4.9
452698	AA481493	Hs.78792	ESTs	4.9
427956	AA416000	Hs.98280	potassium intermediate/small conductance	4.9
432828	A572739	Hs.195471	6-phosphotricin-2-kinase/inositolase-2,5-bi	4.9
408453	A369838	Hs.45127	chondroin sulfate-2-kinase/inositolase-2,5-bi	4.8
428841	AA184340	Hs.104935	ESTs	4.8
416439	AA180363	Hs.118769	ESTs	4.8
447458	A7141082	Hs.158961	ESTs	4.8
429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	4.8
436511	AA727252	Hs.291502	ESTs	4.8
443392	A055821	Hs.293420	ESTs	4.8
423600	A6333559	Hs.310399	ESTs	4.8
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.8
414706	AA340125	Hs.76589	KIAA0097 gene product	4.8
407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypot	4.8
439340	AB032436	Hs.65335	brain-specific Na-dependent inorganic ph	4.7
427624	AA406245	Hs.248955	ESTs	4.7
413248	T48488	Hs.21433	hypothetical protein DKFpZp547A035	4.7
406770	AF160967	Hs.46784	potassium large conductance calcium-acti	4.7
440491	R5252	Hs.136538	ESTs, Weakly similar to 2105200A B cell	4.7
411555	AF113537	Hs.70669	HMP19 protein	4.7
430471	AF064845	Hs.241523	hypothetical protein FLJ10142	4.7
413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	4.7
441990	AF070526	Hs.129035	Homo sapiens clone 24787 mRNA sequence	4.7
425457	AW894667	Hs.165995	chironin (chironin) 1	4.7
458527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serin	4.7
453096	AW294631	Hs.11325	ESTs	4.7

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40125	R17258	Hs.343557	axonal transport of synaptic vesicles	4.7
428001	H87428	Hs.219907	ESTs, Moderately similar to Transforming	4.7
410276	A1554545	Hs.68301	angiopoietin-2	4.7
421637	AF035206	Hs.106300	Homo sapiens clone 23556 mRNA sequence	4.7
421633	AF121860	Hs.106250	sorting nexin 10	4.7
440052	A1533744	Hs.155648	ESTs, Weakly similar to 138022 hypotheti	4.7
429556	AF065387		gh/Homo sapiens full length insert cDNA	4.7
423280	NM_014442	Hs.279751	sialic acid binding Ig-like lectin 8	4.6
402145			Target Exon	4.6
409892	AW956113	Hs.7149	gh:EST1358183 MAGE resequences, MAGD Homo	4.6
458760	A1498631	Hs.111334	femlin, light polypeptide	4.6
453362	H14988	Hs.107375	ESTs	4.6
453734	A1537612	Hs.273758	hypothetical protein FLJ23112	4.6
429925	NM_001195	Hs.315868	Homo sapiens cDNA FLJ22373 fs, clone H	4.6
409041	AB033625	Hs.50081	Hypothetical protein, XP_051650 (R0A119	4.6
428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN 2	4.6
423770	AW976765	Hs.132776	Homo sapiens cDNA FLJ10077 fs, clone HE	4.6
410754	AK091053	Hs.51508	Homo sapiens cDNA FLJ10991 fs, clone PL	4.6
429149	AW193360	Hs.197962	ESTs, Weakly similar to 138022 hypotheti	4.6
437752	T78028	Hs.154679	synaptotagmin 1	4.6
439249	AF060569	Hs.170053	G-protein coupled receptor 88	4.6
416425	AA180738	Hs.210473	Homo sapiens cDNA FLJ14872 fs, clone PL	4.6
425255	BE297811	Hs.155392	calcipain response modulator protein 1	4.6
415257	F03016	Hs.27813	ESTs	4.6
428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	4.6
458814	AF988367	Hs.170661	ESTs, Weakly similar to Z195_HUMAN ZINC	4.6
451320	AW113072		glycylglycyl kinases, zeta (T040D)	4.5
424998	US8515	Hs.154138	chitinase 3-like 2	4.5
422709	AA315331	Hs.153485	ESTs	4.5
420578	AA813546	Hs.59504	GTP-binding protein Rho?	4.5
421977	W54197	Hs.118168	ribosomal protein L26 homolog	4.5
457465	AW301344	Hs.122508	DNA replication factor	4.5
427712	A068024	Hs.283696	ESTs	4.5
444656	A277924	Hs.145199	ESTs	4.5
413469	A1538418	Hs.1449	DEADH (Arg-Glu-Ala-AspHis) box polypep	4.5
428399	AA452244	Hs.16727	ESTs	4.5
450639	A0703186	Hs.277174	ESTs	4.5
452106	A1141031	Hs.21342	ESTs	4.5
424240	A8023185	Hs.143635	calcium/calmodulin-dependent protein kin	4.5
423009	AA791668		gh:cDNA268.s1 NCL CGAP, GCB1 Homo sapiens	4.5
445657	A135191	Hs.250702	ESTs, Weakly similar to 2109260A B cell	4.5
428189	AA424030	Hs.46527	ESTs	4.5
423178	A033140	Hs.124983	Homo sapiens mRNA: cDNA DKFZp564C142 (fr	4.5
445133	AW157645	Hs.198080	ESTs	4.5
418771	AA807981	Hs.25329	ESTs	4.4
438456	AA913381	Hs.20594	ESTs	4.4
410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fs, clone H	4.4
413034	BE295885	Hs.224179	ESTs, Weakly similar to 138022 hypotheti	4.4
419103	Z40229	Hs.56423	hypothetical protein FLJ23033	4.4
420550	AW207748	Hs.59115	ESTs	4.4
439552	H97552	Hs.269690	ESTs	4.4
408577	H50572	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	4.4
445034	AW293376	Hs.143659	ESTs	4.4
402595			Target Exon	4.4
426271	AF026547	Hs.160047	chondroitin sulfate proteoglycan 3 (neur	4.4
457561	AA331517	Hs.280555	chimerin (chimaerin) 2	4.4
130675	AF084865		gh/Homo sapiens envelope protein RIC-3 (4.4
439510	T77925	Hs.259165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.4
452752	AW044058	Hs.33578	KIAA0820 protein	4.4
439108	AW163034	Hs.5407	synaptotagmin 3	4.4
45819			NM_002578 Homo sapiens p21 (CDKN1A) act	4.4
445544	A1631532	Hs.7047	ESTs, Weakly similar to Unkown [E]aspie	4.4
412530	AA766258	Hs.266773	hypothetical protein FLJ13346	4.4
420871	AA702972	Hs.55300	ESTs	4.4
406522	AA505690	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	4.4
423289	AA449013	Hs.59203	ESTs	4.3
427463	AA442224	Hs.37300	ESTs	4.3
425402	A1215981	Hs.24370	ESTs, Weakly similar to B34323 GTP-bindi	4.3
412046	Y07847	Hs.73088	RAS-related on chromosome 22	4.3
427194	AA399018	Hs.250835	ESTs	4.3
437834	AA709294	Hs.263654	gh:cDNA268.s1 NCL CGAP, GCB1 Homo sapiens	4.3
409172	Z99399	Hs.122593	ESTs	4.3
409953	AA332277	Hs.57691	cadherin 16, type 2	4.3
425998	U07616	Hs.173034	amphiphysin (SH-Map) syndrome with br	4.3
452092	BE245374	Hs.77842	hypothetical protein FLJ11210	4.3
438458	AW975186		gh:EST1387294 MAGE resequences, MAGN Homo	4.3
445935	H10207	Hs.47314	ESTs	4.3
433932	AW954599	Hs.169330	neuronal protein	4.3
424900	AL035586	Hs.153203	MyoD family inhibitor	4.3
421998	AW450481	Hs.151333	ESTs	4.3
442832	AW205590	Hs.253569	ESTs	4.3
416596	D44643	Hs.14114	secreted modular calcium-binding protein	4.2
408359	R38438	Hs.182575	solute carrier family 15 (SLC15) transport	4.2

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	450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.2
	449318	AW238021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	4.2
	438624	AA890555	Hs.123468	ESTs	4.2
5	421027	AA161198	Hs.55254	ESTs	4.2
	419412	R20855	Hs.5422	glycoprotein M6B	4.2
	418422	AW161058	Hs.90257	synuclein, beta	4.2
	430228	AW950939	Hs.6382	ESTs, Highly similar to T00391 hypotheti	4.2
	450813	A1739625	Hs.203376	ESTs	4.2
	412505	AA974491	Hs.21734	ESTs	4.2
10	440168	AA865607	Hs.126141	ESTs	4.2
	441707	R42637	Hs.21963	hypothetical protein DKFZp761B0514	4.2
	438703	A1803373	Hs.31599	ESTs	4.2
	444127	M63620	Hs.13281	ESTs	4.2
	447397	BE247678	Hs.18442	C-1 enzyme	4.2
15	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	4.2
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	4.2
	416871	H98716	Hs.13608.s.1	Scanes melanocyte 2N6/HM Ho	4.2
	408538	A1869535	Hs.40369	ESTs	4.2
	425207	R88249	Hs.155524	penut (Drosophila)-like 2	4.2
20	404584			Target Exon	4.2
	436035	AA703679	Hs.106999	ESTs, Weakly similar to SYTS_HUMAN SYNAP	4.2
	404091	AW970395	Hs.269423	ESTs	4.2
	437117	AL149256	Hs.122593	ESTs	4.2
	429643	AA455889	Hs.167279	PYVE-finger-containing RnS effector pro	4.2
25	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (v	4.2
	408177	AJ241733	Hs.43871	ESTs	4.2
	438875	AA827640	Hs.189559	ESTs	4.2
	447877	AJ435184	Hs.164252	ESTs	4.2
30	415402	AA164887	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	4.2
	434859	BE255080	Hs.290315	collapsin response mediator protein-5, C	4.2
	448714	AB033015	Hs.23941	KIAA1159 protein	4.2
	427315	AA179949	Hs.175553	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	4.2
	404541			NM_030795:Homo sapiens stathmin-like 4 (4.1
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fs, clone PL	4.1
35	422253	AW732669	Hs.1519	protein kinase, cAMP-dependent, regulato	4.1
	404483	AI200836	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	4.1
	429421	AL031658		ESTs	4.1
	432882	NM_013257	Hs.279595	Human DNA sequence from clone RPI-310013	4.1
40	424001	Hs.7883	Hs.137476	serum/glucocorticoid induced regulated kinase-6	4.1
	427210	A1919149	Hs.112432	patently expressed 10	4.1
	445292	AW553264	Hs.13982	anti-Müllerian hormone	4.1
	450407	NM_000810	Hs.24959	Homo sapiens cDNA FLJ14665 fs, clone NT	4.1
	429401	AW296102	Hs.99272	gamma-aminobutyric acid (GABA) A recepto	4.1
45	428950	AA1707814	Hs.14545	ESTs, Weakly similar to S32567 A4 prot	4.1
	415796	R07548	Hs.78854	long fatty acyl-CoA synthetase 2 gene	4.1
	446619	AU076643	Hs.313	ATPase, Na ⁺ transporting, beta 2 polypep	4.1
	457211	AW972555	Hs.32389	secreted phosphoprotein 1 (osteopontin,	4.1
	416547	HE2914	Hs.280946	ESTs, Weakly similar to SG1797 vasodilat	4.1
50	412777	A1335773	Hs.270123	ESTs, Weakly similar to PC4239 fentin	4.1
	445225	A1216555	Hs.202398	ESTs	4.1
	408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	4.1
	417873	BE266958	Hs.263659	Down syndrome cell adhesion molecule	4.1
55	443301	AF733514	Hs.229597	Homo sapiens, Similar to RIKEN cDNA A430	4.1
	429281	AA838956	Hs.29808	ESTs, Moderately similar to ALU5_HUMAN A	4.1
	448966	AW372914	Hs.86149	Homo sapiens cDNA: FLJ21122 fs, clone C	4.1
	453857	AL080235	Hs.13561	phosphoinositide 3-phosphate-binding prot	4.1
	417355	DI3168	Hs.82002	DKFZp586162 protein	4.1
60	410359	R38624	Hs.106313	endothelin receptor type B	4.1
	426529	AF090100	Hs.170241	ESTs	4.1
	433223	AA305132	Hs.159142	Homo sapiens clone IMAGE 23915	4.1
	434833	R91095	Hs.4275	ESTs	4.1
	433331	A1240665	Hs.4275	KIAA1701 protein	4.1
65	422661	NM_014700	Hs.119004	ESTs	4.1
	424726	AK001007	Hs.138760	KIAA0665 gene product	4.0
	416805	F13271	Hs.79981	Homo sapiens cDNA FLJ10145 fs, clone HE	4.0
	441787	AS36853	Hs.214635	Human clone 23560 mRNA sequence	4.0
	424782	R76421	Hs.135694	ESTs	4.0
70	407792	A1077715	Hs.39384	ESTs	4.0
	425390	A1092634	Hs.125114	putative secreted ligand homologous to f	4.0
	435312	AJ243366	Hs.4865	protein tyrosine phosphatase, non-recept	4.0
	424635	AA420687	Hs.115455	voltage-gated sodium channel beta-3 subu	4.0
	423279	AW959861	Hs.209043	Homo sapiens cDNA FLJ14259 fs, clone PL	4.0
	444001	A1093087	Hs.152299	ESTs	4.0
75	410768	AF038185	Hs.66187	ESTs, Moderately similar to S60657 alpha	4.0
	428413	AJ377823	Hs.130729	Homo sapiens clone 23700 mRNA sequence	4.0
	450581	AF081513	Hs.25195	gbc-EST0805: Synovial sarcoma Homo sapien	4.0
	435854	AJ278120	Hs.4996	TGF-beta4	4.0
	433615	AJ722982	Hs.286907	putative ankyrin-repeat containing prote	4.0
80	432058	AA965996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	439774	A1362075	Hs.213493	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	445666	R59907	Hs.282386	Homo sapiens mRNA full length insert cDN	4.0
	450582	A139732		ESTs	4.0
				G-rich RNA sequence binding factor 1	4.0

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5	437814	A008192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.0
	451468	AW503388	Hs.293663	ESTs, Moderately similar to UBR22 hypot	4.0
	449277	AA001064	Hs.43670	ESTs	4.0
	440553	AA889416	Hs.34403	Homo sapiens cDNA FLJ14459 fls, clone HE	4.0
	445888	AF075654	Hs.13415	Homo sapiens clone 24571 mRNA sequence	4.0
10	420111	AA255652	gb:zs21h11.1 NC1_CGAP, GCB1 Homo sapiens	4.0	
	407198	H91679	gb:yy04a07.s1 Soares fetal liver spleen	4.0	
	422564	AI148006	Hs.222120	ESTs	4.0
	434992	AW222228	Hs.322922	ESTs	4.0
	435542	AA687376	Hs.5814	ESTs	4.0
15	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	4.0
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	4.0
	438285	AL133916	Hs.5814	hypothetical protein FLJ20093	4.0
	449655	A021987	Hs.59970	ESTs	4.0
	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypot	4.0
20	412659	AW753865	Hs.74376	oligosaccharide related ER localized protein	4.0
	423805	AW579960	Hs.135150	lung type I-cell membrane-associated gly	4.0
	432563	AW995441	Hs.10475	ESTs	4.0
	410765	AG849572	Hs.66180	nucleosome assembly protein 1-like 2	4.0
	420649	A086694	Hs.124704	ESTs, Moderately similar to S65657 alpha	4.0
25	450927	A0807804	Hs.134542	TASP for testis-specific adenylylase sens	4.0
	448895	AA324885	Hs.27277	carbonic anhydrase XI	4.0
	416426	D08961	Hs.79299	Ipona HMGIC fusion partner-like 2	4.0
	412754	AW160375	Hs.74565	amyloid beta (A4) precursor-like 2	4.0
	416340	H31772	Hs.79226	fasciculation and elongation protein zel	4.0
30	428682	NM_003346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	4.0
	413554	AA319146	Hs.75426	serogelatin II (chromogranin C)	4.0
	415687	A1638959	Hs.227699	ESTs, Weakly similar to T2D3_HUMAN TRANS	4.0
	453438	A1469935	Hs.22782	ESTs	4.0
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	4.0
35	426136	AF230877	Hs.152701	neuronal-interacting protein that ass	4.0
	412326	R07596	Hs.73817	small inducible cytokine A3 (homologous	4.0
	411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	4.0
	439935	S75105	Hs.8358	glutamate receptor, ionotropic, kainate	4.0
	458278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22468 fls, clone H	4.0
40	432809	AA565509	Hs.131703	ESTs	4.0
	458568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fls, clone NT	4.0
	413951	AW051200	Hs.75540	nanuric peptide precursor A	4.0
	435743	T68861	Hs.12662	ESTs	4.0
	447937	AL129716	Hs.20034	Homo sapiens mRNA, full length insert cDN	4.0
45	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.0
	448526	AB028046	Hs.21361	KIAA1023 protein	4.0
	445890	AF055019	Hs.21806	Homo sapiens clone 24570 mRNA sequence	4.0
	425341	AA324628	Hs.155247	adenosine C, nucleoside triphosphate	4.0
	417333	AL157546	Hs.173179	brutonin and PHD finger containing, 3	4.0
50	435832	AA425668	Hs.41641	Grn2 (Drosophila)-like 4, RNA binding	4.0
	410592	R04088	Hs.43569	ESTs	4.0
	443361	A1792628	Hs.133273	ESTs	4.0
	402696		CA001100*gb:5852342gb:AA054015.1 (AF0	4.0	
	437756	AA767537	Hs.197096	ESTs	4.0
55	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	4.0
	414998	NM_002643	Hs.77729	oxidized low density lipoprotein (lectin	4.0
	425652	AB021742	Hs.322431	neurapigen differentiation 2	4.0
	437449	AL390153	Hs.208339	Homo sapiens mRNA: cDNA DKFZp762G113 (H	4.0
	421040	AA715626	Hs.135280	ESTs	4.0
60	454171	AW854332	gb:QV2-CT0261-201099-011-05 CT0261 Homo	4.0	
	463740	R56434	Hs.21062	ESTs	4.0
	411668	AB11973	Hs.136313	ESTs	4.0
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.0
	457183	H81882	Hs.118569	Dvl-binding protein IDAX (inhibition of	4.0
65	438142	TB0309	Hs.269561	ESTs	4.0
	408875	NM_015434	Hs.48604	DKFZP346I68 protein	4.0
	436899	AA764852	Hs.291567	ESTs	4.0
	456487	AW567956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubru	4.0
	416882	L24488	Hs.80409	growth arrest and DNA-damage-inducible,	4.0
70	413199	M67843	Hs.753216	ELAV (embryonic lethal, abnormal vision,	4.0
	410711	AB002316	Hs.65746	KIAA0318 protein	4.0
	454117	BE410100	Hs.40358	adaptor-related protein complex 1, sigma	4.0
	438944	AA302517	Hs.92732	KIAA1444 protein	4.0
	445078	AW699575	Hs.4775	pinophilin 3	4.0
75	424330	AW072653	Hs.333386	Homo sapiens cDNA FLJ13596 fls, clone PL	4.0
	435099	AB037800	Hs.6462	protein kinase C and casein kinase subot	4.0
	449444	AW181436	Hs.23590	solute carrier family 16 (monocarboxylic	4.0
	411252	AB018549	Hs.69828	MD-2 protein	4.0
	448275	BE514434	Hs.200300	vesicle-like 2	4.0
80	434269	AK001191	Hs.3781	similar to murine leucine-rich repeat pr	4.0
	400777		NM_007325*Homo sapiens glutamate recept	4.0	
	419586	AI086485	Hs.144759	ESTs, Weakly similar to UBR22 hypot	4.0
	458072	AB983347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	4.0
	445908	R13590	Hs.13436	Homo sapiens clone 24425 mRNA sequence	4.0
	448451	AW015994	Hs.345433	gb:UH-H8p-ahp-g094-U1.s1 NC1_CGAP_S	4.0
	430183	BE010038	gb:PM3-EN0176-100400-001-g04 EN0176 Homo	4.0	
	430147	R50704	Hs.234434	hairpin-hairpin of split related with YRP	4.0

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	458912	AIS11066	ESTs	3.7
	428110	A0312485	Hs.136294 ESTs, Moderately similar to Z195_HUMAN Z	3.7
	448048	BE281291	Hs.170408 ESTs, Moderately similar to A47582 B-cell	3.7
5	442328	H52962	Hs.124813 hypothetical protein MGC14817	3.7
	422798	R52347	Hs.34574 ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	428873	A1701609	Hs.98908 ESTs	3.7
	432008	AL041224	Hs.65379 ESTs	3.7
	414040	N58513	Hs.32171 ESTs	3.7
	407846	AA476202	Hs.40463 CcpA300-interacting transactivator, wit	3.7
10	408629	NM_009042	Hs.48384 heparan sulfate (glucosamine) 3-O-sulfot	3.7
	425010	T16837	Hs.4241 ESTs	3.7
	427209	H06509	Hs.92423 KIAA1566 protein	3.6
	407603	AW955705	Hs.62604 Homo sapiens, clone HMAE-4299322, mRNA,	3.6
	410128	BE169274	KIAA0036 gene product	3.6
15	426646	AA382787	Hs.122713 ESTs	3.6
	418329	AW247430	Hs.84152 cystathionine-beta-synthase	3.6
	415390	A701162	Hs.90207 hypothetical protein MGC11138	3.6
	441703	AW390254	Hs.152843 leucine zipper protein FSGG14	3.6
	431725	X85724	Hs.2839 Homo discolor (pseudogonia)	3.6
20	448425	A1500359	Hs.346112 ESTs	3.6
	422611	AB011153	Hs.129508 KIAA0591 protein	3.6
	438031	BE263273	Hs.6439 synapton II	3.6
	419235	AW470411	Hs.288433 neurotensin	3.6
	451027	AW519204	Hs.40808 ESTs	3.6
25	428463	A1908539	Hs.184592 KIAA0344 gene product	3.6
	424847	R77952	ESTs, Weakly similar to alternatively sp	3.6
	404150		Target Exon	3.6
	450297	AW901347	Hs.38592 hypothetical protein FLJ23342	3.6
	443715	A1583187	Hs.9700 cyclin E1	3.6
30	435910	A1084152	Hs.21782 ESTs, Weakly similar to ALU7_HUMAN ALU S	3.6
	418084	BE387287	Hs.83384 S100-calmodulin-binding protein, beta (neur	3.6
	432488	AA551010	Hs.216640 ESTs	3.6
	431342	AW971018	Hs.21659 ESTs	3.6
35	437916	BE566249	Hs.20299 hypothetical protein FLJ23142	3.6
	412043	BE158672	Hs.33337 Homo sapiens clone TA40 untranslated mRNA	3.6
	448448	NM_014564	Hs.21235 KIAA0385 protein	3.6
	447818	W75940	Hs.21906 Homo sapiens clone 24670 mRNA sequence	3.6
	445105	AF238899	Hs.283955 Homo sapiens clone GLSH-2 similar to gli	3.6
	409557	BE182096	Hs.211193 ESTs	3.6
40	425202	AW962202	Hs.152049 ESTs, Weakly similar to D80222 hypophi	3.6
	451734	NM_006176	Hs.28844 neurogranin (protein kinase C substrate,	3.6
	425331	AW962128	Hs.28844 gbt-EST174201 MAGE resequences, MAGG Homo	3.6
	412759	A1267506	Hs.28844 gbt-EST174201 Stanley Frontal S8 pool 1	3.6
45	435040	A522350	Hs.152825 ESTs	3.6
	431449	Z43309	Hs.244624 hypothetical protein MGC5469	3.6
	415709	AA649850	Hs.278558 ESTs	3.6
	424051	AL110203	Hs.138411 Homo sapiens mRNA; cDNA DKFZp566J1922 (I	3.6
	437640	AA784053	Hs.272155 ESTs, Weakly similar to D80222 hypophi	3.6
50	445953	A612775	Hs.146710 ESTs	3.6
	449266	AA059050	Hs.59847 ESTs	3.6
	424687	J05070	Hs.151738 matrix metalloproteinase 9 (gelatinase B	3.6
	409327	L41162	Hs.32563 collagen, type IX, alpha 3	3.6
	417615	A0808607	Hs.3781 similar to murine leucine-rich repeat pr	3.6
55	423641	AL137256	Hs.130489 ATPase, aminophospholipid transporter-II	3.6
	443912	R37257	Hs.184780 ESTs	3.6
	424572	M19650	Hs.23-cyclic nucleotide 3' phosphodiester	3.5
	424899	AL115387	Hs.119062 ESTs	3.5
	429726	AW449803	Hs.293707 ESTs, Weakly similar to D80698 zinc fing	3.5
	416490	AF090116	Hs.79348 regulator of G-protein signalling 7	3.5
	408809	AW972512	Hs.20985 sh3-associated polypeptide, 30kD	3.5
	429084	AJ001443	Hs.155614 signaling factor 3b, subunit 3, 130kD	3.5
	407624	AW157431	Hs.248841 ESTs	3.5
	419038	AW134924	Hs.190325 ESTs	3.5
65	451489	NM_005603	Hs.26468 amyloid beta (A4) precursor protein-bind	3.5
	428242	H55709	Hs.2250 tykoma inhibitory factor (choleragen	3.5
	411048	AK011742	Hs.67991 hypothetical protein DKFZp454G0522	3.5
	435575	AF213457	Hs.44234 triggering receptor expressed on myeloid	3.5
	424340	AA339036	Hs.7033 ESTs	3.5
	425790	AW136286	Hs.288446 ESTs	3.5
70	432188	AJ362952	Hs.25278 soluble carrier family 7 (cationic amino	3.5
	438096	AW263443	Hs.245205 KIAA1853 protein	3.5
	434784	AA649051	Hs.164007 ESTs	3.5
	452449	AW068658	Hs.20943 ESTs	3.5
	425212	AW992253	Hs.171618 ESTs	3.5
75	407253	AA411175	Hs.141939 ESTs, Moderately similar to S65657 alpha	3.5
	418049	AA211467	Hs.190488 Homo sapiens, Similar to nuclear localiz	3.5
	421247	BE391727	Hs.102910 general transcription factor IIH, polype	3.5
	455311	R40192	Hs.21527 Human DNA sequence from clone GS-1-11503	3.5
	439450	R51813	Hs.125304 ESTs	3.5
80	435545	AA687415	Hs.29107 ESTs	3.5
	445729	H21066	Hs.13223 Homo sapiens mRNA full length insert cDN	3.5
	448999	AF179274	Hs.22791 transmembrane protein with EGF-like and	3.5
	412590	AL134388	Hs.135033 ESTs, Weakly similar to D80222 hypophi	3.5

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	436527	A1969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	441111	A1808667	Hs.126594	ESTs	3.5
5	418630	A1351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	3.5
	439920	H05430	Hs.288433	neurotrophin	3.5
	421268	A1126821	Hs.30514	ESTs	3.5
	432022	AL162042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	3.5
	412719	AW016610	Hs.816	ESTs	3.5
	435092	AL137310	Hs.4749	Homo sapiens mRNA; cDNA DKFp761E13121 (3.5
10	414178	AW957372	Hs.46791	ESTs, Weakly similar to 180222 hypothetical	3.5
	437252	A433833	Hs.164159	ESTs, Weakly similar to ALU1, HUMAN ALU S	3.5
	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.4
	421183	AL135740	Hs.102447	TSC-22 like	3.4
	441834	AL138034	Hs.7979	KIAA0735 gene product	3.4
15	413812	AW188687	Hs.44746	ESTs	3.4
	446932	A1675444	Hs.263024	ESTs	3.4
	447067	RA2098	Hs.21964	ESTs	3.4
	406296	AL117452	Hs.44155	DKFZP586G1517 protein	3.4
	447028	A0973128	Hs.167257	brain link protein-1	3.4
20	432715	AA247152	Hs.200403	ESTs, Weakly similar to KIAA1074 protein	3.4
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	3.4
	417084	H08370	Hs.33067	ESTs	3.4
	444534	AWZ71626	Hs.42254	ESTs	3.4
	440700	AW952261	Hs.295164	guanine nucleotide binding protein (G pr	3.4
	436637	A1783629	Hs.26766	ESTs	3.4
	412820	BE001236	Hs.gM3-BN0075-240200-101-411 BN0075 Homo	3.4	
	428138	AA773842	Hs.293799	ESTs	3.4
	453033	AA328669	Hs.31463	KIAA0281 gene product	3.4
	453305	R36224	Hs.267997	EHM2 gene	3.4
	459660	M79082	Hs.	ESTs	3.4
30	418821	AA436002	Hs.183161	ESTs	3.4
	436518	WY6326	gb:2505604.11 Soares_fetal_heart_NbH19M/	3.4	
	402379	NM_018432	Hs.	Homo sapiens ovarian cancer related prot	3.4
	437085	AA743935	Hs.202329	ESTs	3.4
	419852	AW503756	Hs.286164	hypothetical protein dJ55 ID2.5	3.4
35	430694	AA010624	Hs.30356	ESTs, Weakly similar to H29H_HUMAN HISTO	3.4
	441287	AW251132	Hs.131373	ESTs	3.4
	425870	R13406	Hs.56782	ESTs	3.4
	443672	AA323362	Hs.9567	butyrolactone (gamma), 2-oxoglutarate di	3.4
40	440404	AJ459882	Hs.gbrk13e01.x1 NCI_OGAP_Luc24 Homo sapiens	3.4	
	452338		Hs.	Target Exon	3.4
	444044	A1015881	Hs.324527	mitochondrial ribosomal protein S5	3.4
	453590	AF150278	Hs.33578	KIAA0620 protein	3.4
	450756	A173348	Hs.144052	ESTs	3.4
45	404283		Hs.	ENSP00000244751-Copine-like protein KIA	3.4
	423257	AW161039	Hs.125878	synapsin III	3.4
	432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.4
	412986	XB1120	Hs.75110	cannabinoid receptor 1 (brain)	3.4
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.4
50	426050	AL118615	Hs.94653	neurochordin	3.4
	431789	A115500	Hs.269222	mitogen-activated protein kinase 4	3.4
	408601	U47928	Hs.86122	protein A	3.4
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PCA259 feni	3.4
	446919	A1674685	Hs.200141	ESTs	3.4
55	425380	AJ291267	Hs.149590	ESTs	3.4
	408554	AA636381	Hs.315111	nuclear receptor co-repressor/hDAC3 comp	3.3
	443257	A1334040	Hs.11614	HSPC085 protein	3.3
	432731	R31178	Hs.287820	Bronectin 1	3.3
	421679	AA475110	Hs.203933	ESTs	3.3
60	453169	AB037615	Hs.32156	KIAA1394 protein	3.3
	437357	AA349847	Hs.4221	hypothetical protein DKFZp761H039	3.3
	444310	BE552018	Hs.133152	ESTs	3.3
	423169	BE347009	Hs.21657	ESTs, Weakly similar to KIAA0927 protein	3.3
	433657	AJ244368	Hs.81294	Phi domain containing protein in retina 1	3.3
65	408449	NM_004408	Hs.166161	dynamitin 1	3.3
	417402	BE503227	Hs.134759	ESTs	3.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78665 vein	3.3
	439753	BE262233	Hs.7423	hypothetical protein from EUROMAGE 2168	3.3
	455646	BE064420	gb:RCA-BT0311-241199-012-c08 BT0311 Homo	3.3	
	450337	A1693256	Hs.202427	ESTs	3.3
70	423420	A571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp761H1224 (f	3.3
	433236	NM_004296	Hs.32121	regulator of G-protein signalling 6	3.3
	417868	AJ078534	Hs.122592	ESTs	3.3
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
75	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	3.3
	448249	T52285	Hs.153115	Homo sapiens mRNA for KIAA1764 protein,	3.3
	418216	AA662240	Hs.283309	AF15q14 protein	3.3
	456060	CI4904	Hs.45164	Homo sapiens cDNA FLJ12284 ts, clone MA	3.3
	449145	AB32122	Hs.198408	ESTs	3.3
80	415101	RA5531	Hs.144534	ESTs	3.3
	401272		Hs.	CS000559^g12314195(mae)(CA99338.1)(A	3.3
	402029	AS28272	Hs.88323	ESTs, Weakly similar to ALU1, HUMAN ALU S	3.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.3
	443761	A1529743	Hs.345187	ESTs	3.3

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	427317	AB028955	Hs.157580	KIAA1032 protein	3.3
	426820	AA393351	Hs.132121	ESTs	3.3
	433894	A907682	Hs.243293	ESTs	3.3
5	454253	AW560717	Hs.47144	DNFZP596N0819 protein	3.3
	419647	AA348947	Hs.91816	hypothetical protein	3.3
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fs, clone HE	3.3
	407581	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	3.3
	428670	AA431682	Hs.134832	ESTs	3.3
	435375	U733610	Hs.187832	ESTs	3.3
10	419043	T19167	Hs.68666	els-variant gene 1	3.3
	403341			Target Exon	3.3
	436282	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	3.3
	436267	BE621702	Hs.29076	hypothetical protein FLJ21841	3.3
15	456209	W60633	Hs.297192	ESTs	3.3
	438810	AW897846	Hs.6421	hypothetical protein DKFZp61N09121	3.3
	411555	AW851728		gb:MR2-CT0222-011195-007-d06 CT0222 Homo	3.3
	418020	X54942	Hs.83758	CDC28 protein kinase 2	3.3
	461254	AIS71016	Hs.172967	ESTs	3.3
	432564	AW023337	Hs.9402	glycoprotein M6B	3.3
20	439842	A1852156	Hs.26346	ESTs	3.3
	433325	AW200986	Hs.143905	ESTs	3.3
	451096	AJ758680	Hs.206132	ESTs	3.3
	435114	AA778232	Hs.19515	ESTs, Highly similar to NRG3_HUMAN PRO-N	3.3
	421686	AB011156	Hs.106794	KIAA0584 protein	3.3
25	429228	A1553633	Hs.326447	ESTs	3.3
	429225	A1305962	Hs.26289	ESTs	3.3
	412350	A1559306	Hs.73826	protein tyrosine phosphatase, non-recept	3.3
	451778	A1826131	Hs.62564	ESTs, Weakly similar to zinc finger prot	3.3
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	3.2
30	450475	AB056334	Hs.205015	ESTs	3.2
	418661	NM_001949	Hs.1168	ECF transcription factor 3	3.2
	439480	AJ271643	Hs.87469	putative acid-sensing ion channel	3.2
	407332	A1801565	Hs.200113	Homo sapiens cDNA FLJ11379 fs, clone HE	3.2
	415131	D61119		gb:u158C118 Clontech human fetal brain	3.2
35	409248	AB033035	Hs.51965	KIAA1209 protein	3.2
	431462	AW583672	Hs.255311	granin-like neuroendocrine peptide precu	3.2
	434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransfe	3.2
	450358	AB010098	Hs.24907	coronin, actin-binding protein, 2b	3.2
40	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	452539	US8281		oxidative 3 alpha-hydroxysteroid dehydro	3.2
	407304	AA555832	Hs.271648	gbm312603.s1 NC_024911 Homo sapiens	3.2
	451697	AW449774	Hs.296380	POM (POM121 rat homolog) and ZP3 fusion	3.2
	435071	DE0683	Hs.35495	ESTs	3.2
45	420352	BE258635		gb:0117374F1 NIH_MGC_16 Homo sapiens c	3.2
	412193	A186467	Hs.144057	ESTs	3.2
	442320	A1287817	Hs.129636	ESTs	3.2
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3.2
	414528	AA148950	Hs.188836	ESTs	3.2
	439764	T26335	Hs.22744	hypothetical protein MQC13105	3.2
50	410425	BE278367	Hs.63510	KIAA0141 gene product	3.2
	429876	AB028977	Hs.225974	KIAA1054 protein	3.2
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	3.2
	439039	A1856707	Hs.48713	ESTs	3.2
	447925	AW292271	Hs.550718	ESTs	3.2
55	447714	AW296313	Hs.255537	ESTs	3.2
	434574	A1424458	Hs.33470	ESTs	3.2
	437269	AA334384	Hs.149420	ESTs	3.2
	416845	H93279	Hs.293786	gb:u20802.s1 Soares fetal liver spleen	3.2
60	452234	AW084176	Hs.223296	ESTs, Weakly similar to 138022 hypothe	3.2
	440274	R24595	Hs.7122	scarap responsive protein 1	3.2
	437698	R01837	Hs.7990	ESTs, Moderately similar to 184505 cald	3.2
	414761	AJ071728	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.2
	445826	F05802	Hs.81907	ESTs	3.2
	423779	AW071837	Hs.57571	ESTs	3.2
65	433790			NM_001334: Homo sapiens cathepsin O (CTS	3.2
	453792	AL134539	Hs.254129	KIAA1678	3.2
	428167	AA770021	Hs.16332	ESTs	3.2
	446413	AA151342	Hs.12677	CGI-147 protein	3.2
	415314	N88802	Hs.5422	glycoprotein M6B	3.2
70	425115	RA4664	Hs.123956	ESTs	3.2
	420625	A234396	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.1
	422772	AL119585	Hs.120228	KIAA0749 protein	3.1
	437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	3.1
75	407981	AW283165	Hs.143334	ESTs	3.1
	435256	AF183766	Hs.13872	cytokine-like protein C17	3.1
	428966	AF052914	Hs.194687	cholesterol 25-hydroxylase	3.1
	413995	BE048146	Hs.73671	synthase 1A (brain)	3.1
	443431	A056847	Hs.206054	ESTs	3.1
80	414217	A039298	Hs.278958	Homo sapiens cDNA: FLJ23165 fs, clone L	3.1
	419617	AL006583	Hs.91622	neuronal pentraxin receptor	3.1
	444326	AW939357	Hs.270710	ESTs	3.1
	436315	BE390513	Hs.27535	hypothetical protein MQC4837	3.1

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5	446131	NM_000929	Hs.290	phospholipase A2, group V	3.1
	432858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFpZp34B0650 (f	3.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	3.1
	432682	AJ376400	Hs.159388	ESTs	3.1
	400661	AW952160	Hs.83849	ESTs	3.1
10	417638	R08916	Hs.191212	ESTs	3.1
	417918	AA209205	Hs.163754	hypothetical protein FLJ12506	3.1
	465032	W31790	Hs.194293	ESTs, Weakly similar to IS437.4 gene NF2	3.1
	442150	AJ34467	Hs.34650	ESTs	3.1
	404632		NM_022490	Homo sapiens hypothetical prot	3.1
15	425537	AB007913	Hs.158291	KIAA0444 protein	3.1
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.1
	420690		Hs.12696	Eos Control	3.1
	454524	AB028945	Hs.12696	coractin SH3 domain-binding protein	3.1
	422949	AA319435	Hs.21903	gb:EST12657 Adrenal gland tumor Homo sap	3.1
20	448750	U95020	Hs.21903	calcium channel, voltage-dependent, beta	3.1
	433560	AI925195	Hs.130891	hypothetical protein MGC2400	3.1
	433042	AW133634	Hs.281905	Homo sapiens cDNA FLJ11660 f6, clone HE	3.1
	449722	BE780074	Hs.23660	cyclin B1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
25	445670	F07693	Hs.65903	Homo sapiens mRNA; cDNA DKFpZp34K2172 (f	3.1
	425519	AW298697	Hs.61884	Homo sapiens, clone IMAGE4289026, mRNA,	3.1
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	3.1
	405605		C2001342.gi127814.gp12643.gi1NAH1_RAT	SO	3.1
	417565	AI203405	Hs.47831	ESTs	3.1
30	439538	AA837323	Hs.56467	ESTs	3.1
	414117	W88559	Hs.1787	proteoglycan protein 1 (Pellegrini-Moriziac	3.1
	430818	AJ311528	Hs.348156	gb:acc3504.1 NCL_CGAP_Kid5 Homo sapiens	3.1
	408508	AI806109	Hs.135736	KIAA1580 protein	3.1
	414884	RS4419	Hs.183745	hypothetical protein FLJ13456	3.1
35	435623	AW247529	Hs.6753	protein-activating factor acetylhydrolase	3.1
	446636	AC002563	Hs.15767	clonin (rho-interacting, serine/threonine	3.1
	417169	R13550	Hs.246773	ESTs	3.1
	450202	AW669758	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	3.1
	420060	AA420616	Hs.249433	ESTs	3.1
40	430528	AF181862	Hs.242407	G-protein-coupled receptor, family C, gr	3.1
	421458	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	3.1
	429163	AA844766	Hs.182874	gb:acc20a1.0a1 Soares_NFL_T_GDC_S1 Homo	3.0
	428180	AI123767	Hs.182874	gb:acc20a1.0a1 Soares_NFL_T_GDC_S1 Homo	3.0
	422631	BE218819	Hs.118793	hypothetical protein FLJ10688	3.0
45	433290	R20077	Hs.302165	Homo sapiens clone Z3618 mRNA sequence	3.0
	412607	L36645	Hs.73964	EphA4	3.0
	415827	H17482	Hs.23079	ESTs	3.0
	428602	AF022246	Hs.210063	cell adhesion molecule with homology to	3.0
	457368	AK479755	Hs.129010	ESTs	3.0
50	441732	AW298818	Hs.127341	ESTs	3.0
	455018	NM_000038	Hs.203662	gb:Homo sapiens adenomatosis polyposis c	3.0
	428384	AA720708	Hs.203662	hypothetical protein FLJ13189 (FLJ13189)	3.0
	436267	AW450938	Hs.180115	ESTs	3.0
	450650	T65617	Hs.101257	hypothetical protein MGC3255	3.0
55	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	3.0
	450080	AW192083	Hs.292655	ESTs	3.0
	417283	BE276738	Hs.74570	DEAD-box (Atp-Glu-Atp-Asp) box polypep	3.0
	432593	AW361003	Hs.51463	ESTs, Weakly similar to hypothetical pro	3.0
	443753	AW367578	Hs.134749	ESTs	3.0
60	445921	AW015211	Hs.146181	ESTs	3.0
	427655	RB3483	Hs.172862	ESTs	3.0
	432623	AI458931	Hs.37282	ESTs	3.0
	453324	W26592	Hs.232089	ESTs	3.0
	421094	AW978202	Hs.289064	hypothetical protein FLJ22251	3.0
65	434544	AA588429	Hs.22481	gb:acc2203.1 NCL_CGAP_P122 Homo sapiens	3.0
	452850	H03230	Hs.22481	ESTs, Moderately similar to A46100 X-in	3.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ar	3.0
	429569	AA454893	Hs.138343	ESTs, Weakly similar to T8885 serine/th	3.0
	428600	AW663261	Hs.242413	hypothetical protein DKFpZp34K1421	3.0
70	443613	AL031260	Hs.9654	similar to pregnancy-associated plasma p	3.0
	433229	AB040925	Hs.91625	KIAA1492 protein	3.0
	429045	X57436	Hs.194772	oligodendrocyte myelin glycoprotein	3.0
	431431	AL035711	Hs.252953	Human DNA sequence from clone RP3-403A15	3.0
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.0
75	432165	AI937547	Hs.126195	hypothetical protein MGC2501	3.0
	440281	MB1886	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.0
	441364	AW450496	Hs.126830	ESTs, Weakly similar to Y008_YEAST HYPOT	3.0
	437056	AI147061	Hs.126830	gb:acc33a1.1 s1 Soares_NSF_F8_9M_OT_PA_P	3.0
	429168	AA984682	Hs.146589	ESTs, Weakly similar to JC5238 galactosyl	3.0
	453739	AL120266		ESTs	3.0

TABLE 15B:

Phy Unique Eos precluster identifier number
CAT number: Gene cluster number
Accession: Combank accession numbers

Phy CAT Number Accession

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Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (G#) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	Nt_position
400533	6581826	Minus	27132-277595
402777	8131663	Plus	70745-71721
401272	5757373	Minus	56274-58558
402145	8018280	Plus	113086-114800
402604	9909420	Plus	20393-20767
402605	9909420	Minus	47650-47873
402855	9862553	Minus	55763-55809
403142	9444521	Plus	89286-90131
403341	8569175	Plus	30699-30910
403656	3135242	Minus	143467-143634
403790	8064657	Minus	7628-87947/85835-90002
404150	7534008	Plus	16581-165943
404283	2276311	Minus	95460-95564
404541	8318559	Plus	103456-103664
404584	9857511	Plus	138551-139153
404632	5796668	Plus	45256-45229
404819	4678240	Plus	16223-16319, 16427-16513, 16736-16859, 16941-17075, 17170-17287, 17389-17529, 18251-18357, 18443-18578
405238	7245119	Minus	51728-51836
405239	7245119	Plus	144345-144454, 144690-144836, 151750-151883, 152407-152484
405340	2917117	Minus	43310-43462
405605	8638195	Minus	117070-117270
405819	4007557	Plus	2830-2997

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TABLE 16A: ABOUT 859 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM
Table 16A lists about 859 genes up-regulated in glioblastoma multiforma (GBM) compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Exon HUG GeneChip array such that the ratio of "average" LGG to "average" CNS tissues was greater than or equal to 3.0. The "average" GBM level was set to be the 85th percentile amongst various GBM tumors. The "average" normal CNS tissue level was set to be the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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Pkey: Unique Eos probe/identifier number
ExAccn: Excerpt/Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of GLIOBLASTOMA MULTIFORMA to CNS

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Pkey	ExAccn	UnigeneID	Unigene Title	R1
414555	N95859	Hs.16422	phospholipase A2, group IIA (platelets,	47.2
422737	N26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	44.9
423961	D13666	Hs.136348	perlestin (OSF-2os)	33.3
433001	AF217513	Hs.279505	clone H20310 PRO0310p1	25.9
445535	W83063	Hs.55446	ESTs	25.8
417308	H60720	Hs.81892	HAA0101 gene product	23.3
424800	AL035588	Hs.153203	MyoD family inhibitor	23.0
414825	X06370	Hs.77432	epidermal growth factor receptor (avian	19.6
431941	AK000108	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	18.7
453392	U22742	Hs.52964	SRV (see distalizing region V)-box 11	17.8
444190	A1878918	Hs.10526	cysteine and glycine-rich protein 2	17.8
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	17.7
417130	AW275858	Hs.81266	S103 calcium-binding protein A4 (calcium	17.5
414217	AB292208	Hs.278918	Homo sapiens cDNA FLJ23165 fs, clone L	17.0
423242	H55709	Hs.2250	leukemia inhibitory factor (choleremic	15.9
425597	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	15.6
424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14255 fs, clone PL	15.2
423243	Y08787	Hs.624	interleukin 8	14.7
422672	X12784	Hs.110129	collagen, type IV, alpha 1	14.7
434078	AW880709	Hs.263983	chromosome 8 open reading frame 4	14.6
408799	D11928	Hs.76845	phosphoserine phosphatase-like	14.2
414761	AJ007728	Hs.77256	enhancer of zeste (Drosophila) homolog 2	14.2
424342	BC262580	Hs.38178	hypothetical protein FLJ23469	14.1
445684	U53445	Hs.15432	downregulated in ovarian cancer 1	14.0
444969	A203334	Hs.160628	ESTs	13.5
430651	CI4187	Hs.103538	ESTs	12.9
425075	AW513691	Hs.270149	ESTs, Weakly similar to 2109250A B cell	12.4
445010	T17502	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 f	12.1
441269	AW015206	Hs.178784	ESTs	11.9
417426	NM_002291	Hs.82124	laminin, beta 1	11.9
430132	AA204696	Hs.234149	hypothetical protein FLJ20647	11.8
422163	AF027208	Hs.112360	protein (mouse)-like 1	11.3
411411	AA345241	Hs.555950	ESTs, Weakly similar to KIAA1330 protein	11.3
449722	BE280074	Hs.233960	cycin B1	11.2
435291	BC569452	Hs.344037	protein regulator of cytokinesis 1	11.0
435020	AW505076	Hs.301855	Dyskerp syndrome critical region gene 8	10.9
412140	AA219691	Hs.73625	RAB5 interacting, kinesin-like (rablines	10.9
415239	AA468183	Hs.104598	Homo sapiens cDNA: FLJ23241 fs, clone C	10.6
417043	NM_004369	Hs.80588	collagen, type VI, alpha 3	10.6
413529	BE501688	Hs.75617	collagen, type IV, alpha 2	10.6

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	420602	AF060877	Hs 99236	regulator of G-protein signaling 20	10.6
	409142	AL136877	Hs 50758	SMC4 (structural maintenance of chromoso	10.4
	406972	M32053		gb.Human H19 RNA gene, complete cds	10.4
5	412586	X81120	Hs 75110	cannabinoid receptor 1 (brain)	10.3
	415508	AI9597938	Hs 80786	ITP binding cassette, sub-family C (CFTR	10.1
	449611	AI970394	Hs 197075	ESTs	10.1
	427581	NM_014788	Hs 179703	KIAA0129 gene product	9.9
	431512	BE270734	Hs 2795	lactate dehydrogenase A	9.9
10	429183	AB014654	Hs 197955	KIAA0704 protein	9.7
	433437	U20536	Hs 3280	caspase 5, apoptosis-related cysteine pr	9.7
	424840	D79987	Hs 153479	extra spindle poles, S, convexia, homo	9.7
	433800	AI034361	Hs 135150	lung type I cell membrane-associated gly	9.7
	433647	AA004367	Hs 222254	ESTs	9.7
	414622	AI752666	Hs 7669	nucleoside N-methyltransferase	9.5
15	413719	BE439580	Hs 75498	small inducible cytokine subfamily A (Cy	9.3
	406461	AA382169	Hs 54483	N-myc (and STAT) interactor	9.3
	409902	AJ337658	Hs 156351	ESTs	9.2
	450375	AA009647		a disintegrin and metalloproteinase doma	9.1
20	445873	AA250970	Hs 251946	poly(A)-binding protein, cytoplasmic 1.4	9.1
	442802	AL133035	Hs 8728	hypothetical protein DKFZp434G171	9.1
	452461	N78223	Hs 108106	transcription factor	9.1
	430464	AW255389	Hs 119768	ESTs	9.1
	422158	L10343	Hs 112241	protease inhibitor 3, shin-derived (SKAL	9.0
25	425187	AW014486	Hs 22509	ESTs	9.0
	434247	BE514387	Hs 333893	c-Myc target JPO1	8.7
	450079	AI795870	Hs 54277	DNA segment on chromosome X (unique) 952	8.7
	410276	AB54545	Hs 63301	angiotensin-2	8.6
	402855			NM_001839 Homo sapiens calpain 3, acid	8.6
	430710	AF086543		gb:Homo sapiens full length insert cDNA	8.6
30	411968	AI207410	Hs 69280	Homo sapiens, clone IMAGE:363629, mRNA,	8.6
	410103	AA245608	Hs 275727	ESTs, homologue of PEM-3 (Ciona savignyi	8.6
	430895	AF037335	Hs 5338	carboxic anhydrase XII	8.6
	418203	X54942	Hs 83758	CDC28 protein kinase 2	8.6
	416892	L24498	Hs 80409	growth arrest and DNA-damage-inducible,	8.6
35	425234	AW152225	Hs 165369	ESTs, Weakly similar to D8022 hypophos	8.5
	449961	AW265634	Hs 131100	ESTs	8.5
	449444	AW181436	Hs 23590	solute carrier family 15 (monocarboxylic	8.4
	417061	AF75944	Hs 188691	Homo sapiens cDNA FLJ12033 fs, clone HE	8.3
	453884	AA355625	Hs 36232	KIAA0186 gene product	8.3
40	424965	NM_002914	Hs 139228	replication factor C (pactivator 1) 2 (40	8.1
	419938	AL076772	Hs 1279	complement component 1, r subcomponent	8.1
	411078	AI222020	Hs 182364	Coccolip	8.1
	406550	AF624300	Hs 172528	collagen, type I, alpha 1	8.0
	447725	AL137638	Hs 19358	melanin 2	8.0
45	432955	AA111581	Hs 88338	ras homolog gene family, member E	8.0
	416658	U03272	Hs 79432	fibrillin 2 (congenital contractural ara	7.9
	439451	AF086270	Hs 278554	heterochromatin-like protein 1	7.9
	458814	AI408957	Hs 170981	ESTs, Weakly similar to Z195_HUMAN ZINC	7.9
	447004	AW296968	Hs 157539	ESTs	7.9
50	436140	W87355	Hs 269697	ESTs	7.9
	436607	AW661783	Hs 211061	ESTs	7.7
	422809	AK001379	Hs 121028	hypothetical protein FLJ10549	7.7
	440052	AB337444	Hs 195640	ESTs, Weakly similar to D3022 hypophos	7.7
55	422106	DB4239	Hs 111732	Fc fragment of IgG binding protein	7.7
	418113	AI272141	Hs 83484	SRY (sex determining region Y)-box 4	7.7
	410286	AI739159	Hs 61896	DKFZP586N2124 protein	7.7
	424687	J55070	Hs 151738	major metalloproteinase 9 (gelatinase B	7.6
	422048	NM_012445	Hs 289128	spardin 2, extracellular matrix protein	7.6
60	421988	AW450481	Hs 161333	ESTs	7.6
	452620	AA436504	Hs 119286	ESTs	7.6
	453341	U39817	Hs 36820	Bloom syndrome	7.5
	416737	AF154335	Hs 79610	LIM domain protein	7.5
	425289	AW139342	Hs 155530	interiorin, gamma-inducible protein 16	7.5
	418400	BE243026	Hs 301989	KIAA0246 protein	7.5
65	437036	AI571514	Hs 133022	ESTs	7.5
	421899	AJ011895	Hs 109781	Nel-associated factor 1	7.4
	409731	AA125965	Hs 55145	thymosin, beta, identified in neuroblast	7.4
	427528	AU077143	Hs 179565	minichromosome maintenance deficient (S,	7.4
	427871	AW992405	Hs 59622	Homo sapiens, clone IMAGE:3507281, mRNA,	7.3
70	446935	AJ076596	Hs 22591	nuclear receptor subfamily 2, group E, m	7.3
	415079	RA3179	Hs 22899	hypothetical protein FLJ23548	7.3
	449571	AW015812	Hs 200266	ESTs	7.3
	427899	AA829286	Hs 332053	serum amyloid A1	7.3
	447458	AI41082	Hs 158961	ESTs	7.3
75	430530	AA263920	Hs 2621	cystatin A (cistatin A)	7.2
	411252	AB018549	Hs 69328	MD-2 protein	7.2
	432731	R31178	Hs 287820	fibronectin 1	7.2
	454117	BE410100	Hs 40368	adaptor-related protein complex 1, sigma	7.2
	407881	AA072003	Hs 40996	heparan sulfate (glycosaminic) 3-O-sulfat	7.2
80	428728	NM_015625	Hs 191381	hypothetical protein	7.1
	416111	AA033813	Hs 79018	chromatin assembly factor 1, subunit A	7.1
	432281	AK001239	Hs 274263	hypothetical protein FLJ10377	7.1
	410434	AF051152	Hs 63668	cell-he receptor 2	7.1

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420018	U56387	Hs.94376	protoporphyrinogen oxidoreductase 1	7.1
418293	A1224483	Hs.16063	hypothetical protein FLJ121877	7.1
424954	NM_000546	Hs.1946	tumor protein p53 (Li-Fraumeni syndrome)	7.0
445900	AF070326	Hs.125936	Homo sapiens clone 24787 mRNA sequence	7.0
419741	NM_007019	Hs.53002	ubiquitin carrier protein E2-C	7.0
422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S cerevisiae)	7.0
434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.9
416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	6.9
424381	AA382948	Hs.146329	protein kinase C-2	6.9
410064	XS3416	Hs.195464	filamin A, alpha (actin-binding protein)	6.9
415682	A1347128	Hs.191870	ESTs	6.9
421977	W94197	Hs.110195	ribosomal protein L26 homolog	6.8
429447	AHW12452	Hs.132036	ESTs, Weakly similar to S14747 aphragmy	6.8
423198	M81933	Hs.1634	cell division cycle 25A	6.8
413627	BE182082	Hs.246973	ESTs	6.8
412777	A1335773	Hs.270123	ESTs	6.8
409479	X33552	Hs.56729	lymphocyte-specific protein 1	6.8
451129	BE072881	gc-R1C2-BT0548-200,300,412.e09	BT0548 Homo	6.8
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.7
446131	NM_000520	Hs.290	phospholipase A2, group V	6.7
441703	AW390554	Hs.192843	isucine zipper protein FKSG14	6.7
423211	AW445044	Hs.38207	Human DNA sequence from clone RP4.530015	6.7
425202	AW562282	Hs.152049	ESTs, Weakly similar to D80227 hypotheti	6.7
408161	AW952912	Hs.300383	hypothetical protein MGC3032	6.7
440704	M89241	Hs.162	intra-fil-like growth factor binding prote	6.7
407161	AA312551	Hs.230157	ESTs	6.7
445837	A1261700	Hs.145544	ESTs	6.6
433376	A1249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	6.6
431211	M86849	Hs.323933	gap junction protein, beta 2, 26kD (conn	6.6
447439	AA313565	Hs.158620	ESTs, Weakly similar to KIAA1203 protein	6.5
407235	D05659	Hs.169407	SAC2 (suppressor of actin mutations 2, y	6.5
450506	NM_004460		fibroblast activation protein, alpha	6.5
432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	6.5
418054	NM_002318	Hs.83354	lysoyl oxidase-2	6.5
432799	A1948829	Hs.213786	ESTs	6.5
446557	A1335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	6.4
424247	X14008	Hs.234734	lysosomal (renal amyloidosis)	6.4
444394	N20617	Hs.194397	leptin receptor	6.4
422560	AW207748	Hs.59115	ESTs	6.4
419465	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	6.3
420649	A1866964	Hs.124704	ESTs, Moderately similar to S65657 alpha	6.3
457465	AW301344	Hs.122908	DNA replication factor	6.3
446332	A1276517	Hs.168051	ESTs	6.3
446246	AW411120	Hs.23363	hypothetical protein FLJ110983	6.3
413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.2
448275	BE514434	Hs.20830	kinesin-like 2	6.2
440286	U25589	Hs.7138	cholinergic receptor, muscarinic 3	6.2
435518	W76328	Hs.100004.01	Scoraei, fetal heart, Nbl-H119W	6.1
412567	A1750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	6.1
426635	NM_000088	Hs.172928	collagen, type I, alpha 1	6.1
456977	AK000252	Hs.169758	hypothetical protein FLJ120245	6.1
428450	NM_014791	Hs.154339	KIAA0175 gene product	6.0
411225	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	6.0
413786	AW613780	Hs.13500	ESTs	6.0
410555	U92649	Hs.54311	a disintegrin and metalloproteinase doma	5.9
400419	AF304545		Target	5.9
405380	AF123950	Hs.44532	ubiquitin	5.9
426108	AA622037	Hs.166468	programmed cell death 5	5.9
418774	X02419	Hs.77274	plasminogen activator, urokinase	5.9
437865	AA769202	Hs.192142	ESTs	5.9
409463	AA58165	Hs.17296	hypothetical protein MGC23376	5.8
411048	AK001742	Hs.67991	hypothetical protein DKF7p434G0522	5.8
443731	A1083028	Hs.145418	ESTs	5.8
405568			Target Exon	5.8
422094	AF129635	Hs.272027	-beta-actin only protein 5	5.8
429113	D82835	Hs.195334	prostaglandin-endoperoxide synthase 2 (p	5.8
425882	U83115	Hs.161002	absent in melanoma 1	5.8
412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	5.8
425149	AW193360	Hs.197962	ESTs, Weakly similar to D80022 hypotheti	5.7
434807	H71217	Hs.5332	guanine nucleotide binding protein (G pr	5.7
435905	AE032959	Hs.318684	novel C3HC4 type Zinc finger (ring finger	5.7
414053	BE391636	Hs.75725	transgelin 2	5.7
436805	AA731533	Hs.270751	ESTs	5.7
442201	AW516704	Hs.208785	ESTs	5.7
453361	AA035197	Hs.107375	ESTs	5.6
429083	Y09397	Hs.227817	BCL2-related protein A1	5.6
426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	5.6
423381	AF262992	Hs.123159	sperm associated antigen 4	5.6
407013	U35637		gH-human melanin mRNA, partial cets	5.5
405478			Target Exon	5.5
435937	AA830893	Hs.119769	ESTs	5.5
453362	H14988	Hs.107375	ESTs	5.5
449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fs, clone PL	5.5

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5	442547	AA305997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.5
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibitor	5.5
	429643	AA455889	Hs.167279	FYVE finger-containing Rab5 effector pro	5.5
	407862	BE482467	Hs.337986	Homo sapiens cDNA FLJ10934 fls, clone OV	5.4
	407624	AW157431	Hs.248941	ESTs	5.4
10	448769	H66537	Hs.38173	ESTs	5.4
	417124	BE122662	Hs.25338	ESTs	5.4
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	5.4
	457292	AW21270	Hs.281462	hypothetical protein FLJ14251	5.3
	418596	AW678721	Hs.293327	ESTs	5.3
15	410295	AA741357	Hs.5174	nidogen (enactin)	5.3
	433323	AA805132	Hs.159142	ESTs	5.3
	412326	R07566	Hs.17817	small inducible cytokine A3 (homologous	5.3
	418630	AJ351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	5.3
	420075	AF142482	Hs.203846	TEA domain family member 3	5.2
20	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	5.2
	407729	T40707	Hs.270862	ESTs	5.2
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	5.2
	441432	AA143654	Hs.345072	gb:z65a02.1 Stratiopene pancreas, 630720	5.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	5.2
25	424998	U58516	Hs.154138	chitinase 3-like 2	5.2
	407603	AW555705	Hs.62664	Homo sapiens, clone IMAGE:4295322, mRNA,	5.2
	445118	AJ208162	Hs.345072	ESTs	5.2
	408523	AW633259	Hs.314287	ESTs	5.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	5.2
30	449300	AJ656953	Hs.346514	ESTs	5.2
	429732	UJ20158	Hs.2498	lymphocyte cytosolic protein 2 (SH2 doma	5.2
	423757	ALC49337	Hs.132571	Homo sapiens mRNA, cDNA DKF Zp564P016 (fr	5.1
	439570	T79525	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (beta D, chr	5.1
35	443604	CD3577	Hs.9616	myosin regulatory light chain 2, smooth	5.1
	421247	BE391727	Hs.102910	general transcription factor IIR, polyep	5.1
	416913	AW594714	Hs.93913	gb:RC1-DT0001-031259-01-a11 DT0001 Homo	5.1
	419968	XD4430	Hs.93913	interleukin 6 (interferon, beta 2)	5.0
	424409	F11690	Hs.93913	gb:HS3C0041 normalized infant brain cDN	5.0
40	412833	SP98915	Hs.83942	cathepsin K (lysosomal acidosis)	5.0
	429469	ME4590	Hs.27	glycine dehydrogenase (decarboxylating);	5.0
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosaminine) 3-O-sulfat	5.0
	418397	RA5137	Hs.21868	ESTs	5.0
45	453331	AJ240865	Hs.213586	ESTs	4.9
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.9
	426044	AA502490	Hs.170290	ESTs	4.9
	444161	NS2543	Hs.142340	ESTs	4.9
	423227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.9
50	432442	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.9
	447752	M73700	Hs.105938	lactotransferrin	4.9
	439627	BE621702	Hs.29076	hypothetical protein FLJ21841	4.9
	402274		C19000498	g14567179gMAD23607 1JAC00	4.9
	444656	AJ277924	Hs.145159	ESTs	4.9
55	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	4.9
	443744	AJ084326	Hs.271548	ESTs, Weakly similar to I78885; senile	4.9
	416871	H98716	Hs.271548	gb:y13008.1 Soxies melanocyte 2N94M Ho	4.9
	402112	BE43971	Hs.50649	quinine oxidoreductase homolog	4.8
	403481			Target Exon	4.8
60	434507	R56434	Hs.21062	ESTs	4.8
	430025	U80743	Hs.300394	trinucleotide repeat containing 12	4.8
	429163	AA584766	Hs.300394	gb:n20a10.11 Soares, NFL_T_GBC_S1 Homo s	4.8
	451418	BE387790	Hs.26369	hypothetical protein FLJ20827	4.8
	428403	AJ393048	Hs.326159	leucine rich repeat (in FLJ) interaction	4.8
65	430968	AW572830	Hs.326159	gb:EST34925 MAGe resequences, MAGL Homo	4.8
	425212	AW982223	Hs.176168	ESTs	4.8
	409205	AJ552884	Hs.14832	ESTs, Moderately similar to unnamed prot	4.8
	431176	AJ026984	Hs.253662	ESTs	4.8
	420092	AA814043	Hs.88045	ESTs	4.8
70	437834	AA769294	Hs.283654	gb:n336g02.s1 NC1_CGAP, GC3B1 Homo sapiens	4.8
	432363	AA534489	Hs.283654	gb:n336g02.s1 NC1_CGAP, GC3B1 Homo sapiens	4.8
	403011			ENSP00000215330*Probable serine/threonine	4.7
	405348			C7001664:g12698051dbJBAR21649.11 (AB	4.7
	447072	D61594	Hs.17279	thymoprotein sulfotransferase 1	4.7
75	443318	AJ051603	Hs.131141	ESTs	4.7
	421027	AA761198	Hs.55254	ESTs	4.7
	449318	AW260021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	4.7
	429170	NM_001394	Hs.2389	dual specificity phosphatase 4	4.7
	411852	AA578140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	4.7
80	402166	AA426904	Hs.107515	ESTs	4.7
	438456	AA913381	Hs.20594	ESTs	4.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	4.7
	438527	AF695251	Hs.115325	R4B7, member RAS oncogene family like 1	4.7
	458946	AA029716	Hs.42311	ESTs	4.7
	454980	AW835767	Hs.152701	gb:QV4.LT0016.240200-110-b08.LT0016 Homo	4.7
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.6
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.6

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	422648	D85893	He 118893	Melanoma associated gene	4.6
	431319	AA873350	He 302232	ESTs	4.6
	445666	R59660	He 282386	ESTs	4.6
5	416405	D85951	He 75259	ipoma HMGC fusion partner-like 2	4.6
	422887	A1751848	He 49215	ESTs	4.6
	422938	NM_001809	He 1594	centromere protein A (17kD)	4.6
	405141	Y14443		zinc finger protein 200	4.6
	440210	AW674682	He 125296	ESTs	4.6
10	432527	AW974028	He 102754	ESTs	4.6
	435726	AW440893	He 293707	ESTs, Weakly similar to G8598 zinc fing	4.6
	435143	R12375	He 194600	ESTs	4.6
	422170	A1791949	He 112432	anti-Mullerian hormone	4.6
	462574	A0001061	He 30525	hypothetical protein FLJ10193	4.6
15	406295	A1979168	He 344056	glycoprotein (transmembrane) nmh	4.5
	412568	A878826	He 74034	cavovirin 1, cavovirae protein, 22kD	4.5
	426215	AW663419	He 155223	stannocalcin 2	4.5
	413076	U10564	He 75188	wee1 (S. pombe) homolog	4.5
	456769	BE291190	He 127792	delta (Drosophila) like 3	4.5
20	419735	AW750055	He 169577	Homo sapiens cDNA FLJ114743 fs, clone NT	4.5
	433675	AW577653	He 75319	ribonucleotide reductase M2 polypeptide	4.5
	441217	A822183	He 131246	ESTs	4.5
	435542	AA681737		ESTs	4.5
	404435	AL042201	He 21273	transcription factor MYD-ap10	4.5
25	406288	X06256	He 149609	integrin, alpha 5 (fibronectin receptor,	4.5
	416114	A055549	He 183858	glucuronidase, beta	4.5
	437323	AA371146	He 194397	iodin receptor	4.5
	425139	AW630458	He 25336	penicillin, sorine, 23	4.5
	423678	AW953357	He 7847	ESTs	4.5
30	403951			Target Exon	4.5
	443462	A064890	He 171176	ESTs	4.5
	414843	BE25075	He 221847	ESTs	4.5
	428873	A1701609	He 58958	ESTs	4.5
	410268	AA316181	He 61635	slk transmembrane epithelial antigen of	4.5
35	408298	A1745325	He 271923	Homo sapiens cDNA: FLJ22785 fs, clone K	4.5
	439145	A1632122	He 198408	ESTs	4.4
	435674	A4607186	He 168190	ESTs	4.4
	423955	AW579960	He 135150	lung type-I cell membrane-associated gly	4.4
	453387	A1990741	He 252809	ESTs	4.4
40	447444	AK000318	He 18616	hypothetical protein FLJ20311	4.4
	433507	A817336	He 191791	ESTs	4.4
	448049	BE281291	He 170408	ESTs, Moderately similar to A45782 B-cell	4.4
	421064	A1245432	He 101382	tumor necrosis factor, alpha-induced pro	4.4
	402604			Target Exon	4.4
45	446291	BE397753	He 14523	interferon, gamma-inducible protein 30	4.4
	424503	NM_002205	He 149509	integrin, alpha 5 (fibronectin receptor,	4.4
	423600	A633559	He 310359	ESTs	4.4
	403391			NM_002210: Homo sapiens integrin, alpha	4.4
	408432	AW195262		glnrnf/605-x1 NCI_CGAP_CML1 Homo sapiens	4.4
50	424459	T48831	He 274470	D-tiglic acid precursor,	4.3
	442264	A1278777	He 263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3
	447247	AW939351	He 287955	Homo sapiens cDNA FLJ13090 fs, clone NT	4.3
	417018	M16036	He 80887	v-yes-1 Yamaguchi sarcoma viral related	4.3
	414020	NM_002884	He 75763	small inducible cytokine A4 (hemopoiesis	4.3
55	438565	AF085387		gloHomo sapiens full length insert cDNA	4.3
	425242	D13635	He 155287	KIAA0010 gene product	4.3
	423529	T87316	He 120411	ESTs	4.3
	438538	AA637323	He 56407	ESTs	4.3
	433602	T72703		gdyd71e08L1 Soares fetal liver spleen	4.3
60	425259	AL049280	He 155397	Homo sapiens mRNA: cDNA DKF2564K143 (fr	4.3
	417818	AA205205	He 153754	hypothetical protein FLJ12606	4.3
	428640	A914936	He 57152	ESTs	4.3
	438575	AA627540	He 189509	ESTs	4.3
	445968	BE165357	He 207428	ESTs	4.3
65	426509	M31155	He 2050	penicillin-related gene, rapidly induced b	4.3
	428853	AW247090	He 57101	minichromosome maintenance deficient (S,	4.3
	423059	AW665996	He 130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3
	430694	AA510624	He 30535	ESTs, Weakly similar to H2B_HUMAN HISTO	4.3
	441523	AW514263	He 301771	ESTs, Weakly similar to ALUF_HUMAN H	4.2
70	443950	NM_001425	He 9999	epithelial membrane protein 3	4.2
	419895	295352		gb.HS299362 DKF Zp5470065	4.2
	452294	AW952597	He 31305	KIAA1547 protein	4.2
	420841	A1625251	He 94037	hypothetical protein FLJ23053	4.2
	441255	R05350	He 171635	ESTs	4.2
75	414626	AA186258	He 210473	Homo sapiens cDNA FLJ14572 fs, clone PL	4.2
	411785	AF245555	He 72157	Adipon	4.2
	409638	AA505420	He 21335	ESTs	4.2
	439192	AW970536	He 105413	ESTs	4.2
	440984	AL253123	He 127356	ESTs, Highly similar to S21424 nestin (H	4.2
	437470	AL390747	He 134742	hypothetical protein DKF Zp5470065	4.2
80	432343	NM_002960	He 2951	S100 calcium-binding protein A3	4.2
	401454			NM_014228: Homo sapiens renal tumor ant	4.2
	431770	BE221880	He 288555	5'-3' exon/bicoidase 5	4.2
	442326	HS2952	He 124813	hypothetical protein MGC14817	4.2

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	419402	Z68155	Hs.90291	laminin, beta 2 (laminin 5)	4.2
	435703	AW630133	Hs.83313	GK003 protein	4.2
	444609	AW571659	Hs.278081	ESTs	4.2
5	404407			Target Exon	4.2
	450581	AF081513	Hs.25195	TGF-beta 4	4.2
	407838	BE146411	Hs.40342	putative nuclear protein	4.1
	410407	X68639	Hs.63287	carbonic anhydrase IX	4.1
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.1
	438998	A1815963	Hs.100243	ESTs	4.1
10	421674	T10707	Hs.296355	hypothetical protein FLJ123138	4.1
	445921	AW015211	Hs.146181	ESTs	4.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC-9658, mRNA, comp	4.1
	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	4.1
15	427463	AA442224	Hs.97000	ESTs	4.1
	450639	A1073186	Hs.271714	ESTs	4.1
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransferase	4.1
	437629	AA334384	Hs.149420	ESTs	4.1
	415688	AA161863	Hs.186680	gb-m85d01.s1 Stratiogene ovarian cancer	4.1
20	414300	A0304670	Hs.8333	ESTs	4.1
	413278	BE563085	Hs.8333	interferon-stimulated protein, 15 kDa	4.1
	415024	A1963961	Hs.189114	ESTs	4.1
	408102	U46351	Hs.621	lactin, galactoside-binding, soluble, 3	4.1
	448919	AW947164	Hs.165641	ESTs, Moderately similar to U88022 hypol	4.1
25	451433	AA021140	Hs.269285	ESTs, Weakly similar to A46010 X-linked sarcoplasm	4.1
	446523	NM_003063	Hs.334629	sarcoplasm	4.1
	427700	AA262294	Hs.160383	acid specificity phosphatase 5	4.1
	402229			Target Exon	4.1
	432713	AW754182	gc.RC2-C10321-131199-011-e01 C10321 Homo	4.1	
30	437814	A1088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	4.1
	414948	C15240	Hs.182155	ESTs	4.1
	421307	BE339976	Hs.103305	Homo sapiens mRNA: cDNA DKFZp434B0425 (f	4.0
	427375	AL035480	Hs.177536	metallocarboxypeptidase CPX-1	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
35	449655	A1021987	Hs.59970	ESTs	4.0
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fs, clone HE	4.0
	432942	AA674083	Hs.334822	hypothetical protein MGC4485	4.0
	422822	AF619225	Hs.114309	apolipoprotein L	4.0
	452574	AF127481	Hs.301946	lymphoid blast crisis oncogene	4.0
40	449256	AA059050	Hs.59847	ESTs	4.0
	453385	AW296101	Hs.252806	ESTs	4.0
	443715	A1583187	Hs.9700	cyclin E1	4.0
	451778	A1826131	Hs.62954	ESTs, Weakly similar to zinc finger prot	4.0
	441287	AW293132	Hs.131373	ESTs	4.0
45	418681	NM_001949	Hs.1189	CBF transcription factor 3	4.0
	420894	AA744597	Hs.88854	ESTs	4.0
	454120	AB032990	Hs.40719	hypothetical protein KIAA1164	4.0
	441627	AA947552	Hs.58085	branched chain aminotransferase 1, cytos	4.0
	455948	A1970797	Hs.64859	ESTs	4.0
50	444170	AW613879	Hs.102408	ESTs	4.0
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	418216	AA662240	Hs.283099	AF15q14 protein	4.0
	435105	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	4.0
55	430890	X54232	Hs.2699	glypican 1	3.9
	429490	A1971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.9
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.9
	436265	AA731331	Hs.199468	ESTs	3.9
	407304	AA656839	Hs.271649	gbm32N03.s1 NCI_CGAP_AA1 Homo sapiens	3.9
60	433244	AB040943	Hs.271285	KIAA1510 protein	3.9
	446960	AW294936	Hs.156762	ESTs	3.9
	406627	T64904	Hs.163780	ESTs	3.9
	402552	AK000492	Hs.389605	hypothetical protein	3.9
	402062			C18000743-g16678363yefHP_033416 t1 t	3.9
65	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.9
	449966	AW372914	Hs.86149	phosphoinositide 3-kinase-binding prot	3.9
	421527	A180657	Hs.293441	immunoglobulin heavy constant mu	3.9
	422564	A1180006	Hs.222120	ESTs	3.9
	418781	T41160	Hs.8404	ESTs	3.9
70	431820	AW410408	Hs.271167	L-lipoic acid oxidase	3.9
	413095	AA944359	Hs.30715	potassium voltage-gated channel, Ish-rel	3.9
	430837	BE160081	Hs.266280	S100 calcium-binding protein A11 (calgiz	3.9
	443539	A1076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	3.9
	422173	BE385823	Hs.250619	phorbol-like protein MDS019	3.9
75	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	3.8
	403849			Target Exon	3.8
	406646	M33600	Hs.308026	major histocompatibility complex, class	3.8
	445075	A1851827	Hs.344767	ESTs	3.8
	402004	AW915532	Hs.164039	ESTs, Moderately similar to U88022 hypol	3.8
80	449670	FO7183	Hs.85503	Homo sapiens mRNA: cDNA DKFZp434K2172 (f	3.8
	424479	AF064238	Hs.146066	smoothelin	3.8
	449625	NM_014253		ozd (Oz1/en m, Drosophila) homolog 1	3.8
	418641	BE243136	Hs.86847	a disintegrin and metalloproteinase doma	3.8
	439979	AW602291	Hs.6823	hypothetical protein FLJ10430	3.8

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427266	AW732602	Hs.2132	epidermal growth factor receptor pathway	3.8
453920	AI133148	Hs.36602	I factor (complement)	3.8
453857	AL080235	Hs.35861	DKF ZP586E1621 protein	3.8
406872	AI705903		gb w19908.x1 NC_024047 Homo sapiens	3.8
423696			C40011007.g15552342g15A054915.11 (AF0	3.8
417791	AW065339	Hs.111471	ESTs	3.8
418036	Z37976	Hs.83337	latent transforming growth factor beta b	3.8
404209			Target Exon	3.8
431454	AW915960	Hs.292918	ESTs	3.8
410422	AL042014	Hs.63346	Homo sapiens, clone MGC:15203, mRNA, com	3.8
406739	AI566701	Hs.182426	ribosomal protein S2	3.8
450810	BE075588	Hs.334360	transforming growth factor beta 1 induce	3.8
457876	AI821540		ESTs, Moderately similar to ALU1_HUMAN A	3.8
435718	R05699	Hs.265634	ESTs	3.8
429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.8
442710	AI015631	Hs.23210	ESTs	3.8
450534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.8
413764	BE262524	Hs.53183	vascular-stimulated phosphoprotein	3.8
436674	AA725002	Hs.272018	low molecular mass ubiquitin-binding pr	3.8
406896	AI510447	Hs.46778	riban protein	3.8
423300	AW601773	Hs.270259	ESTs	3.8
432866	BE159628	Hs.275704	chromatin accessibility complex 1	3.8
424090	XQ3999	Hs.139262	XOAP associated factor 1	3.7
420202	AL036357	Hs.95910	putative lymphocyte G/G1 switch gene	3.7
427584	BE410293	Hs.179718	v-myb avian myeloblastic virus oncogen	3.7
426579	AA728449	Hs.137429	ESTs	3.7
409638	Y14443		zinc finger protein 200	3.7
412590	AL134388	Hs.135033	ESTs, Weakly similar to 130222 hypothel	3.7
406714	AI219304	Hs.266559	hemoglobin, gamma G	3.7
412014	AI820850	Hs.43761	ESTs, Weakly similar to A63010 X-linked	3.7
415713	AW960359	Hs.523381	nucle (nucleoside diphosphate linked mo	3.7
449115	AW959952	Hs.37528	ESTs, Weakly similar to AF-090944 1 PRO06	3.7
408955	BE315170	Hs.8087	Target CAT	3.7
441352	BE514410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	3.7
413774	AA131782	Hs.162314	ESTs	3.7
440225	BE285782	Hs.159	tumor necrosis factor receptor superfam	3.7
414528	AA148950	Hs.188638	ESTs	3.7
436137	AI056769	Hs.133512	ESTs	3.7
414733	BE514335	Hs.717171	minichromosome maintenance deficient (S	3.7
407845	AA580361		gb w106053.x1 NC_024047 Homo sapiens	3.7
443361	AI792628	Hs.133273	ESTs	3.7
434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.7
409557	BE126986	Hs.211193	ESTs	3.7
426300	AA282345	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
427695	R84463	Hs.172682	ESTs	3.7
407756	AA116021	Hs.38250	ubiquitin specific protease 18	3.6
437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6
434503	AW083954	Hs.5459	pleckstrin homology domain-containing, f	3.6
444371	BE540274	Hs.239	forward box M1	3.6
437616	AI823445	Hs.280699	ESTs	3.6
405605			C2001342.g1127814spP26434NA44_RAT SO	3.6
444754	AI419991	Hs.145225	ESTs	3.6
435640	AI024522	Hs.106357	Homo sapiens cDNA: FLJ22105 fs, clone H	3.6
429747	M87507	Hs.2490	casepase 1, apoptosis-related cysteine pr	3.6
453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.6
403267			Target Exon	3.6
440370	AA084000	Hs.8173	hypothetical protein FLJ10803	3.6
447467	AW161254	Hs.205722	ESTs	3.6
428600	AW863261	Hs.242413	hypothetical protein DKF Zp34K1421	3.6
428715	AI0293716	Hs.53126	ESTs	3.6
416087	BE387371	Hs.118564	hypothetical protein FLJ20085	3.6
453438	AA089265	Hs.22762	ESTs	3.6
427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.6
434577	R73716	Hs.179769	Homo sapiens cDNA: FLJ22487 fs, clone H	3.6
452785	AI359942	Hs.296434	erythroid differentiation and deacetyl	3.6
434467	BE552386	Hs.231853	Homo sapiens cDNA: FLJ13445 fs, clone PL	3.6
435523	162648	Hs.11090	membrane-spanning 4-domains, subfamily A	3.6
418287	AI872319	Hs.78535	methylome aminopeptidase, eIF-2-associ	3.6
422156	NA3524		glycy56410.s1 Scores, multiple_sclerosis,	3.6
441224	AI007684	Hs.7753	calumenin	3.6
458072	AW863347	Hs.271923	Homo sapiens cDNA: FLJ22765 fs, clone X	3.6
435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.6
433325	AW206986	Hs.143905	ESTs	3.6
420663	AA530158	Hs.271305	ESTs	3.6
443206	AB011420	Hs.9075	serine/threonine kinase 17a (apoptosis-i	3.6
454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.6
404584			Target Exon	3.5
428311	NM_005851	Hs.183671	tyrosophan 2,3-dioxygenase	3.5
425922	AL151466	Hs.162751	Homo sapiens mRNA: cDNA DKF Zp761E2423 (f	3.5
413131	DB1119		gb HUM158C11B Contect human fetal brain	3.5
412971	AA889628	Hs.35125	ESTs	3.5
451593	AF151879	Hs.26706	CGI-121 protein	3.5
410427	BE244050	Hs.73307	RacGdc42 guanine exchange factor (GEF)	3.5

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	427809	MD6380	Hs.180878	lipoprotein lipase	3.5
	443303	U67319	Hs.9216	caseinase 7, apoptosis-related cysteine pr	3.5
	422765	AAW409701	Hs.1578	baculoviral IAP repeat-containing 5 (bur	3.5
	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	3.5
5	411537	BE012290	gib.MRO-BT0551-046100-102-a05 BT0551 Homo	3.5	
	432260	AA452088	Hs.274170	Gp-interacting protein 2	3.5
	458438	AH141520	Hs.151464	ESTs, Weakly similar to ALLOC_HUMAN H	3.5
	407263	AA411175	Hs.141939	ESTs, Moderately similar to S66567 human	3.5
	410507	AA355288	Hs.76064	transitional epithelia response protein	3.5
10	417436	AA669089	gib.mut76101.1 NCL_CGAP_Pv1 Homo sapiens	3.5	
	416933	BE551850	Hs.80506	small nuclear ribonucleoprotein polypept	3.5
	437681	A1207958	Hs.165556	Home sapiens, Similar to TEA domain fami	3.5
	408247	AA053451	Hs.225632	leucine zipper protein 3	3.5
	440074	AA49E045	Hs.10599	ESTs, Weakly similar to T00050 hypotheti	3.5
15	422448	AW372922	Hs.116774	integrin, alpha 1	3.5
	420676	AA434780	Hs.4248	vav 2 oncogene	3.5
	417863	R07483	Hs.184641	ESTs	3.5
	451085	AA930705	Hs.4190	Home sapiens cDNA: FLJ23269 fic, clone C	3.5
20	451446	AH826288	Hs.171637	hypothetical protein MGC26:28	3.5
	414727	BE466904	Hs.190162	gib.hz2093.1 NCL_CGAP_GCG Homo sapiens	3.5
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	3.5
	427413	BE547547	Hs.177781	hypothetical protein MGC5518	3.5
	414039	ME3221	Hs.859	v-rel vira1 reticuloendotheliosis viral	3.5
	456304	AH820973	gib.nc21c02.y5 NCL_CGAP_Pv1 Homo sapiens	3.5	
25	449162	AH632740	Hs.10476	ESTs	3.5
	437774	AA3078199	Hs.291648	ESTs, Weakly similar to 180022 hypother	3.5
	429527	AA061705	Hs.172655	methylcrotonylhydroxylase dehydrogenase	3.5
	452203	XS7522	Hs.26289	transporter 1, ATP-binding cassette, sub	3.4
	450325	AH395962	Hs.26289	ESTs	3.4
30	452711	AA972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	3.4
	419726	US5336	Hs.1274	bone morphogenetic protein 1	3.4
	417400	BE272506	Hs.82109	syndecan 1	3.4
	412811	H06382	Hs.10476	ESTs	3.4
	430798	T91568	Hs.270616	ESTs, Moderately similar to A34087 hypot	3.4
35	425769	U72513	Hs.159486	human RPL13-2 pseudogene mRNA, complete	3.4
	452682	AA48193	Hs.5071	progesterone membrane binding protein	3.4
	429500	X47595	Hs.289114	hexabrachion (tenascin C, cytotactin)	3.4
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	3.4
	443376	AA392520	Hs.5280	proteasome (prosome, macropain) subunit,	3.4
40	445134	AH161234	Hs.13953	TBP-like 1	3.4
	418669	U85992	Hs.87197	Human clone IMAGE:35527 unknown protein	3.4
	425006	R36885	Hs.222746	ESTs	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	453379	AA035281	Hs.61753	ESTs	3.4
45	448224	RA4700	Hs.20733	Home sapiens cDNA: FLJ23356 fic, clone H	3.4
	455899	BE155112	gib.PM1-41T0350-151299-a03 HT0350 Homo	3.4	
	422017	NM_003877	Hs.110076	STAT induced STAT inhibitor-2	3.4
	417395	BE564245	Hs.82064	integrin beta 3 binding protein (beta3-a	3.4
	425046			C2000576.gib2904-9.gib1401575.1 (AB	3.4
50	423178	AH031340	Hs.124983	Home sapiens mRNA, cDNA DKFZ564C142 (f	3.4
	455142	AA061840	gib.CMO-CT0337-250200-243-g01 CT0337 Homo	3.4	
	418819	AA228776	Hs.191721	ESTs	3.4
	424269	M05301	Hs.2253	complement component 2	3.4
55	417299	A267606	gib.SP11N03.x1 Stanley Frontal S8 pool 1	3.4	
	403108		ENSP00000241415*Hypothetical 67.7 kDa p	3.4	
	421637	AF035290	Hs.106300	Home sapiens clone Z3556 mRNA, sequence	3.4
	419373	NM_003244	Hs.50077	TG-interacting factor (TALE family home	3.4
	424048	AF54613	Hs.146428	collagen, type V, alpha 1	3.4
60	451061	AA291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.4
	433576	BE336886	Hs.3416	adipose differentiation-related protein	3.4
	439867	AA847510	Hs.161292	ESTs	3.4
	445249	TS5285	Hs.193115	Home sapiens mRNA for KIAA1764 protein,	3.4
	420982	AA575180	Hs.100729	KIAA0992 protein	3.4
	440826	AA383618	Hs.346256	ESTs, Moderately similar to ALLOC_HUMAN A	3.4
65	427687	AA003067	Hs.1570	Histamine receptor h1	3.4
	420533		ENSP0000020537P-PRED65 protein (Fragmen	3.3	
	496314	AH983409	Hs.189226	ESTs	3.3
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	3.3
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.3
70	422729	BE262604	Hs.50077	mitochondrial ribosomal protein S2	3.3
	410807	U24389	Hs.65436	hyal oxidase-like 1	3.3
	424614	XS4486	Hs.151242	serine (or cysteine) proteinase inhibito	3.3
	443338	R59575	Hs.302908	ESTs	3.3
	433062	AK001757	Hs.281348	hypothetical protein FLJ10895	3.3
75	455303			Target Exam	3.3
	410889	XS1862	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.3
	406673	M34956	Hs.198253	major histocompatibility complex, class	3.3
	431721	AB032996	Hs.268044	KIAA1170 protein	3.3
	425746	X3626	Hs.2057	uridine monophosphatyl synthetase (arout	3.3
80	425262	O27119	Hs.155418	GS3955 protein	3.3
	424947	R77952	Hs.155418	ESTs, Weakly similar to alternatively sp	3.3
	437634	AA293046	Hs.255158	ESTs	3.3
	437014	AA806757	Hs.222531	ESTs, Weakly similar to S59501 interfero	3.3

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	411688	AW563440		gb EST365510 IMAGE resequences, MAGB Homo	3.3
	447499	AW262580	Hs.147674	protocadherin beta 16	3.3
	432625	AI283596	Hs.04830	ESTs, Moderately similar to T03094 A-kin	3.3
	435644	AA700867	Hs.26959	ESTs	3.3
5	496060			Target Exon	3.3
	428018	BE245277	Hs.154196	EAF transcription factor 1	3.3
	450728	AW162523	Hs.25353	presenilin 2 (Alzheimer disease 4)	3.3
	443105	X96753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	3.3
	441759	AF25416	Hs.71326	insulin-like growth factor binding prote	3.3
10	435375	AF33610	Hs.167832	ESTs	3.3
	432693	AW449630	Hs.253790	ESTs	3.3
	445340	AW235786	Hs.155359	hypothetical protein MGC10954	3.3
	422530	AK672300	Hs.118110	bone marrow chromatin cell antigen 2	3.3
	448022	Y15227	Hs.20145	deleted in lymphocytic leukemia, 1	3.3
15	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	3.3
	429125	AA446854	Hs.271004	ESTs, Weakly similar to U38022 hypotheti	3.3
	452526	W36537	Hs.260740	hypothetical protein MGC3040	3.3
	415664	HT2760	Hs.20280	ESTs	3.3
	444511	U06117	Hs.250	xanthine dehydrogenase	3.3
20	453644	AA831765	Hs.171914	Homo sapiens cDNA FLJ14209 fs, clone NT	3.3
	433042	AW193534	Hs.261895	Homo sapiens cDNA FLJ11660 fs, clone HE	3.3
	444546	AB580834	Hs.136594	ESTs	3.3
	411373	BE326276	Hs.8861	ESTs	3.3
	431865	AA521106	Hs.136375	ESTs, Weakly similar to S65824 reverse t	3.3
25	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	3.3
	410006	AW132628	Hs.57763	cytokinetic transition initiation factor	3.3
	442455	BE092285	Hs.26724	hypothetical protein FLJ13167	3.3
	416379	N38657	Hs.203933	ESTs	3.3
	416306	AW261942	Hs.23626	3 beta-hydroxy-delta 5-C27-steroid oxido	3.3
30	427954	J03060	Hs.247551	metastin 1	3.3
	459660	MT6682		ESTs	3.3
	419829	AF242228	Hs.115165	ESTs, Moderately similar to PC4259 ferri	3.3
35	437545	T78519		glycylserine C181 Scores fetal liver spleen	3.3
	400850			Target Exon	3.3
	457244	AA581385	Hs.162473	ESTs, Weakly similar to U38022 hypotheti	3.3
	430462	AB84156	Hs.105640	Homo sapiens, clone IMAGE:41397/5, mRNA,	3.3
	457653	AB207119	Hs.154662	DnaI (Hsp40) homolog, subfamily A, membe	3.3
	431836	AF176332	Hs.271411	beta-site APP-cleaving enzyme 2	3.2
40	445933	AD206217	Hs.142679	ESTs	3.2
	418079	AA026164	Hs.69911	ESTs	3.2
	414280	BE410769	Hs.75873	zysyn	3.2
	425296	AA431366	Hs.37251	ESTs	3.2
	408872	AA767139	Hs.13261	ESTs	3.2
45	416857	AA189775	Hs.292433	ESTs	3.2
	429599	AA806108	Hs.123594	ESTs	3.2
	437437	AA226869		hypothetical protein DKFZp762L0311	3.2
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.2
	403349	NM_001406		ephrin-B3	3.2
50	449385	AF650471	Hs.347290	ESTs	3.2
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.2
	419865	NM_007020	Hs.53202	U1-snRNP binding protein homolog (70kD)	3.2
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.2
	432044	AW972727		gb EST334019 IMAGE resequences, MAGL Homo	3.2
55	412460	AW603564	Hs.288850	Homo sapiens cDNA, FLJ22526 fs, clone H	3.2
	408431	AI338631	Hs.43266	Homo sapiens cDNA, FLJ22536 fs, clone H	3.2
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.2
	448789	BE539103	Hs.22051	hypothetical protein MGC15548	3.2
	439332	AW842747	Hs.300870	Homo sapiens mRNA, cDNA DKFZp547M072 (fr	3.2
	418030	BE207573	Hs.83321	neuromedin B	3.2
60	426876	AA436884	Hs.48926	ESTs	3.2
	451527	AF222813	Hs.26516	transmembrane 4 superfamily member 7	3.2
	426406	AI42261	Hs.159565	complement component 1, epsilon component	3.2
	448432	AI763566	Hs.206575	ESTs	3.2
	433894	AI907682	Hs.243293	ESTs	3.2
65	436270	AE254240	Hs.151624	ESTs	3.2
	433751	AA719362	Hs.112716	ESTs	3.2
	450150	AI754361	Hs.23510	Kruppel-like factor 12	3.2
	427513	AI476318	Hs.152480	ESTs	3.2
70	423769	AK002084	Hs.132851	hypothetical protein FLJ11122	3.2
	451350	AF791447	Hs.791447	ghn13a05.y5 HCl, C2AP, Ccd Homo sapiens	3.2
	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13183 fs, clone NT	3.2
	416784	AA334592	Hs.79514	lumican	3.2
	405851	AA607984		major histocompatibility complex, class	3.2
	426032	AW959704	Hs.114653	Homo sapiens cDNA FLJ13536 fs, clone PL	3.2
75	412646	NM_008025	Hs.74356	transmembrane protein (6-3kD), endoplasm	3.2
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	3.2
	415709	AA649850	Hs.276558	ESTs	3.2
	422798	R02347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.2
80	437807	AS17875	Hs.138429	ESTs	3.2
	425171	AW732240	Hs.16365	ESTs	3.2
	448108	AW300021	Hs.170685	ESTs	3.2
	402523			C100117.3" g[15743439]gbJAA7599.32 (AF2	3.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA, FLJ22930 fs, clone K	3.2

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	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3,2
	422081	AW136820	Hs.156011	ESTs	3,2
	436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	3,2
5	410886	AW805224	gbMIR4-310121-141059-010-G06_1	510121 Ho	3,2
	442605	AL020976	Hs.8518	retrovirus N	3,2
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	3,2
	441544	AW300043	Hs.127137	ESTs	3,2
	437860	AA333063	Hs.279858	Homo sapiens cDNA: FLJ23165 fis, clone L	3,2
10	419652	AL157405	Hs.61973	hypothetical protein	3,2
	443623	AA345519	Hs.5641	complement component 1, q subcomponent,	3,2
	415198	AW009480	Hs.943	natural killer cell transcript 4	3,2
	441701	AW339628	Hs.127497	ESTs	3,2
	426384	AA12078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	3,2
15	420886	AA054453	Hs.5596	ESTs, Weakly similar to T29012 hypoteti	3,2
	428896	AW261532	Hs.59836	ESTs	3,2
	458253	AW269952	Hs.196802	ESTs	3,2
	456895	AA354771	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	3,2
	434819	AA650097	Hs.5596	ESTs	3,2
20	424278	AK000723	Hs.144517	hypothetical protein FLJ20716	3,2
	434131	AI858275	Hs.143659	ESTs	3,1
	441111	AU017574	Hs.17405	cysteine-rich protein 1 (intestinal)	3,2
	443021	AA368546	Hs.8904	lg superfamily protein	3,1
	415677	TE3470	Hs.334840	ESTs, Moderately similar to 178885 senn	3,1
	429973	AI423317	Hs.164680	ESTs	3,1
25	422545	XO2761	Hs.267820	fibronectin 1	3,1
	444036	BE395085	Hs.10086	type 1 transmembrane protein Fr14	3,1
	420115	NM_013241	Hs.55231	PHF1P2 domain-containing protein	3,1
	401841			NM_015113.Homo sapiens KIAA0399 protein	3,1
	414416	AW409585	Hs.76084	hypothetical protein MGC27221	3,1
30	431019	NM_005249	Hs.2714	torhead box G1B	3,1
	453707	AW003979	Hs.126522	ESTs, Weakly similar to 178885 senn	3,1
	432188	AI362552	Hs.2528	solute carrier family 7 (cationic amino	3,1
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3,1
	430701	AI740333	Hs.25971	ESTs	3,1
35	425963	AA154653	Hs.136343	ESTs, Weakly similar to 178885 senn	3,1
	458918	HS6459	Hs.252892	ESTs, Weakly similar to 138022 hypoteti	3,1
	439764	T26535	Hs.22744	hypothetical protein MGC13105	3,1
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	3,1
40	403969			ENSP0000034963.Zinc finger protein 131	3,1
	427329	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23065 fis, clone L	3,1
	414356	BE548266	Hs.79057	galactose-4-epimerase, UDP-	3,1
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	3,1
	414403	AW965551	Hs.76064	ribosomal protein L27a	3,1
45	444168	AW375875		gbrHC1-AT0256-01199-011-01 HT0256 Homo	3,1
	410595	AW625223	Hs.64794	zinc finger protein 183(RING finger, C3	3,1
	444881	AI623288	Hs.192805	ESTs	3,1
	440381	AA517808	Hs.100455	ESTs	3,1
	416207	NM_014745	Hs.73077	Homo sapiens, clone MGC.2908, mRNA, comp	3,1
50	429130	AA308090	Hs.124707	ESTs	3,1
	457579	AB030816	Hs.36761	HRAS-like suppressor	3,1
	406736	AI254733	Hs.182426	ribosomal protein S2	3,1
	420172	AA801122	Hs.95655	secreted and transmembrane 1	3,1
	423660	AA420516	Hs.240483	ESTs	3,1
55	444143	AW747596	Hs.180999	ESTs, Moderately similar to A56194 throm	3,1
	409154	U72882	Hs.50842	interferon-induced protein 35	3,1
	449426	T29251	Hs.158882	ESTs	3,1
	458760	AA49631	Hs.111334	lentin, light polypeptide	3,1
	450811	AI735486	Hs.246547	ESTs	3,1
60	425331	AW962128		gb:EST1374201 MAGE resequencs, MAGE Homo	3,1
	445211	BE045601	Hs.118248	ESTs, Weakly similar to YC18_HUMAN HYPOT	3,1
	441318	AW102334	Hs.176130	ESTs	3,1
	453625	AW970707		gb:EST182188 MAGE resequencs, MAGE Homo	3,1
	437640	AA764853	Hs.272155	ESTs, Weakly similar to 138022 hypoteti	3,1
	446672	Z95636	Hs.11669	laminin, alpha 5	3,1
65	407047	X65965		gb:H sapiens SOD-2 gene for manganese su	3,1
	413834	BE256986	Hs.224179	ESTs, Weakly similar to 138022 hypoteti	3,1
	439155	AW749482	Hs.77873	B7 homolog 3	3,1
	435520	AA297950	Hs.5315	HN0EL-iso protein	3,1
	414598	AA094221	Hs.135150	lung type-I cell membrane-associated gly	3,1
70	440948	AW188311	Hs.128619	ESTs	3,1
	412851	AB056522	Hs.106140	ESTs	3,1
	417336	R70429	Hs.81988	disfused (Drosophila) homolog 2 (mitogen	3,1
	417944	AU077196	Hs.82595	collagen, type V, alpha 2	3,1
	411671	BE043054		ESTs	3,1
75	430444	AW026421	Hs.121035	ESTs	3,1
	425843	BE313280	Hs.159627	death associated protein 3	3,1
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	3,1
	433903	AA534163	Hs.5476	Homo sapiens, clone MAGE-350123, mRNA,	3,1
	449523	NM_002619	Hs.54443	chemokine (C-C motif) receptor 5	3,1
80	435564	AK030087	Hs.269819	ESTs	3,1
	453085	AW554243		KIAA0251 protein	3,1
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	3,0
	447527	A702895	Hs.42091	ESTs	3,0

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5	432682	AI375400	Hs.159588	ESTs	3.0
	416941	BE000150	Hs.48778	niban protein	3.0
	455481	AW948317	Hs.13434	gb:RC0-MT0015-280300-021-a09 MT0015 Homo	3.0
	445906	T29939	Hs.15174	Homo sapiens clone 24418 mRNA sequence	3.0
	408716	AB67830	Hs.15443	Homo sapiens mRNA for KIAA1789 protein, mitochondria maintenance deficient (S.	3.0
10	424308	AW975531	Hs.128746	ESTs	3.0
	436443	AW138211	Hs.157145	tetracycline transporter-like protein	3.0
	425421	L11669	Hs.100533	nitrogen-activated protein kinase kinase	3.0
	427725	U65839	Hs.144391	hypothetical protein FLJ10547	3.0
	456816	AK001509	Hs.157145	hypothetical protein FLJ10547	3.0
15	404632			NM_022490 Homo sapiens hypothetical prot	3.0
	411565	AW851728	Hs.2076	gb:NR2-CT0222-011159-007-006 CT0222 Homo	3.0
	426917	AA37337	Hs.16589	ESTs	3.0
	424684	H12692	Hs.13310	ESTs	3.0
	452483	AI903731	Hs.106357	valosin-containing protein	3.0
20	404453			C8000963-gb:G3299159gb:GAA86452.1j (A8	3.0
	426931	NM_000416	Hs.176275	zinc finger protein 7 (K0X 4, clone HF.1	3.0
	455646	BE004420	Hs.50009	gb:RC4-BT0311-241159-012 -c88 BT0311 Homo	3.0
	452188	AB64208	Hs.221024	ESTs	3.0
	400703	NM_006187	Hs.29279	2'-5'-oligoadenylate synthetase 3 (100 k	3.0
25	413922	AI538895	Hs.221024	ESTs	3.0
	432367	U71287	Hs.27087	eyes absent (Drosophila) homolog 2	3.0
	434070	AF116652	Hs.27087	hypothetical protein PR00013	3.0
	406679	AA070786		gb:zm6607.r1 Stratagene neuroepithelium	3.0
	414747	U30972	Hs.77204	centromere protein F (350/400kd, mitosis	3.0
30	435472	AW672330	Hs.263022	gating receptor expressed on myeloid	3.0
	429612	AF362549	Hs.255587	pharyngeal tumor-transforming 1	3.0
	408989	AW361666	Hs.49500	KIAA0746 protein	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
	418877	SS3308	Hs.87224	SPY (sex determining region Y)-box 5	3.0
35	425765	AA743603	Hs.121218	nucleoprotein 89d	3.0
	400295	W72838		AW905687.IL-BT095-19019-019 BT095 Homo	3.0
	429751	M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2)	3.0
	429940	W25215		gb:zb67a09.r1 Soares_senescent_fibroblasts	3.0
	411281	AB10054	Hs.14119	ESTs	3.0
40	434858	AW500458	Hs.29565	KIAA0460 protein	3.0
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 (H	3.0
	459727	AF96454		gb:RC-BT113-060495-024 BT113 Homo sapien	3.0
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.0
	458729	AI354504	Hs.53967	ESTs, Weakly similar to NBKUL3 domain p	3.0
45	402105			C18000230-pj1258552jgb:Q9Y201J257_HU	3.0
	425248	AW957442	Hs.257266	ESTs	3.0
	404995	T57773	Hs.10263	ESTs	3.0
	411360	AO91713	Hs.106597	Homo sapiens, Similar to RKEIN cDNA 1110	3.0
	432692	AW974944	Hs.200577	ESTs	3.0
50	428899	AA744610	Hs.194431	palladin	3.0
	452811	AA937079	Hs.118983	hypothetical protein FLJ12150	3.0
	447183	AI554733	Hs.173162	ESTs	3.0
	429679	NM_029290	Hs.211500	tumor necrosis factor, alpha-induced pro	3.0
	416605	H66470	Hs.16004	ESTs	3.0
55	420144	AA811813	Hs.119421	ESTs	3.0
	439184	AW021842	Hs.16533	myosin phosphatase, target subunit 1	3.0
	438033	T25413	Hs.6059	EGF-containing fibulin-like extracellular	3.0
	464276	AF069475		gb:AF069475 Homo sapiens astrocytoma lb	3.0
	441035	AW944309	Hs.126458	ESTs	3.0
60	458810	BE407125	Hs.231510	ESTs	3.0
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALLU1_HUMAN ALU S	3.0
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.0
	450879	AI742885	Hs.210347	ESTs	3.0
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	3.0
65	403780			C4501759-gj133200-gj133200-gj133200-gj133200	3.0
	411543	AW851248	Hs.7179	gb:LA-CT0220-160200-066-FP1 CT0220 Homo	3.0
	452139	AA093969	Hs.16331	RAD1 (S. pombe) homolog	3.0
	443943	AI672096	Hs.16331	Homo sapiens cDNA: FLJ21482.1f, clone C	3.0
	413945	NA_003091	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	3.0
70	433681	AK004377	Hs.200360	CD14 antigen	3.0
	422605	H16646	Hs.118666	Homo sapiens cDNA FLJ13027.1f, clone NT	3.0
	443502	AI074528	Hs.133949	hypothetical protein PPS91	3.0
	410781	AI375672	Hs.165028	ESTs	3.0
	449428	AB51280	Hs.156485	ESTs	3.0
75	436671	AW137159	Hs.146151	ESTs	3.0
	TABLE 16B				
	Phy:	Unique Ecs probe/identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
80	Phy:	CAT Number	Accession		
	403432	1058667_1	AW195262 R27868 AW811262		
	410886	1225822_1	AW809324 BE144977 BE144956		
	411537	1248899_1	BE073250 BE073378 BE073379 AWR50533 AWR50529		
	411543	1249127_1	AW851248 AWR51425 AWR50805 AWR51021 AWR50905		

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5	411565	1249756_1	AWB51728 AWB51607 AWB51621 AWB51702 AWB51647 AWB51727 AWB51658 AWB51617 AWB51628
	411671	125369_1	BE049094 AA0700765 H66770 AA094646 RD2483 CD3685 N56170
	411688	1254076_1	AWB53440 T08189 AWB57085
	412338	125439_1	AA085089 AA135130 AA084059 AA102419 AWB77755
	412799	132817_1	A026766 AA121046 AA126251
10	412811	132843_1	H06382 AWB97730 AA352014 R13591 AA121201 D04020 BE263253 BE047862 Z41952 AA424991 AB93507 AB63108 AA099050 A0191148 AA598689
	414372	143009_1	R35887 AA13482 AW0616452 H06383 R14807 A1364268 AA620528 A1741940 AW089149 AW090713 AA008675 Z38240 AA121202 R17734
	415131	152368_1	AA143654 AW753140 AA127370 AW970865 AA569075 AA492132
	415588	154643_1	D61119 D61508 D61734
	416871	1626761_1	AA156963 AW971218 AA439342
15	416913	163001_1	H98716 N90792 N24283
	416986	1686662_1	AW934714 BE1615007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	420688	197344_1	Z99357 Z99363
	421256	212379_1	AA056453 AA2381379
	423713	231290_1	N34524 AA305071 AW954803 AA502335 AA433430 A203697 AW026670 AA255323 AW850787 AA173564 AW993643 AW835572 AW385512
20	424029	234177_1	A034966 W32951 H62656 H53902 R89904 AWB35732
	424947	245247_1	AW754182 AW754198 AA329583
	425331	250199_1	F11690 AW95370 AA333366 D00800
	429163	300543_1	R77952 AA348809 AW959960 AW959962 A565552 AW070702 AA973910 R89593
	429960	310884_1	AW962128 AA355353 AA427363
25	432383	345469_1	AA844166 AW974271 AA0292975 AA447312
	432968	352620_1	H25215 AA461079 AA61351
	432944	340773_1	AW972530 AA527847 AA489820 AA570362
	432383	345469_1	AW972727 AA524829 AW972733
	433542	407744_1	AA534489 AW970240 AW970323
30	437437	43709_1	AWB67378 W14234 AW755033
	439495	44580_1	A022869 AA206516 AW058953 AA186390 AL359619 AA565195 AA148427 R22748 A033624 BE548838 H53327 AW579751 BE161649 AA397533
	439518	44580_1	BE517136 AA236444 T89945 AA247450 N56777 W38725 A743846 A1080406 AA922229 A051464 W04713 R11251 W19656 A042319 AA489276
	439566	47387_1	A1224533 H
	439710	545347_1	T78519 H58988 W12518
35	442476	545347_1	W73525 AF08341 W72300
	444168	535829_1	AF086307 W7784 W72711
	445925	8115_1	AF086543 W96291 W65225
	450106	82677_1	AF069475 AF069477 AF069476
	450375	83327_1	AK375873 AF12625512014
40	450506	836_1	NM_014523 AF100772 BE088769 AL022718 BE161779 AW836569 BE161640 AL030960 BE166542 AW265554 AA321393 AA235370 AW779760
	450625	84022_1	AA08741 AF375997 R45432 D59344 A203107 F07491 R35360 R25094 AA193631 AA488402 Z1382 A016320 H45526 T51415 AA331486
	451129	859870_1	AA429504 R14904 AA279467 H09648 AA007206
	451350	86649_1	AA009647 AA112514 AA3421293 AW954405 H09410 AW063684 AA151196 BE157467 BE157601 H04364 W46291 AW963674 H04021 H01532
	452203	903_2	AA159923 H03291 H56966 H01642 AA832876 AA113758 AW626015 AA746952 A161014 AA099554 R09067
45	452625	91427_1	NM_004480 LU9278 H76833 AW630005 AW471133 C02434 W45237 AW793518 BE070112 A159749 A1624429 AW190535 AA46661 A418772
	453331	96214_1	AW022667 AA528235 AA599775 AWE13820 A435793 AW949230 A051768 A0200109 A680296 AA4336611 AW609728 W42634 AA06584 AA050569
	453582	977454_1	A059553 AWC
	454080	123732_1	AW970107 AA513261 AA014046
	454144	1254807_1	AW072681 BE072946 A072181
50	45481	1253182_1	A0791447 A0791327 AW686809
	45546	1345557_1	X57522 AW285947 A048197 A1304693 L21205 L21206 L21207 L21208 L21204 NM_000593 F06770 F12630 X57521 R16264 T74482 AA4346259
	45589	1351547_1	AW602508 A0504076 F08426 H23432 AA313731 AA353782 H78052 A0484741 AA487637 AA135770 AA333161 A181978 AA05458 A1346733
	456304	17820_1	AW051447 A4
	457876	24814_2	AW954328 AA482930 AA412476 AA828434 AA814538 A027418 A192435 W52897 AA443666 AA031913 A16833306 AA916481 A1183314 D83907
55	458480	123732_1	A1206632 AA057122 D83836 D83838 D82533 A1761290 A191125 A143749 AW1771905 A1241336 W76267 W56507 A0447787 AW588922 T10502
	458548	1253182_1	A1247870
	458566	1345557_1	AW954328 AA482930 AA412476 AA828434 AA814538 A027418 A192435 W52897 AA443666 AA031913 A16833306 AA916481 A1183314 D83907
	45899	1351547_1	A1206632 AA057122 D83836 D83838 D82533 A1761290 A191125 A143749 AW1771905 A1241336 W76267 W56507 A0447787 AW588922 T10502
	459304	17820_1	AW051447 A4
60	459786	24814_2	AW954328 AA482930 AA412476 AA828434 AA814538 A027418 A192435 W52897 AA443666 AA031913 A16833306 AA916481 A1183314 D83907
	460096	24814_2	AW954328 AA482930 AA412476 AA828434 AA814538 A027418 A192435 W52897 AA443666 AA031913 A16833306 AA916481 A1183314 D83907
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
65	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
70	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
75	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
80	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517
	460442	29 BE064435	BE064429 BE064435 BE064441 BE064440 BE064517

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	402855	9662953	Minus	59763-59909
	403011	6693597	Minus	3468-3623
	403108	8980955	Plus	93253-93667
5	403267	7887182	Plus	116076-121885
	403349	8569773	Minus	167015-168374
	403351	8570313	Minus	112496-112687
	403481	9965004	Plus	93496-93933
	403696	3135242	Minus	143467-143634
10	403780	8076989	Plus	93160-93409
	403849	7700655	Plus	92043-95519
	403961	7596976	Minus	110393-110503
	403969	8569909	Plus	31237-31375,32405-32506
	404209	5006246	Minus	11247-11514
15	404407	7325316	Minus	45154-49499
	404453	7657714	Plus	27768-29179
	404584	9857511	Plus	13865-1129153
	404632	9796668	Plus	45096-45229
	405046	7596829	Minus	4373-4526
20	405141	8969211	Plus	90961-100054
	405303	2078453	Minus	130607-130802
	405348	2914717	Minus	43310-43462
	405558	1621110	Plus	4622-4644,5963-6083
	405605	5636195	Minus	117070-117270
	406038	8389537	Plus	37764-37877
25	406060	6899623	Minus	20339-20746
	406478	9857502	Plus	68314-66523,68853-68950

TABLE 17A: ABOUT 1040 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT TISSUES

Table 17A lists about 1040 genes up-regulated in glioblastoma multiforma (GBM) compared to normal normal adult tissues. These were selected from 55680 probesets on the Affymetrix/Exon Hu30 GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" GBM level was set to be the 85th percentile amongst various GBM tumors. The "average" normal tissue level was set to be the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Play: Uniqe Eos probeid identifier number

ExAcon: Exemplar Accession number, Genbank accession number

UniqeneID: Uniqene number

Uniqene Title: Uniqene gene title

Ratio: Ratio of GLIOBLASTOMA MULTIFORMA compared to NORMAL ADULT TISSUES

40	Phy	ExCon	UniqeneID	Uniqene Title	RI
	431917	D16181	Hs.2868 <td>peripheral myelin protein 2</td> <td>57.9</td>	peripheral myelin protein 2	57.9
	428321	A169994	Hs.2866 <td>peripheral myelin protein 2</td> <td>50.1</td>	peripheral myelin protein 2	50.1
	427343	A188004	Hs.176977 <td>protein kinase C binding protein 2</td> <td>49.6</td>	protein kinase C binding protein 2	49.6
45	413472	BE242870	Hs.75379 <td>solute carrier family 1 (glut high affinity)</td> <td>43.9</td>	solute carrier family 1 (glut high affinity)	43.9
	415817	U89967	Hs.78867 <td>protein tyrosine phosphatase, receptor-1</td> <td>42.9</td>	protein tyrosine phosphatase, receptor-1	42.9
	435147	AL_133731	Hs.4774 <td>Homo sapiens mRNA, cDNA DKFZp761C1712 (f)</td> <td>42.5</td>	Homo sapiens mRNA, cDNA DKFZp761C1712 (f)	42.5
	430838	N46664	Hs.165395 <td>hypothetical protein FLJ12015</td> <td>37.9</td>	hypothetical protein FLJ12015	37.9
	418375	NM_003081	Hs.84369 <td>synapsoosomal-associated protein, 290D</td> <td>37.1</td>	synapsoosomal-associated protein, 290D	37.1
	446494	AW237014	Hs.315369 <td>Homo sapiens cDNA: FLJ23075 fs, clone L</td> <td>37.0</td>	Homo sapiens cDNA: FLJ23075 fs, clone L	37.0
	425088	A466372	Hs.165395 <td>hypothetical protein FLJ12015</td> <td>32.7</td>	hypothetical protein FLJ12015	32.7
	425842	A1587490	Hs.159623 <td>HK-2 (Drosophila) homolog B</td> <td>32.4</td>	HK-2 (Drosophila) homolog B	32.4
	419078	M83119	Hs.89584 <td>insulinoma-associated 1</td> <td>32.1</td>	insulinoma-associated 1	32.1
	423849	AL157425	Hs.133315 <td>Homo sapiens mRNA, cDNA DKFZp761J1324 (f)</td> <td>31.7</td>	Homo sapiens mRNA, cDNA DKFZp761J1324 (f)	31.7
55	402389	AB020779	Hs.301261 <td>Homo sapiens mRNA, chromosome 1 specific</td> <td>29.8</td>	Homo sapiens mRNA, chromosome 1 specific	29.8
	413333	M74028	Hs.75297 <td>fibrinectin growth factor 1 (acidic)</td> <td>28.5</td>	fibrinectin growth factor 1 (acidic)	28.5
	417183	RS2089	Hs.172717 <td>ESTs</td> <td>27.6</td>	ESTs	27.6
	426325	D28114	Hs.188309 <td>myelin-associated oligodendrocyte basic</td> <td>27.6</td>	myelin-associated oligodendrocyte basic	27.6
	412733	A4584472	Hs.74554 <td>KIAA0803 protein</td> <td>26.8</td>	KIAA0803 protein	26.8
60	422656	A1870435	Hs.1569	LIM homeobox protein 2	26.6
	436678	BE465204	Hs.47448	ESTs	24.9
	437204	AL110216	Hs.22826	ESTs, weakly similar to I55214 salivary	24.3
	429007	D06042	Hs.15739	ghrHUN052:050 Human fetal brain (Tfujwa)	23.1
	429776	AF056085	Hs.198612	G protein-coupled receptor 51	22.1
65	409395	U46745	Hs.336678	dystrobrevin, alpha	23.0
	435708	A162949	Hs.75169	ESTs	22.5
	453392	U23752	Hs.32964	SRF (sex determining region Y)-box 11	22.2
	431941	AK003106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	22.1
	418110	RA3523	Hs.217554	hypothetical protein FLJ22202	22.0
	416829	AB013805	Hs.80220	catenin (cadherin associated protein), d	21.7
70	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	20.9
	433551	A185544	Hs.12450	proteolipin 9	19.8
	452744	A267852	Hs.245107	Homo sapiens mRNA, cDNA DKFZp434E082 (f)	19.1
	425057	A4826434	Hs.1619	achetate-scutel complex (Drosophila) homolog	19.0
75	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	19.0
	447004	AW298968	Hs.157539	ESTs	18.6
	425046	H05468	Hs.164502	ESTs	18.2
	427897	NM_017413	Hs.303084	apelin, peptide ligand for APJ receptor	18.0
	421264	AL039123	Hs.103042	microtubule-associated protein 1B	18.0
	453542	A270936	Hs.34074	dispeptidyl/dipeptidase VI	17.8
80	421416	Z40521	Hs.141308	myelin oligodendrocyte glycoprotein	17.7
	444471	AB020684	Hs.11217	KIAA0877 protein	17.7
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	17.2
	430691	C14187	Hs.103538	ESTs	16.7

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5	433800	A034361	Hs.135150	lung type-I cell membrane-associated gly	16.6
	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	16.6
	408562	A0436323	Hs.31141	Home sapiens mRNA for KIAA1568 protein,	16.5
	423853	AB011537	Hs.133466	shl (Drosophila) homolog 1	16.4
	431019	NM_005249	Hs.2714	forhead box G1b	16.4
10	449539	W80363	Hs.58446	ESTs	16.4
	450133	AW569769	Hs.105201	ESTs	16.1
	425799	T08133	Hs.182906	Home sapiens mRNA for KIAA1872 protein,	16.0
	447359	NM_012053	Hs.18258	adenylate kinase 5	15.4
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
15	459516	A049662	Hs.246858	EST	14.9
	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	14.7
	425466	M85935	Hs.12827	ESTs	14.7
	425679	AW502201	Hs.8823	hypothetical protein FLJ10430	14.7
	443785	AW449552	Hs.190125	basic-helix-loop-helix-PAS protein	14.6
20	439415	F05538	Hs.4273	ESTs	14.5
	408604	D01408	Hs.21925	ESTs	14.5
	444378	R41339	Hs.47860	neurotrophic tyrosine kinase, receptor,	14.5
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	14.0
	418738	AW386633	Hs.6682	solute carrier family 7, (cationic) amino	14.0
25	409799	D11928	Hs.76845	phosphoserine phosphatase-like	13.9
	439239	A031540	Hs.235331	ESTs	13.8
	428342	A0739168		Home sapiens cDNA FLJ13458 fls, clone PL	13.7
	448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
	441285	NM_002374	Hs.167	microtubule-associated protein 2	13.5
30	428892	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	13.4
	441440	A007981	Hs.30465	ESTs	13.0
	412959	D87458	Hs.75090	KIAA0282 protein	12.8
	413597	AW302885	Hs.117183	ESTs	12.8
	440106	AW138853	Hs.25845	ESTs	12.7
35	418338	NM_002622	Hs.84154	neural pentrasin I	12.6
	423419	RS5336	Hs.23539	ESTs	12.6
	445495	BE622641	Hs.38489	ESTs, Weakly similar to 138022 hypothei	12.6
	441497	RS1064	Hs.21372	ESTs	12.4
	424893	AW295112	Hs.153548	Home sapiens cDNA FLJ13303 fls, clone ON	12.2
40	453941	U39817	Hs.36820	Bloom syndrome	12.2
	427701	AA411101	Hs.243685	nuclear autoantigenic sperm protein (his	12.2
	446782	A0633048	Hs.144006	ESTs	12.1
	437268	A0754847	Hs.227571	regulator of G-protein signaling 4	12.1
	411411	AA343241	Hs.55590	ESTs, Weakly similar to KIAA1330 protein	11.9
45	448302	AA480206	Hs.182908	Home sapiens mRNA for KIAA1872 protein,	11.9
	407034	U84540		gbHuman dystrobrevin isoform DTN-3 (DTN	11.9
	449625	NM_014263		ozc (odd Oz/ten-m, Drosophila) homolog 1	11.7
	451059	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	11.7
	424432	AB037821	Hs.146858	procadherin 10	11.6
50	451996	AW514021	Hs.245510	ESTs	11.4
	423678	AW963357	Hs.7847	ESTs	11.4
	465041	T64183	Hs.28392	solute carrier	11.3
	442613	AB044032	Hs.132622	Mr channel-interacting protein 1	11.2
	419721	NM_001650	Hs.289650	aquaporin 4	11.2
55	446711	AF169892	Hs.12450	protocadherin 9	11.1
	412886	X81120	Hs.75110	carnitide receptor 1 (brain)	11.0
	412140	AA219691	Hs.73325	RAB6-interacting, kinesin-like (rablins)	10.7
	428728	NM_016625	Hs.191381	hypothetical protein	10.6
	415849	R20629	Hs.6806	ESTs	10.6
60	447198	D61523	Hs.283435	ESTs	10.5
	420602	AF968877	Hs.59236	regulator of G-protein signalling 20	10.3
	455793	AB037734	Hs.49593	KIAA1313 protein	10.3
	409049	AH423132	Hs.146343	ESTs	10.2
	449611	A070394	Hs.193075	ESTs	10.2
65	402604			Target Exon	10.1
	434277	X77748	Hs.3785	glutamate receptor, metabotropic 3	10.0
	440435	AL042201	Hs.21273	transcription factor NYD-sp10	10.0
	438080	AA777381	Hs.291530	ESTs, Weakly similar to ALUC_HUMAN	10.0
	419271	NL34901	Hs.236532	ESTs	9.9
70	425344	H41821	Hs.322466	transcriptional activator of the c-fos p	9.8
	448605	AW138581	Hs.198416	ESTs	9.8
	408081	AW451597	Hs.167409	ESTs	9.8
	452526	W38537	Hs.280740	hypothetical protein MGC3040	9.8
	411305	BE241596	Hs.69547	myelin basic protein	9.8
75	443455	AB001025	Hs.53949	ryanodine receptor 3	9.8
	427540	R12014	Hs.20978	ESTs	9.7
	424790	AL119344	Hs.13328	ESTs, Weakly similar to 2004399A chromos	9.7
	410892	L24498	Hs.80405	growth arrest and DNA-damage-inducible,	9.6
	452461	U78223	Hs.108106	transcription factor	9.6
80	449433	A0672096	Hs.9012	ESTs, Weakly similar to T26650 DNA-bndi	9.6
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	9.5
	439199	RA0373	Hs.26299	ESTs	9.5
	433896	AW294729	Hs.274461	ESTs	9.3
	419572	AL110370	Hs.79000	growth associated protein 43	9.3
	444119	R41231	Hs.184261	ESTs, Weakly similar to T26666 hypothei	9.2
	435624	AF218942	Hs.24889	formin 2	9.2
	412788	AA120960	Hs.198416	ESTs	9.2

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5	409902	AI337858	Hs.156351	ESTs	9.2
	427304	AA761526	Hs.163853	ESTs	9.2
	429918	AW073896	Hs.118383	ESTs	9.1
	429910	AI365130	Hs.11367	ESTs, Weakly similar to 119326 hypothetical	9.1
10	425187	AW014486	Hs.22509	ESTs	9.1
	436954	AA740151	Hs.130425	ESTs	9.1
	442710	AI015631	Hs.23210	ESTs	9.1
	411078	AI222620	Hs.182364	CoosaCrisp	9.0
15	432029	AL129659	Hs.6111	aryl-hydrocarbon receptor nuclear transd	8.9
	437036	AI571514	Hs.133022	ESTs	9.0
	448672	AI955511	Hs.225106	ESTs	9.0
	451952	AL120173	Hs.301663	ESTs	8.9
20	448743	AB032962	Hs.21896	KIAA1136 protein	8.9
	412068	S7043	Hs.71333	metallothionein 3 (growth inhibitory fac	8.9
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	8.8
	419088	AI538323	Hs.52620	integrin, beta 8	8.8
25	445873	AA250870	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	8.8
	410102	AW424508	Hs.279727	ESTs, homologue of PEM-3 (Ciona savignyi)	8.8
	448571	AW016812	Hs.200266	ESTs	8.7
	425354	U52027	Hs.155935	complement component 3a receptor 1	8.7
30	452355	NS4926	Hs.29202	G protein-coupled receptor 34	8.7
	412276	AI554545	Hs.63801	angiotensin 2	8.7
	435501	AW051819	Hs.129908	KIAA0591 protein	8.6
	407728	AW071502	Hs.175931	ESTs	8.6
35	415293	RI49462	Hs.106541	ESTs	8.6
	416857	AA188175	Hs.292453	ESTs	8.6
	425234	AW151225	Hs.165809	ESTs, Weakly similar to 138022 hypothetical	8.5
	450376	AA009647		a disintegrin and metalloproteinase doma	8.5
40	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	8.4
	435380	T06430	Hs.61394	chondroitin sulfate proteoglycan DEHA8b	8.4
	421659	NM_014459	Hs.106511	protocadherin 17	8.3
	418097	RA5137	Hs.21868	ESTs	8.3
45	429183	AB014604	Hs.197955	KIAA0704 protein	8.2
	424945	AL221919		hypothetical protein FLJ10582	8.2
	455601	AI368680	Hs.816	GRIY (see determining region Y)-box 2	8.2
	453884	AA355925	Hs.36232	KIAA0195 gene product	8.2
50	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfat	8.1
	436887	AW963157	Hs.193235	hypothetical protein DKFZp470155	8.1
	431721	AB032996	Hs.268344	KIAA1170 protein	8.1
	417160	NT6497	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	8.1
55	490941	AB033025	Hs.50081	hypothetical protein, XP_051860 (KIAA119	8.1
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	8.1
	436039	AW023323	Hs.121070	ESTs	8.0
	449444	AWB19436	Hs.23590	sukkle carrier family 16 (monocarboxylic	8.0
60	427463	AA442224	Hs.97900	ESTs	8.0
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	7.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.8
	451621	AB79148	Hs.26770	faty acid binding protein 7, brain	7.7
65	419929	U92028	Hs.50810	central cavernous malformations 1	7.7
	419644	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	7.7
	448555	AC36697	Hs.150863	ESTs	7.7
	414372	AA143854		gb:z05a02r1 Stratagene panoseas (B3720	7.7
70	438527	AB99251	Hs.115325	RAB7, member RAS oncogenes family like 1	7.7
	402993	NS1002	Hs.306480	Homo sapiens mRNA, cDNA DKFZp761E2112 (f	7.7
	420362	U79734	Hs.97206	huntinglin interacting protein 1	7.6
	430132	AA204686	Hs.234149	hypothetical protein FLJ20847	7.5
75	448643	AW897741	Hs.21380	Homo sapiens mRNA, cDNA DKFZp596P1124 (f	7.5
	436140	W87355	Hs.265887	ESTs	7.4
	443404	AW235786	Hs.195359	hypothetical protein MGCT0954	7.4
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	7.4
80	454117	BE410100	Hs.40308	adipocyte-related protein complex 1, sigma	7.4
	410434	AF051152	Hs.63668	foli-like receptor 2	7.4
	454048	H05626	Hs.6921	ESTs	7.4
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUUF_HUMAN !!!	7.4
85	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	7.4
	438330	AW456572	Hs.257316	ESTs	7.4
	433656	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	7.3
90	445900	AF070526	Hs.125036	Homo sapiens clone 24787 mRNA sequence	7.3
	422855			NM_001639? Homo sapiens calpainin 3, acid	7.2
	422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	7.2
	439772	AL365405	Hs.10268	Homo sapiens mRNA full length insert cDN	7.2
95	433447	U29195	Hs.3281	neuronal pentraxin II	7.2
	412709	AL022327	Hs.74518	R1A0027 protein	7.2
	445745	AB007924	Hs.13245	KIAA0455 gene product	7.2
	447101	NT7185	Hs.44189	ESTs	7.2
100	448935	AL078596	Hs.22591	nuclear receptor subfamily 2, group E, m	7.1
	409248	AB033035	Hs.51965	KIAA1209 protein	7.1
	452785	AL358942	Hs.296434	eyfmod differentiation and desiccatio	7.1
	424998	US9515	Hs.154138	chitinase 3 like 2	7.1
105	436607	AW661783	Hs.211061	ESTs	7.1
	447197	R36075		gb:yh38d01.s1 Soares; placenta Nb2HP Homo	7.1
	419249	X14767	Hs.89788	gamma-aminobutyric acid (GABA) A recept	7.1

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	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.1
	421633	AF121860	Hs.106260	sorting nexin 10	7.0
	428976	AL037824	Hs.194695	ras homolog gene family, member 1	7.0
	444783	AK001468	Hs.62180	actin (Drosophila Scappa homolog), act	7.0
5	408096	BE250162	Hs.83765	dihydrodipicolinate reductase	7.0
	426269	HI5302	Hs.168650	Homo sapiens mRNA, cDNA DKFZp566A1046 (I	6.9
	439978	BE139460	Hs.124673	Homo sapiens cDNA FLJ11477 fs, clone HE	6.9
	439570	U78925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.9
	422980	U46569	Hs.76722	CCAAT/enhancer binding protein (CEBP),	6.9
10	415279	F04237	Hs.1447	glial fibrillary acidic protein	6.9
	456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	6.9
	447773	HA23930	Hs.36790	ESTs, Weakly similar to putative p150 (H	6.9
	429297	NM_001115	Hs.2522	adenylosuccinate cyclase 8 (farn)	6.9
	447459	AW262580	Hs.147674	protodactherin beta 16	6.8
15	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	6.8
	447255	R06350	Hs.171635	ESTs	6.8
	428556	X06508	Hs.211564	neurofilament, light polypeptide (58KD)	6.8
	439566	AF086387		gh:Homo sapiens full length insert cDNA	6.8
	435191	RI5912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	6.8
20	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	6.8
	430668	AW972630		gb:EST364925 MAGE resequences, MAGL Homo	6.8
	455332	AF003341	Hs.220491	ESTs	6.8
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.7
	413627	BE182082	Hs.246973	ESTs	6.7
25	415079	R43179	Hs.22885	hypothetical protein FLJ23548	6.7
	418677	S83308	Hs.87224	SV4V size determining region Y-box 5	6.7
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.7
	425741	AF052152	Hs.159412	Homo sapiens clone 24628 mRNA sequence	6.7
30	421141	AW117261	Hs.125914	ESTs	6.6
	409629	NM_006042	Hs.48394	heparan sulfate (glucosamine) 3-O-sulfat	6.6
	432154	AT105123	Hs.112577	ESTs	6.6
	425202	AW962282	Hs.152048	ESTs, Weakly similar to 138022 hypothet	6.6
	434164	AW207019	Hs.148135	serine/threonine kinase 33	6.6
	407182	AA312551	Hs.230157	ESTs	6.6
35	445034	AW293376	Hs.143869	ESTs	6.6
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	6.6
	441102	AA973905		intermediate filament protein syncollin	6.6
	425834	AB338627	Hs.105685	KIAA1658 protein	6.6
40	429339	AA448419	Hs.45329	ESTs	6.6
	414715	AI308876	Hs.103849	hypothetical protein DKFZp761D112	6.5
	449300	AB658959	Hs.346514	ESTs	6.5
	446727	AB011095	Hs.16032	KIAA0523 protein	6.5
	429520	U56535	Hs.198338	hypothetical rich basic protein	6.5
45	420540	AW207748	Hs.59115	ESTs	6.5
	448321	NM_005883	Hs.20912	adenomatous polyposis coli like	6.5
	441390	AB925860	Hs.131175	ESTs	6.5
	407168	RA5175	Hs.117183	ESTs	6.4
	447414	DS2343	Hs.74736	neuroblastoma (nerve tissue) protein	6.4
50	407235	D02059	Hs.165407	SAC2 (suppressor of acin mutations 2, y	6.4
	433597	AA708205	Hs.100343	ESTs	6.4
	414528	AA148950	Hs.188836	ESTs	6.4
	414214	D49958	Hs.75819	glycoprotein MGA	6.4
	446682	Z44514		Homo sapiens mRNA for KIAA1763 protein,	6.4
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	6.4
55	440152	AB002376	Hs.7006	KIAA0378 protein	6.4
	453785	AB068235	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.3
	412530	AA786268	Hs.286673	hypothetical protein FLJ13346	6.3
	448902	Z45998	Hs.22543	Homo sapiens mRNA, cDNA DKFZp7611912 (I	6.3
60	452799	AB948829	Hs.213786	ESTs	6.3
	425523	AB007948	Hs.158244	KIAA0479 protein	6.3
	444396	U75213	Hs.4257	ESTs	6.3
	432094	AF129535	Hs.27207	F-box only protein 5	6.3
	420649	AB66964	Hs.124704	ESTs, Moderately similar to S65657 alpha	6.3
	424028	AF055084	Hs.153692	Homo sapiens cDNA FLJ14354 fs, clone Y7	6.2
65	447350	AA375572	Hs.172634	ESTs	6.2
	448148	NM_015678	Hs.20590	HIV p6 associated protein-8	6.2
	436936	AL134451	Hs.197478	ESTs	6.2
	448243	AW369771	Hs.52620	integrin, beta 8	6.2
	414727	BE466904	Hs.193162	gb:hc2803.x1 NC1_GCAP_GCE Homo sapiens	6.2
70	420608	BE548277	Hs.103104	ESTs	6.2
	432949	AA319435		gb:EST121657 Adrenal gland tumor Homo sap	6.2
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	6.1
	428242	H65709	Hs.2250	leukemia inhibitory factor (cholinergic	6.1
	423261	AW170055	Hs.47628	ESTs	6.1
75	417417	F05745	Hs.86512	ATPase, Ca transporting, plasma membrane	6.1
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	6.1
	415651	AA207162	Hs.3815	stathmin-like protein RB3	6.0
	418030	BE205753	Hs.83321	neurotrophin B	6.0
	429469	MA5490	Hs.27	neuronic dihydrodipicolinate (decarboxylating;	6.0
80	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	6.0
	429900	AA460421	Hs.30875	ESTs	6.0
	416439	AA180363	Hs.118789	ESTs	6.0
	439845	AL335743	Hs.56653	Homo sapiens EST from clone 41214, full	6.0

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425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	6.0
436518	W76326		gtr:z60204.1 Soares_fetal_heart_NBMH19W	6.0
428919	AL041228		ELAV (embryonic lethal, abnormal vision,	6.0
440492	K039127	Hs.21433	hypothetical protein DKFZp73J036	5.9
433328	A0572739	Hs.195471	G-phosphatidyl-2-kinase/phospho-2.5-bi	5.9
444190	A0878918	Hs.10526	cysteine and glycine-rich protein 2	5.9
425984	AW838277	Hs.195636	hypothetical protein DKFZp751C07121	5.9
425977	R15136	Hs.165570	Homo sapiens clone Z6052 mRNA sequence	5.9
443315	AW230211	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5130	5.9
457465	AW301344	Hs.122908	DNA replication factor	5.9
453362	H14988	Hs.107375	ESTs	5.9
453924	R49295	Hs.24886	ESTs	5.9
414825	X05310	Hs.77432	epidermal growth factor receptor (avian	5.8
433701	AW445023	Hs.15155	ESTs	5.8
412777	A335773	Hs.270123	ESTs	5.8
419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	5.8
433604	AA778628	Hs.165309	ESTs	5.8
416427	BE244050	Hs.79307	RacGdp42 guanine exchange factor (GEF)	5.8
400292	AA250737	Hs.72472	BMP-R1B	5.8
407748	AL079409	Hs.38176	KIAA0506 protein; SCN Circadian Oscillat	5.8
453313	BE005771	Hs.153746	hypothetical protein FLJ22490	5.8
433189	AL049242	Hs.254794	Homo sapiens mRNA; cDNA DKFZp564B093 (fr	5.8
411252	AB018549	Hs.69328	MD-2 protein	5.8
448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.7
446052	A0633744	Hs.199548	ESTs, Weakly similar to G80222 hypothi	5.7
419704	AA429104	Hs.45957	ESTs	5.7
420077	AW512260	Hs.87767	ESTs	5.7
448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.7
436511	AA721252	Hs.291502	ESTs	5.7
424560	AA158127	Hs.150155	protein predicted by clone 23/33	5.7
423346	A0267077	Hs.127146	cytoplasmic 1	5.7
439249	AF060600	Hs.170053	G-protein coupled receptor 88	5.7
428588	F12101	Hs.185701	Homo sapiens mRNA, full length insert cDN	5.7
450927	A0807804	Hs.134342	TASP for testis-specific androgenin sens	5.7
451752	AB032997	Hs.26966	KIAA1171 protein	5.7
458814	A1498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.6
416406	D66961	Hs.79299	lipoma HMGR fusion partner-like 2	5.6
448275	BE514454	Hs.20830	kinesin like 2	5.6
415492	D87470	Hs.75400	KIAA0209 protein	5.6
444630	R41398	Hs.6996	ESTs	5.6
421988	AW450481	Hs.161333	ESTs	5.6
434397	A040984	Hs.133029	ESTs	5.6
433244	AB040943	Hs.271785	KIAA1510 protein	5.5
458809	AW972512	Hs.20985	sh3-associated polypeptide, 300D	5.5
448499	BE611030	Hs.77550	hypothetical protein MGC1780	5.5
447458	A1741082	Hs.159861	ESTs	5.5
436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	5.5
401886	AW698608	Hs.100028	ESTs	5.5
448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.5
418630	A1351311	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.5
415734	NM_014747	Hs.78748	KIAA0237 gene product	5.5
410059	AA081630		KIAA0036 gene product	5.5
453128	AW028516	Hs.31791	acylphosphatase 2, muscle type	5.5
444670	H58373	Hs.332938	hypothetical protein MGC5370	5.5
420345	AW295230	Hs.25231	ESTs	5.5
420092	AA814043	Hs.88045	ESTs	5.5
414821	M53835	Hs.77424	Fc fragment of IgG, high affinity Ia re	5.4
428876	AB028977	Hs.225974	KIAA1054 protein	5.4
419863	AW952691	Hs.93485	Homo sapiens mRNA, cDNA DKFZp751D191 (fr	5.4
428149	AW193630	Hs.193962	ESTs, Weakly similar to G80222 hypothi	5.4
415085	H11214	Hs.13294	ESTs, Weakly similar to Z109260A B cell	5.4
429643	AA455889	Hs.161279	TYNE finger-containing Rals1 vector pro	5.4
446657	A1335191	Hs.260702	ESTs, Weakly similar to Z109260A B cell	5.4
439662	H97552	Hs.269090	ESTs	5.4
441855	AL131443	Hs.10441	hypothetical protein FLJ11236	5.4
429192	AW610536	Hs.105413	ESTs	5.3
448789	N66037	Hs.38173	ESTs	5.3
410555	U92649	Hs.64311	a disintegrin and metalloprotease doma	5.3
424922	BE386547	Hs.217112	hypothetical protein MGC10825	5.3
423905	AW579985	Hs.135150	lung type-I cell membrane-associated gly	5.3
429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	5.3
427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006, fig. clone L	5.3
422544	AB018299	Hs.118140	KIAA0715 gene product	5.3
420547	AF155140	Hs.58738	gonadotropin regulated testicular RNA he	5.2
424524	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.2
441797	A0398333	Hs.214635	ESTs	5.2
428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN81_HUMAN Z	5.2
418079	R40058	Hs.6911	ESTs	5.2
445740	T78081	Hs.13228	Homo sapiens clone Z5181 mRNA sequence	5.2
416126	AA180256	Hs.210473	Homo sapiens cDNA FLJ14187, fig. clone PL	5.2
436109	AA922153	Hs.132750	hypothetical protein MGC15129	5.2
433647	AA603387	Hs.222294	ESTs	5.2
452786	R61362	Hs.105642	ESTs, Weakly similar to T09052 hypothi	5.1

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5	436443	AW138211	Hs.128746	ESTs	5.1
	408243	Y00787	Hs.624	interleukin 8	5.1
	404819			NM_002688* Homo sapiens peanut (Orsoph)	5.1
	424914	AA348410	Hs.119065	ESTs	5.1
	455331	AQ40865		ESTs	5.1
10	444656	AQ777594	Hs.145199	ESTs	5.1
	437387	A198874	Hs.28847	ADQ26 protein	5.1
	421027	AA761198	Hs.55254	ESTs	5.1
	410651	AA086469	Hs.417171	ESTs	5.1
	454293	A49739	Hs.134013	ESTs, Moderately similar to HK61_HUMAN H	5.1
15	416220	A49776	Hs.170954	hypothetical protein MGC10946	5.1
	415498	AL036591	Hs.20887	hypothetical protein FLJ10392	5.1
	421040	AA159266	Hs.135280	ESTs	5.1
	415170	RA4386	Hs.164578	ESTs	5.0
	412590	AL134388	Hs.135033	ESTs, Weakly similar to I38022 hypothet	5.1
20	448985	AA324885	Hg.22777	carbonic anhydrase XJ	5.0
	433929	AQ35499	Hs.27379	ESTs	5.0
	409638	AAW454020	Hs.21335	ESTs	5.0
	437916	BC566249	Hs.20999	hypothetical protein FLJ23142	5.0
	406533			ENSPO0000209376* PRED65 protein (Fosmen	5.0
25	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFpZp761G02121 (5.0
	437372	AA321968	Hs.263531	hypothetical protein DKFpZp547G183	5.0
	414737	A160286	Hs.125097	ESTs	5.0
	422964	AA318323	Hs.12827	gb:EST200390 Retina II Homo sapiens cDNA	5.0
	428878	AA436884	Hs.48926	ESTs	5.0
30	428841	AA18430	Hs.104935	ESTs	5.0
	428110	AQ12485	Hs.139294	ESTs, Moderately similar to Z195_HUMAN Z	5.0
	444170	AW613879	Hs.102408	ESTs	4.9
	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFpZp547D086 (fr	4.9
	452106	A1141031	Hs.21342	ESTs	4.9
35	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	4.9
	414300	AQ304870	Hs.189640	ESTs	4.9
	429399	AA452244	Hs.16727	ESTs	4.9
	430726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	4.9
	428873	A701689	Hs.99508	ESTs	4.9
40	451516	AIS98015	Hs.12804	ESTs	4.9
	407792	AQ077715	Hs.39384	putative secreted ligand homologous to f	4.9
	418836	D54745	Hs.80247	cholecystokinin	4.9
	447247	AW368351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.9
	436605	AA731533	Hs.270251	ESTs	4.9
45	423175	WZ7566	Hs.547310	hypothetical protein FLJ14627	4.9
	415402	AA164687	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	4.9
	422263	AA307639	Hs.129908	KIAA0591 protein	4.8
	443715	A563167	Hs.9700	cyclin E1	4.8
	413248	TA489	Hs.21433	hypothetical protein DKFpZp547J036	4.8
50	434811	AW971205	Hs.114280	ESTs	4.8
	441287	AW293132	Hs.131373	ESTs	4.8
	428882	NM_000346	Hs.2316	SRY (sex determining region Y) box 9 (ca	4.8
	413834	BE298968	Hs.224175	ESTs, Weakly similar to I38022 hypothet	4.8
	443740	R56434	Hs.21062	ESTs	4.8
55	416871	H89716		gbrx1.3d08.s1 Soares melanocyte 2N8HM Ho	4.8
	441916	AA959371	Hs.129075	ESTs	4.8
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU1_HUMAN A	4.8
	424240	AB923185	Hs.141535	calcium/calmodulin-dependent protein kin	4.8
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.8
60	448425	A500359	Hs.346112	ESTs	4.8
	423600	AB633559	Hs.310359	ESTs	4.8
	424687	JQ5079	Hs.151738	mutic metallopeptidase 9 (gelatinase B	4.8
	423669	BE400301	Hs.134012	C1q-related factor	4.8
	425402	A215881	Hs.24970	ESTs, Weakly similar to B34523 GTP-bind	4.7
65	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.7
	407808	AA603559	Hs.279789	histone disacetylase 3	4.7
	428748	AW553206	Hs.98785	Ksp.37 protein	4.7
	434859	BE255080	Hs.299315	collapsin response mediator protein-5; C	4.7
	431820	AW410408	Hs.271167	Lip-specific acid oxidase	4.7
70	409100	H89216	Hs.42245	ESTs, Moderately similar to I38022 hypot	4.7
	420133	AA425117	Hs.155543	ESTs	4.7
	420297	AG62872	Hs.88533	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.7
	443462	AA064990	Hs.171176	ESTs	4.7
	424481	R19453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	4.7
75	431454	AW915980	Hs.292918	ESTs	4.7
	432682	AL378400	Hs.156588	ESTs	4.7
	434933	R81095	Hs.4276	KAA1701 protein	4.7
	421247	BE391727	Hs.102910	general transcription factor IIB, polype	4.7
	435538	AB011540	Hs.4530	low density lipoprotein receptor-related	4.7
80	441703	AW230054	Hs.192843	leucine zipper protein PRC314	4.6
	418661	NM_001949	Hs.1189	E2F transcription factor 3	4.7
	412266	N59006	Hs.26133	ESTs	4.6
	417675	AB080877	Hs.3781	similar to murine leucine-rich repeat pr	4.6
	422564	AI148006	Hs.222120	ESTs	4.6
	427250	R35941	Hs.25418	ESTs	4.6
	427695	R88483	Hs.172862	ESTs	4.6
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	4.6

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5	407603	AW955705	Hs.62804	Homo sapiens, clone IMAGE:4299322, mRNA,	4.6
	427687	AW030867	Hs.1570	histamine receptor H1	4.6
	427194	AA399018	Hs.250635	ESTs	4.6
	440285	U25591	Hs.7138	cholinergic receptor, muscarinic 3	4.6
	427099	AB032953	Hs.173600	oid Oculin-m homolog 2 (Drosophila, mouse)	4.6
10	458760	AI496631	Hs.111334	ferlin, light polypeptide	4.6
	433675	AW977653	Hs.75319	noncatalytic reductase M2 polypeptide	4.6
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.6
	427712	AB36024	Hs.28386	ESTs	4.6
	437834	AA769294	Hs.283854	glucn3.36g0.3a.1 NCI_CGAP_GCB1 Homo sapiens	4.6
15	408947	AL080093	Hs.49117	Homo sapiens mRNA, cDNA DKF2p564N1662 (f	4.6
	424458	M29273	Hs.1780	myelin associated glycoprotein	4.6
	456568	AL025078	Hs.25159	Homo sapiens cDNA FLJ10784 fs, clone NT	4.6
	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fs, clone PL	4.6
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2105260A B cell	4.6
20	428409	AW1117207	Hs.98523	ESTs	4.5
	424745	AL035633		Human DNA sequence from clone RPS-1046G1	4.5
	421977	VS91197	Hs.110165	ribosomal protein L26 homolog	4.5
	440105	AA694010	Hs.6932	Homo sapiens clone Z3809 mRNA sequence	4.5
	422411	AW749443	Hs.22511	ESTs	4.5
25	443361	AJ792628	Hs.133273	ESTs	4.5
	453957	AL080235	Hs.39861	DKF2P566E121 protein	4.5
	408432	AW195262		gb:ex67805.x1 NCI_CGAP_CML1 Homo sapiens	4.5
	444127	N53620	Hs.13281	ESTs	4.5
	417435	NM_005181	Hs.62129	carbonic anhydrase II, muscle specific	4.5
30	446264	NM_014700	Hs.119504	KIAA0655 gene product	4.5
	446864	AQ253123	Hs.127335	ESTs, Highly similar to 21424 neslin [H]	4.5
	407365	AA610150	Hs.272072	ESTs, Weakly similar to 138022 hypohelit	4.5
	425256	BE297611	Hs.155352	collapsin response mediator protein 1	4.5
	441364	AA494646	Hs.126530	ESTs, Weakly similar to YD38_YEAST HYPOPT	4.5
35	430471	AF064845	Hs.241523	hypothetical protein FLJ10142	4.5
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	4.5
	426503	AA380153		gb:EST30903 Skin tumor 1 Homo sapiens cd	4.5
	418771	AA807881	Hs.25329	ESTs	4.4
	414706	AW341125	Hs.75989	KIAA0057 gene product	4.4
40	424800	AL035588	Hs.153203	MyoD family inhibitor	4.4
	441217	AI922183	Hs.213246	ESTs	4.4
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	4.4
	446619	ALJ076543	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.4
	444153	AK001610	Hs.10414	hypothetical protein FLJ10745	4.4
45	435542	AA687376		ESTs	4.4
	443912	R37257	Hs.184780	ESTs	4.4
	414822	CD00723	Hs.77831	glycine cleavage system protein H (amino	4.4
	423527	AW975028	Hs.100754	ESTs	4.4
	410082	AA081594	Hs.155311	Musashi (Drosophila) homolog 1	4.4
50	446936	H10207	Hs.47314	ESTs	4.4
	425212	AW962253	Hs.171618	ESTs	4.4
	426925	NM_001196	Hs.315518	Homo sapiens cDNA FLJ22373 fs, clone H	4.4
	427221	LT15409	Hs.174007	von Hippel-Lindau syndrome	4.4
	439274	AF096092	Hs.46372	ESTs	4.4
55	412799	AI257606		gb:ac91103.x1 Stanley Frontal S8 pool 1	4.4
	435676	AF084866		gb:homo sapiens envelope protein PIC-3 (4.4
	450348			C7021654-p1258895 Jctb [BA021946.1] (AB	4.4
	419412	AW161058	Hs.90297	synuclein, beta	4.3
	447397	BE247676	Hs.18442	E-1 enzyme	4.3
60	409125	R17289	Hs.343567	axonal transport of synaptic vesicles	4.3
	433323	AA805132	Hs.159142	ESTs	4.3
	450530	NM_009668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.3
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (C)	4.3
	408622	AA066000	Hs.202577	Homo sapiens cDNA FLJ12155 fs, clone MA	4.3
65	433610	AA066622	Hs.112547	ESTs	4.3
	426021	AA330566	Hs.23968	Homo sapiens cDNA FLJ21122 fs, clone C	4.3
	451320	AW118072		diacylglycerol kinase, zeta (104d)	4.3
	430979	AA479755	Hs.129010	ESTs	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
70	438456	AA913381	Hs.20594	ESTs	4.3
	433236	NM_004296	Hs.33221	regulator of G-protein signaling 6	4.3
	445133	AW157646	Hs.198689	ESTs	4.3
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.2
	432882	NM_013257	Hs.278696	serum lipocalin/calmodulin regulated kinase 1	4.2
75	407646	AA426202	Hs.40403	Chap300-interacting transactivator, wt	4.2
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	4.2
	424489	T48851	Hs.274470	D-sialic precursor,	4.2
	453662	T79103		ghy:yl1605.1 Soares fetal liver spleen	4.2
	445568	H02018	Hs.268744	KIAA1756 protein	4.2
80	448526	AB028946	Hs.21361	KIAA1023 protein	4.2
	426457	AW894667	Hs.169955	chimerin (chimerin) 1	4.2
	415796	R87548	Hs.78854	ATPase, Na ⁺ /K ⁺ transporting, beta 2 polypep	4.2
	438815	AA827640	Hs.189509	ESTs	4.2
	428001	H97428	Hs.215907	ESTs, Moderately similar to Transforming	4.2
	410361	BE391804	Hs.62561	guanylate binding protein 1, interferon-	4.2
	445921	AW015211	Hs.146181	ESTs	4.2
	412190	R16160	Hs.274461	ESTs	4.2

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445666	R59960	Hs.282386	ESTs	4.2
439538	AA837323	Hs.56407	ESTs	4.2
437814	A088192	Hs.135474	ESTs, Weakly similar to DD39_HUMAN ATP-D	4.2
410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fs, clone PL	4.2
409691	AW570386	Hs.269423	ESTs	4.2
458527	AW577586	Hs.291735	ESTs, Weakly similar to I78855 sorcinin	4.2
426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	4.2
432731	R31178	Hs.287820	fibronectin 1	4.2
423135	HE1655	Hs.26411	ESTs	4.2
446131	NM_000929	Hs.290	phospholipase A2, group V	4.2
424736	AF230877	Hs.152701	microtubule-interacting protein that ass	4.2
408298	A1745325	Hs.271923	Homo sapiens cDNA FLJ22785 fs, clone K	4.2
452234	AW064178	Hs.223296	ESTs, Weakly similar to I58022 hypophth	4.2
451468	AW502398	Hs.293653	ESTs, Moderately similar to I58022 hypophth	4.2
429421	AL031658		Human DNA sequence from clone RP1-310013	4.2
422374	AW732869	Hs.1519	protein kinase, cAMP-dependent, regulate	4.1
402145			Target Exon	4.1
440493	A1200836	Hs.150396	ESTs	4.1
425018	BE245277	Hs.154196	EAF transcription factor 1	4.1
448046	BE281291	Hs.170408	ESTs, Moderately similar to A47532 B-cel	4.1
445868	BE169357	Hs.207428	ESTs	4.1
431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.1
433575	AF219457	Hs.44224	triggingin receptor expressed on myeloid	4.1
424726	AK001007	Hs.138750	Homo sapiens cDNA FLJ10145 fs, clone HE	4.1
450326	A1935962	Hs.26289	ESTs	4.1
450639	AJ031186	Hs.277174	ESTs	4.1
445102	AW204610	Hs.22270	ESTs	4.1
416547	H62914	Hs.265946	ESTs, Weakly similar to PC4259 farnitin	4.1
430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.1
408296	AL117452	Hs.44155	DKFZP566G1517 protein	4.1
435619	AA837118	Hs.118366	ESTs	4.1
442326	H92662	Hs.124613	hypothetical protein MGC14817	4.1
404190			Target Exon	4.1
420805	L10333	Hs.99947	reticulin 1	4.1
429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypophth	4.1
427362	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fs, clone HE	4.1
446534	AW271626	Hs.42294	ESTs	4.1
437414	AW894071	Hs.48448	hypothetical protein DKFZ547C176	4.1
418512	AW489974		diacylglycerol kinase, zeta (104kD)	4.1
414217	A1309298	Hs.279898	Homo sapiens cDNA FLJ23165 fs, clone L	4.1
449328	A1962493	Hs.345363	ESTs	4.1
432683	AW995441	Hs.10475	ESTs	4.1
435312	A1243396	Hs.4865	voltage-gated sodium channel beta-3 subu	4.1
429163	AA844766		gbr.amC0810.s1 Soares_NFL_T_GBC_S1 Homo s	4.1
450996	AW294631	Hs.11325	ESTs	4.0
414683	S78296	Hs.76888	hypothetical protein MGC12702	4.0
433523	H29882		ESTs	4.0
422170	A1791949	Hs.112432	anti-Müllerian hormone	4.0
424120	T80579	Hs.296270	ESTs	4.0
448548	R13209	Hs.21413	solute carrier family 12, (potassium-chl	4.0
433009	AA761668		gbr.mz24c08.s1 NC1_CGAP_GDB1 Homo sapiens	4.0
434834	AF156774	Hs.324020	1-acylglycerol-3-phosphate O-acyltransfe	4.0
439059	AB037800	Hs.5462	protein kinase C and casein kinase subcl	4.0
444001	AB050397	Hs.152269	ESTs, Moderately similar to S59567 alpha	4.0
413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	4.0
423279	AW959861	Hs.290943	ESTs	4.0
457211	AW972665	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.0
445681	AF381513	Hs.29195	TGF-beta 4	4.0
436654	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.0
433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
424001	W67883	Hs.137476	internally expressed 10	4.0
432058	AW865996	Hs.130729	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
423713	AW754182		gbr.RC2-C10321-131199-011-c01 CT0321 Homo	4.0
419629	AB020595	Hs.91662	KIAA0888 protein	4.0
439108	AW163034	Hs.6467	synaptogyrin 3	4.0
444086	AJ703103	Hs.271360	hypothetical protein MGC16275	4.0
422807	A751648	Hs.495215	ESTs	4.0
405331			NM_024560:Homo sapiens hypothetical prot	4.0
457005	AJ007421	Hs.172597	saf (Drosophila)-like 3	4.0
437948	AA772920	Hs.303527	ESTs	4.0
440471	AA861466	Hs.307844	ESTs	4.0
432149	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	4.0
449655	AJ021987	Hs.59970	ESTs	4.0
448299	AA497044	Hs.20687	hypothetical protein FLJ10392	4.0
435743	T68661	Hs.12962	ESTs	4.0
412659	AW733865	Hs.74376	alpha-fetoprotein related ER localized prot	4.0
430694	AA810624	Hs.30936	ESTs, Weakly similar to H28H_HUMAN HISTO	3.9
437807	AJ017875	Hs.138826	ESTs	3.9
440085	BE270761	Hs.23158	ESTs	3.9
449722	BE280074	Hs.23960	cyclin G1	3.9
445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	3.9
420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	3.9
407198	H91679		gbr.yv0407.s1 Soares fetal liver spleen	3.9

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447519	U46258	Hs.330665	ESTs	3.9
425038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	3.9
414761	A0077228	Hs.17256	enhancer of zeste (Drosophila) homolog 2	3.9
404534			Target Egen	3.9
449670	F07693	Hs.85603	Homo sapiens mRNA cDNA DKF-Zp434K2172 (f)	3.9
414117	W88559	Hs.1787	proteolipid protein 1 (Polineus-Merzbach)	3.9
433290	R20077	Hs.302185	Homo sapiens clone Z0618 mRNA sequence	3.9
447107	R42637	Hs.21963	hypothetical protein DKF-Zp76180S14	3.9
431789	H15500	Hs.265222	mitogen-activated protein kinase 4	3.9
434149	Z43829	Hs.244624	hypothetical protein MGCS5469	3.9
466896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.9
411555	AF113537	Hs.70689	HMP19 protein	3.9
426646	A4382187	Hs.122713	ESTs	3.9
450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.9
429228	A553633	Hs.326447	ESTs	3.9
451433	AA021140	Hs.269265	ESTs, Weakly similar to A46910 X-linked	3.9
447937	AL109116	Hs.29034	Homo sapiens mRNA full length insert cDNA	3.9
436734	A507612	Hs.273558	hypothetical protein FLJ23112	3.9
417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransferase	3.9
417632	R20855	Hs.5422	glycoprotein M6B	3.9
414245	BE148072	Hs.75850	VAS protein family, member 1	3.9
418203	JX5492	Hs.83756	CDC26 protein kinase 2	3.9
453438	A469603	Hs.22792	ESTs	3.9
408449	NM_004408	Hs.166151	dynamitin 1	3.8
411048	AK001742	Hs.67991	hypothetical protein DKF-Zp434G0622	3.8
408819			NM_002576 Homo sapiens p21 (CDKN1A)-actin	3.8
445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	3.8
432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	3.8
457292	A521270	Hs.281462	hypothetical protein FLJ14251	3.8
432553	AW367103	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.8
413889	AW462631	Hs.313903	ESTs, Highly similar to AF157833 1 noncl	3.8
426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	3.8
410768	AF038185	Hs.66187	Homo sapiens clone Z3700 mRNA sequence	3.8
417791	AF065339	Hs.111471	ESTs	3.8
454123	AB032990	Hs.40715	hypothetical protein KIAA1164	3.8
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	3.8
449145	A632122	Hs.198408	ESTs	3.8
446957	AA383439	Hs.16759	Sp1-1 protein	3.8
407304	AA558332	Hs.271645	gh-MSD03.1 NCL_OGAP_AA1 Homo sapiens	3.8
437269	AA334384	Hs.145420	ESTs	3.8
443539	AJ076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	3.8
426855	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKF-Zp566P013 (f)	3.8
418821	AA436002	Hs.163161	ESTs	3.8
409875	NM_015434	Hs.48604	DKF-ZP434B168 protein	3.8
422175	N79885	Hs.6382	ESTs, Highly similar to T00391 hypothi	3.8
432488	AA551010	Hs.216640	ESTs	3.8
450582	AI339732		G-rich RNA sequence binding factor 1	3.8
425380	A1291287	Hs.140990	ESTs	3.8
451407	AA113176	Hs.343809	fibroblast growth factor 12B	3.8
451778	A1826131	Hs.62954	ESTs, Weakly similar to zinc finger prot	3.8
425652	AB021742	Hs.322431	neurogenic differentiation 2	3.8
412820	BE601236		gh-CHG-BN0075-249200-101-d11 BN0075 Homo	3.8
412193	A1884467	Hs.144057	ESTs	3.8
431117	AF003522	Hs.265090	delta (Drosophila)-like 1	3.8
433042	AW190334	Hs.281895	Homo sapiens cDNA FLJ11660 f1s, clone HE	3.8
437156	AA761537	Hs.191096	ESTs	3.8
451367	AA923729	Hs.26332	cell cycle related kinase	3.8
425390	A092634	Hs.156114	protein tyrosine phosphatase, non-recept	3.8
445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 f1s, clone NT	3.8
425843	BE313280	Hs.159627	death associated protein 3	3.8
445331	AF333614	Hs.220657	ESTs, Moderately similar to ALU5_HUMAN A	3.7
440210	AW674562	Hs.125296	ESTs	3.7
430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUK	3.7
437252	AA433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
405327	LA1162	Hs.53563	collagen, type IX, alpha 3	3.7
429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130KD	3.7
457183	H81882	Hs.118669	Dvl-binding protein IDAX (inhibition of	3.7
403696			CA001100 ^g gH5852342) gH/AADS4015 1) (AF0	3.7
408670	AF160567	Hs.45784	potassium large conductance calcium-acti	3.7
416577	T80470	Hs.334840	ESTs, Moderately similar to T80855 acin	3.7
422253	W81526	Hs.118329	ESTs, Moderately similar to GAD_HUMAN GA	3.7
450154	R15891	Hs.281587	Human (clone CTG-4A) mRNA sequence	3.7
408453	AA369838	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.7
440553	AA883416	Hs.344543	Homo sapiens cDNA FLJ14459 f1s, clone HE	3.7
428536	A143139	Hs.2238	visinin-like 1	3.7
426413	AA377823		gh:EST00805 Synovial sarcoma Homo sapien	3.7
409172	Z99399	Hs.122593	ESTs	3.7
441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	3.7
418216	AA662240	Hs.263099	AF15c14 protein	3.7
408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	3.7
437449	AL390153	Hs.208339	Homo sapiens mRNA; cDNA DKF-Zp752G113 (f)	3.7
436035	AA703679	Hs.100999	ESTs, Weakly similar to SYTS_HUMAN SYNA	3.7
451697	AW449774	Hs.296380	POM (PCMB21 rat homolog) and ZP3 fusion	3.7

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436961	AW375974	Hs.156704	ESTs	3.7
409953	AA322277	Hs.57691	cadherin 18, type 2	3.7
435832	AA425688	Hs.41641	Bruno (Drosophila)-like 4, RNA binding	3.7
424343	AW955360	Hs.47448	adenylyl cyclase activating polypeptide	3.6
437470	AL390147	Hs.134742	hypothetical protein DKFZp470M05	3.6
440168	AA868507	Hs.126141	ESTs	3.6
427624	AA406245	Hs.24895	-ESTs	3.6
418293	AL224483	Hs.16063	hypothetical protein FLJ21877	3.6
445883	AF070554	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.6
458912	A1911066	Hs.13415	ESTs	3.6
419390	A1701162	Hs.90207	hypothetical protein MGSC11138	3.6
449256	AA059050	Hs.59847	ESTs	3.6
425010	T16837	Hs.4241	ESTs	3.6
412754	AW163975	Hs.74565	amyloid beta (A4) precursor-like protein	3.6
407077		NM_007325	Homo sapiens glutamate receptor	3.6
438831	BE263273	Hs.6439	synapsin II	3.6
419235	AW170411	Hs.289433	neurotrophin	3.6
424947	R77552	Hs.289433	ESTs, Weakly similar to alternatively sp	3.6
407624	AW157431	Hs.248941	ESTs	3.6
440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.6
440404	AF015881	Hs.324527	mitochondrial ribosomal protein S5	3.6
435967	AA267747	Hs.173212	ESTs, Weakly similar to A46010 X-linked	3.6
424340	AA339306	Hs.7033	ESTs	3.6
423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.6
418064	BE387287	Hs.83364	S100 calcium-binding protein, beta (neur	3.6
429483	AF038339	Hs.184592	KIAA0244 gene product	3.6
463875	AW001783	Hs.232711	ESTs	3.6
430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	3.6
431552	AH15063	Hs.255873	axonal transport of synaptic vesicles	3.6
424278	AK000723	Hs.144517	hypothetical protein FLJ20716	3.6
434131	AB682276	Hs.143869	ESTs	3.6
435923	BE301930	Hs.5010	Homo sapiens clone 24672 mRNA sequence	3.6
415709	AA649850	Hs.278558	ESTs	3.6
437640	AA764893	Hs.272159	ESTs, Weakly similar to I38022 hypot	3.6
415585	A208485	Hs.144759	ESTs, Weakly similar to I38022 hypot	3.6
414040	NS8513	Hs.32171	ESTs	3.6
427315	AA178949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.6
410711	AB002316	Hs.65746	KIAA0318 protein	3.6
445953	AS127275	Hs.145710	ESTs	3.6
444794	AJ185991	Hs.145525	ESTs	3.6
411968	AJ207410	Hs.69280	Homo sapiens, clone IMAGE:363629, mRNA,	3.6
428180	AJ129767	Hs.182874	guanine nucleotide binding protein (G pr	3.6
415283	RA0504	Hs.21245	ESTs	3.6
433160	AW227002	Hs.134342	TASIP for testis-specific adriamycin sens	3.5
410386	W26187	Hs.3327	Homo sapiens cDNA: FLJ22219 fls, clone H	3.5
430818	AJ319128	Hs.348156	gb:qp89H04.x1 NC1_CGAP_Kd5 Homo sapiens	3.5
433932	AW954599	Hs.169330	neuronal protein	3.5
426378	AA813546	Hs.59034	GTP-binding protein Rho7	3.5
456723	Z43602	Hs.4748	adenylyl cyclase activating polypeptide	3.5
416340	N31772	Hs.79226	lacculation and elongation protein zel	3.5
451455	AJ037227	Hs.8821	hapdinin antimicrobial peptide	3.5
412719	AW016610	Hs.818	ESTs	3.5
438910	A084152	Hs.217182	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.5
439340	AB032436	Hs.6535	brain-specific Na-dependent inorganic ph	3.5
458072	AW90347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	3.5
439710	AF086543		gb:Homo sapiens full length insert cDNA	3.5
433896	AF253483	Hs.255205	KIAA1863 protein	3.5
427225	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.5
449599	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fls, clone PL	3.5
439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.5
443332	AA338919	Hs.101615	ESTs	3.5
456407	AW967656	Hs.123848	ESTs, Weakly similar to AF108460 1 ubinu	3.5
442264	AJ278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
404295			Target Exon	3.5
427209	H06559	Hs.92423	KIAA1566 protein	3.5
429627	BE621102	Hs.290276	hypothetical protein FLJ21841	3.5
427513	AJ476318	Hs.192480	ESTs	3.5
458435	AJ418718	Hs.144121	ESTs, Weakly similar to T46916 hypot	3.5
435545	AA687415	Hs.28107	ESTs	3.5
413198	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	3.5
441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	3.5
452449	AW068058	Hs.20943	ESTs	3.5
443257	AJ334040	Hs.11614	HSPC065 protein	3.5
423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-4	3.5
427581	NM_014788	Hs.179703	KIAA0129 gene product	3.5
424090	X99099	Hs.135262	XIAP associated factor-1	3.5
422906	U80773	Hs.121580	Human EST clone 42944 member transposon	3.5
429698	AA083086	Hs.26339	ESTs, Weakly similar to S21348 probable	3.5
439510	H05430	Hs.288433	neurotrophin	3.5
436899	AA764852	Hs.291567	ESTs	3.5
414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypot	3.5
418365	AW014345	Hs.161690	ESTs	3.4
414598	AJ094221	Hs.135150	lung type-I cell membrane associated gly	3.4

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452571	W31518	Hs.34665	ESTs	3.4
443633	AL031290	Hs.9654	similar to pregnancy-associated plasma p	3.4
408955	BE315170	Hs.8087	Target CAT	3.4
443206	AB011420	Hs.9075	serine/threonine kinase 17a [apoptosis-i	3.4
419617	AL008283	Hs.9122	neuronal pentamer receptor	3.4
454171	AW854832	Hs.10261	glt-0v2-C10261-201099-011-05 C10261 Homo	3.4
265259	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	3.4
440652	AJ216751	Hs.143877	ESTs	3.4
450813	AJ739625	Hs.203378	ESTs	3.4
429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.4
439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDN	3.4
409892	AW956113	Hs.7149	glt-EST358183 MAGC resequences, MAGD Homo	3.4
439963	AW243529	Hs.6753	platelet activating factor acetylhydrola	3.4
416658	U03272	Hs.79432	filovlin 2 (congenital contractual dra	3.4
453740	AL120295	Hs.211809	ESTs, Moderately similar to PC4259 form	3.4
435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
453305	R35224	Hs.267597	EHMZ gene	3.4
425287	R88249	Hs.155524	peanut (Thiosiphila)-like 2	3.4
417663	R07483	Hs.180461	ESTs	3.4
448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.4
441834	AL138034	Hs.7979	KIAA0736 gene product	3.4
457876	AJ221940	Hs.225526	ESTs, Moderately similar to ALUS_HUMAN A	3.4
407842	BE410100	Hs.40368	scaptor-related protein complex 1, sigma	3.4
422676	D28481	Hs.1570	histamine receptor H1	3.4
408926	AF217525	Hs.49002	Down syndrome cell adhesion molecule	3.4
430762	AI343652	Hs.105667	ESTs	3.4
430950	XS4232	Hs.2559	glycocalyx 1	3.4
445078	AI069975	Hs.4775	juncophilin 3	3.4
423257	AW161039	Hs.125878	synapsin III	3.4
417402	BE003227	Hs.134759	ESTs	3.4
410011	AB029641	Hs.57865	PF4746 protein kinase 1	3.4
404541		NM_000795	Homo sapiens slathern-like 4 (3.4
436291	BE569452	Hs.344037	protein regulator of cytokinesis 1	3.4
443672	AA323352	Hs.9587	bulbocystine (gamma), 2-oxoglutarate di	3.4
421140	AK009494	Hs.273558	hypothetical protein FLJ20397	3.4
451061	AW091487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.4
425782	U66466	Hs.159525	cell growth regulatory with EF-hand dome	3.4
420692	AW976345	Hs.159525	glt-EST358454 MAGC resequences, MAGN Homo	3.4
410507	AA355288	Hs.76064	translational epithelia response protein	3.4
412436	AA680988	Hs.159525	glt-76061 c1 NCL, CCAP, Axl Homo sapiens	3.4
448112	AW245919	Hs.34969	hypothetical protein DKFZ5566N004	3.4
429269	AA449013	Hs.99203	ESTs	3.4
408037	AW271720	Hs.42223	hypothetical protein FLJ10300	3.3
416858	AW961605	Hs.211145	hypothetical protein RG083W05.2	3.3
400090	AL118615	Hs.94653	neurochondin	3.3
436277	R88820	Hs.120917	ESTs	3.3
430412	AW341754	Hs.189305	ESTs	3.3
428524	AA086381	Hs.315111	nuclear receptor co-repressor/NRAC3 comp	3.3
432653	AS84317	Hs.120589	ESTs	3.3
449919	AI674585	Hs.200141	ESTs	3.3
438509	RA5367	Hs.101191	ESTs	3.3
429037	X81895	Hs.194765	H. sapiens GENX-5524 mRNA, 3' UTR	3.3
445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	3.3
425537	AB007913	Hs.158291	KIAA0444 protein	3.3
408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	3.3
449886	AW072813	Hs.270858	ESTs, Moderately similar to ALU4_HUMAN A	3.3
417323	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.3
410592	R94088	Hs.43569	ESTs	3.3
439444	AJ277652	Hs.54578	ESTs, Weakly similar to 38022 hypoteti	3.3
453575	AI733610	Hs.187832	ESTs	3.3
409746	NM_004794	Hs.56294	RAS33A, member RAS oncogene family	3.3
425688	F07396	Hs.46527	ESTs	3.3
412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP1	3.3
425242	D13635	Hs.155287	KIAA0010 gene product	3.3
417280	AW173136	Hs.250103	ESTs	3.3
423746	AI149048	Hs.307211	hypothetical protein FLJ22313	3.3
452856	AF034793	Hs.30881	protein tyrosine phosphatase, receptor 1	3.3
419103	Z40229	Hs.96423	hypothetical protein FLJ23033	3.3
453718	R06569	Hs.269534	ESTs	3.3
445286	TS2285	Hs.193155	Homo sapiens mRNA for KIAA1754 protein,	3.3
423770	AW976796	Hs.132776	Homo sapiens cDNA FLJ10077 fls, clone HE	3.3
409557	BE182896	Hs.211193	ESTs	3.3
439285	AL133916		hypothetical protein FLJ20093	3.3
421183	AL135740	Hs.102447	TSC-22-like	3.3
433894	AP07682	Hs.243293	ESTs	3.3
445225	AP216555	Hs.202398	ESTs	3.3
411379	AI816344	Hs.12554	ESTs, Weakly similar to NPLA_HUMAN NUCLE	3.3
436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.3
438870	AW204219	Hs.155560	catenexin	3.3
441751	AW372449	Hs.612711	hypothetical protein FLJ21159	3.3
408547	AA574291	Hs.57837	ESTs	3.3
420982	AW576160	Hs.100729	KIAA0692 protein	3.3
451625	R56793	Hs.106576	alanine-glyoxylate aminotransferase 2-4	3.3

5	418932	L34059	Hs.89484	cathepin 4, type 1, R-cathepin (retinal)	3.3
	453496	AA442103	Hs.33054	solute carrier family 2 (facilitated glu	3.3
	423169	BE047009	Hs.21837	ESTs, Weakly similar to KIAA0927 protein	3.3
	418949	AA211467	Hs.19048	Homo sapiens, Similar to nuclear localiz	3.3
	441243	AV157556	Hs.19302	ESTs	3.3
	444427	H25094	Hs.253663	ESTs, Moderately similar to 138022 hypot	3.3
	449115	AW059952	Hs.37528	ESTs, Weakly similar to AF050944 1 PRO06	3.3
	445416	AV055299	Hs.163595	ESTs	3.3
	437162	178028	Hs.154079	synaptotagmin I	3.3
10	450336	AA046814	Hs.289528	Homo sapiens cDNA: FLJ23296 fs, clone H	3.3
	433842	AI652156	Hs.26346	ESTs	3.3
	444124	RA3097	Hs.6818	ESTs	3.3
	423588	AL137326	Hs.133483	Homo sapiens mRNA: cDNA DNFZp43490505 (I	3.3
	454792	AW020794	Hs.252405	hypothetical protein FLJ12296 similar to	3.3
15	412775	AA709046	Hs.27552	Homo sapiens mRNA: cDNA DNFZp566N2424 (I	3.3
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	3.2
	413981	AW051200	Hs.75640	natriuretic peptide precursor A	3.2
	433325	AW026896	Hs.143805	ESTs	3.2
	449092	U51641	Hs.22585	alpha2,8-sialyltransferase	3.2
20	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypothet	3.2
	424699	AL119387	Hs.115052	ESTs	3.2
	454263	AW067117	Hs.47144	DNFZP586N0819 protein	3.2
	410126	BE165274		KIAA0036 gene product	3.2
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	3.2
25	405303			Target Exon	3.2
	420871	AA702972	Hs.65300	ESTs	3.2
	442432	BE790369	Hs.38178	hypothetical protein FLJ23468	3.2
	428769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	3.2
30	442320	A/287817	Hs.129636	ESTs	3.2
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	3.2
	439764	T25535	Hs.22144	hypothetical protein MGC13105	3.2
	410425	BE278367	Hs.63510	KIAA0141 gene product	3.2
	422156	N34524		ghy56d10.s1 Soares_multiple_alderscos_	3.2
	451489	NM_005503	Hs.26468	amyloid beta (A4) precursor protein-bind	3.2
35	457358	AA179755	Hs.129010	ESTs	3.2
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	3.2
	452372	AI885742	Hs.228474	ESTs	3.2
	459660	MT9082		ESTs	3.2
	437085	AA435335	Hs.202329	ESTs	3.2
40	418832	AW362756	Hs.286184	hypothetical protein dJ55102.5	3.2
	440080	AW051597	Hs.143707	ESTs	3.2
	449714	AB033015	Hs.23941	KIAA1189 protein	3.2
	450407	NM_000910	Hs.24959	gamma-aminobutyric acid (GABA) A recepto	3.2
	423165	AB375447	Hs.124915	hypothetical protein MGC2501	3.2
45	449861	AW026534	Hs.133100	ESTs	3.2
	454036	AA347456	Hs.33660	Homo sapiens mRNA for KIAA1771 protein,	3.2
	419865	NM_007020	Hs.93802	U1 snRNP binding protein homolog (70kD)	3.2
	423420	AI571364	Hs.126382	Homo sapiens mRNA: cDNA DNFZp76111224 (I	3.2
	420332	BE258535		glc-6011173141: NM_MGC_16 Homo sapiens c	3.2
50	424641	AB001106	Hs.151413	glia maturation factor, beta	3.2
	453544	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fs, clone NT	3.2
	447877	AA38194	Hs.164252	ESTs	3.2
	419683	AA348897	Hs.45874	ESTs	3.2
55	451026	AA013218	Hs.157492	cor-34 (mouse) homolog	3.2
	422709	AA315331	Hs.153485	ESTs	3.2
	432809	AA645509	Hs.131703	ESTs	3.2
	446503	W79572	Hs.13277	hypothetical protein FLJ22054	3.2
	457728	AW374811		griEST386915 MAGC resequences, MAGN Homo	3.2
	407390			NM_001334* Homo sapiens cathepsin O (CTS	3.2
60	445413	AA151342	Hs.12677	CGI 147 protein	3.2
	438703	AB033373	Hs.31699	ESTs	3.1
	434571	R07316	Hs.170769	Homo sapiens cDNA: FLJ22487 fs, clone H	3.1
	422772	AL115895	Hs.120238	KIAA0749 protein	3.1
	433434	AA588429		gln2203.s1 NCI_CGAP_P22 Homo sapiens	3.1
65	427961	AW293165	Hs.143134	ESTs	3.1
	414430	AA364201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	420552	AK000452	Hs.98906	hypothetical protein	3.1
	456209	W65633	Hs.297792	ESTs	3.1
	418819	AA228776	Hs.131721	ESTs	3.1
70	436944	AA302517	Hs.92732	KIAA1444 protein	3.1
	433095	AF085447		glt-Homo sapiens full length insert cDNA	3.1
	451734	NM_005176	Hs.26944	neurogranin (protein kinase C substrate,	3.1
	415267	F03016	Hs.27513	ESTs	3.1
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.1
75	432675	AF191851	Hs.105884	ESTs	3.1
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	3.1
	435092	AL137310	Hs.4749	Homo sapiens mRNA: cDNA DNFZp76151212 (I	3.1
	439039	AI656707	Hs.48713	ESTs	3.1
	453358	AB010098	Hs.24907	corvinn, actin-binding protein, 2B	3.1
80	400890			Target Exon	3.1
	417636	R08916	Hs.191212	ESTs	3.1
	425790	AW136286	Hs.288466	ESTs	3.1
	415314	N88802	Hs.5422	glycoprotein M6B	3.1

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5	436456	AW292677	Hs.248122	G protein-coupled receptor 24	3.1
	408601	U47928	Hs.86122	protein A	3.1
	420886	AA805453	Hs.5454	ESTs, Weakly similar to T99012 hypothel	3.1
	437162	AW005505	Hs.167700	thyroid hormone receptor coactivating pr	3.1
	445734	AA832142	Hs.296184	ESTs, Moderately similar to 180022 hypot	3.1
10	440700	AW952281	Hs.7799	guanine nucleotide binding protein (G pr	3.1
	414747	U30872	Hs.7799	centromere protein F (350400KD, mitotin	3.1
	431553	X78075	Hs.7294	cartilage linking protein 1	3.1
	426549			CD001342-p1.278144p[26434]NAHL_RAT GO	3.1
	431467	N71831	Hs.295398	Homo sapiens mRNA, cDNA DKFpZp434E0526 (I	3.1
15	457561	AA331517	Hs.286055	chimerin (chimerin) 2	3.1
	412507	L36645	Hs.73964	EphA4	3.1
	413448	AL134667	Hs.25307	Homo sapiens clone 24812 mRNA sequence	3.1
	444168	AW379879		gb.RC11-H10255-681159-011-011 H10256 Homo	3.1
	400090			Eos Control	3.1
20	433642	BE466341	Hs.189746	ESTs, Weakly similar to 180022 hypothel	3.1
	422508	NM_001809	Hs.1559	centromere protein A (17c3)	3.1
	426318	AA375125	Hs.147112	Homo sapiens cDNA: FLJ22322 fls, clone H	3.1
	428896	AW251932	Hs.98936	ESTs	3.1
	429277	AA001064	Hs.43670	ESTs	3.1
25	426509	M31166	Hs.2050	penicillin-related gene, rapidly induced b	3.1
	412216	AW051517		gb.RC5-NAH1013-310300-021-C03 NH1013 Homo	3.1
	428845	AL157579	Hs.153610	KIAA0751 gene product	3.1
	431512	BE207334	Hs.2795	lactate dehydrogenase A	3.1
	418113	AJ272141	Hs.83494	SRY (sex determining region Y)-box 4	3.0
30	450661	AW552180	Hs.83494	ESTs	3.0
	456448	NM_014954	Hs.21239	KIAA0985 protein	3.0
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.0
	419687	A1638659	Hs.227699	ESTs, Weakly similar to T203_HUMAN TRANS	3.0
	450933	A164668	Hs.48832	ESTs	3.0
35	439660	AJ422719	Hs.120912	ESTs, Weakly similar to fork head like p	3.0
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.0
	437348	AL359620	Hs.14217	hypothetical protein DKFp762P2111	3.0
	439401	R44477	Hs.10056	hypothetical protein FLJ14621	3.0
	417837	AF154335	Hs.76691	LIM domain protein	3.0
40	445314	A1689948	Hs.65489	Homo sapiens cDNA: FLJ21517 fls, clone C	3.0
	425870	R13406	Hs.56782	ESTs	3.0
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.0
	414604	AA160138	Hs.107524	ESTs	3.0
	413995	BE048146	Hs.75671	synectin 1A (brain)	3.0
45	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	426384	AJ472078	Hs.303562	hypothetical protein FLJ13189 (FLJ13189)	3.0
	430747	BE0704	Hs.23434	hairy enhancer of split related with YRP	3.0
	425264	AA333563	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.0
	406917	X65964		gb.H.sapiens nestin gene	3.0
50	425262	D87119	Hs.155418	GS3955 protein	3.0
	401558			ENSP00000220478-9-SECRET00GRANN III.	3.0
	438345	AW444759	Hs.146171	ESTs	3.0
	414865	AA157155	Hs.274414	hypothetical protein FLJ114457	3.0
	453976	BE463830	Hs.163714	ESTs	3.0
55	404283			ENSP0000024751-1-Copine-like protein KIA	3.0
	432990	NM_014442	Hs.279751	static acid binding Ig-like lectin 8	3.0
	451491	AJ72084	Hs.286221	Homo sapiens cDNA FLJ11741 fls, clone PL	3.0
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.0
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.0
60	443753	AW367578	Hs.134749	ESTs	3.0
	417688	AJ078534	Hs.122592	ESTs	3.0
	443998	AW904296	Hs.9550	Sec1 gamma	3.0
	438869	AF075009		gb.Homo sapiens full length insert cDNA	3.0
	453900	AW003682	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.0
65	447714	AW265313	Hs.255337	ESTs	3.0
	426581	AB040968	Hs.136950	KIAA1523 protein	3.0
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	3.0
	410762	AF226053	Hs.66170	HSKM-B protein	3.0
	431462	AW036772	Hs.255311	gram-like neuroendocrine peptide precu	3.0
70	452221	C21322	Hs.286057	hypothetical protein FLJ22242	3.0
	412326	R01566	Hs.73817	small inducible cytokine A3 (homologous	3.0
	428600	AW863261	Hs.24213	hypothetical protein DKFpZp434K1421	3.0
	428601	AW043782	Hs.293616	ESTs	3.0
	405558			Target Ecan	3.0
75	421483	NM_003388	Hs.104717	hypothetical protein MGC11333	3.0
	446681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	3.0
	452108	AW135982	Hs.203013	hypothetical protein FLJ12748	3.0
	429569	AA454933	Hs.136343	ESTs, Weakly similar to 178855 senecio	3.0
	450728	AW152523	Hs.26363	presenilin 2 (Alzheimer disease 2)	3.0
80	429371	NM_001703	Hs.200586	brain-specific angiogenesis inhibitor 2	3.0
	437435	AA249439	Hs.27027	hypothetical protein DKFpZp62H1311	3.0
	432188	AB062592	Hs.29228	solute carrier family 7 (cationic amino	3.0
	404632			NM_022450 Homo sapiens hypothetical prot	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE-2298026, mRNA,	3.0
	421458	NM_003654	Hs.104576	carbohydrate (sulfate) sulfatase (GAL-6) sul	3.0
	419036	AW134924	Hs.190325	ESTs	3.0
	453563	AW608906	Hs.181163	hypothetical protein MGC5629	3.0

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3.0

Genbank accession numbers

Number	Accession
1	AM1106262, DQ3969, AM0411062

T07735 AA484549 W60090 D52685 T23811

AA211402 AJ204899 AL366472 AW827081 A

AW901517 AW901523 AW901521 AW901524
AA66E0B0 AA13E130 AA4840E0 AA102419

BE001236 BE001177 BE001180 BE001234

1_1 H98716 N90792 N24283

2 A1909154 AAF26337 AA244193 A1909153

AW976345 AA279423 AA761070

1 N34524 AA305071 AW954803 AA502335 A

AA319435 NS6456 AA319377 AW961532 I
AL035633 E11794 E11783 H18042 T66089

AW754182 AW754198 AA329983

A1806660 A1982626 D81263 D53937 D5249

1 AA377823 AW954494 AM22588

AL041228 D82C04 D61361 AI203314 AJ990

AIC85630 AA731340

1 AL031658 AF693758 AL040619 AW977914

AF084866 AF084870 AF084864 AF084867

3_1 AW972830 AA527647 AA489820 AA57036

W29882 AWE65533 AW149601 A1572917 A

AF075009 R63109 R63068

AL133916 N79113 AF086101 N76721 AW9

1 AF086387 W72884 W72711

AA973906 AI299888 AA917019 H63235 T9

3_1 Z44514 A1352097 A1803984 AW235923 AV

NM_014253 AF100772 BEC88769 AL0227
N48674 A1375997 B45433 D59344 A12031

AA190993 H03231 H59505 H01642 AA852

AW118072 AI631982 T15734 AA224195 A

1 AI240665 T53681 N77468 H51833 AA147

R73906 R75632 H03612 AA909684 NS069

4_1 T79703 T96307 AL079725

AW974811 AA651634 AA650072
A1821940 N67106 A1744264 AA806846 AA

759 1000 1000 1000 1000 1000 1000 1000 1000 1000

Unique number corresponding to an Eos probe set

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Ref: Sequence source The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

5

10

15

20

25

30

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400777	8131663	Plus	70745-71121
402850	1927510	Minus	4506-4691
401558	7196618	Plus	103510-104090
402145	8018280	Plus	113086-114000
402604	9909420	Plus	20393-20767
402855	9962953	Minus	59763-59909
403696	3135242	Minus	143457-143534
403790	8284957	Minus	87825-87947,89803-90002
404150	7534008	Plus	165811-165943
404283	2276311	Minus	99489-99564
404295	9855683	Minus	75741-75747
404541	8318558	Plus	103458-103654
404584	9857511	Plus	138651-139153
404632	9796668	Plus	45096-45229
404819	4578240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17528,18261-18357,18443-18578
405229	7249119	Plus	144345-144464,144690-144836,151750-151883,152407-152484
405303	2078453	Minus	130607-130802
405331	3236226	Minus	32502-32690
405348	2914717	Minus	43310-43462
405558	1621110	Plus	4562-4644,5063-6083
405605	5836196	Minus	117070-117270
405819	4007557	Plus	2830-2957

TABLE 18A: ABOUT 446 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT CNS

Table 18A lists about 446 CNS-enriched genes significantly down-regulated in glioblastoma multiforma (GBM) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Exon Hu30 GeneChip array such that the ratio of "average" normal CNS to "average" GBM was greater than or equal to 2. The "average" normal CNS level was set to the 85th percentile amongst various normal CNS tissues. The "average" GBM level was set to the 85th percentile amongst various tumor samples. To enrich for CNS-specific genes, the ratio of "average" normal CNS to "average" normal non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

Pkey: Unique Exon probe identifier number
 ExAcon: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of CNS to GLIOBLASTOMA MULTIFORMA
 R2: Ratio of CNS to NON-CNS NORMAL ADULT TISSUES

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Pkey	ExAcon	UnigeneID	Unigene Title	R1	R2
425489	M58594	Hs.1905	protactin	38.8	10.5
410330	AW025630	Hs.159426	ESTs	23.4	23.4
403538	AB024335	Hs.243821	differentiation-associated Na-dependent	22.6	22.6
417275	X63578	Hs.295448	parvalbumin	22.4	6.0
453590	AF159278	Hs.33578	KIAA0820 protein	22.3	22.3
428505	AL035461	Hs.1281	chromogranin B (secretogranin 1)	21.8	21.8
453220	AB033089	Hs.32452	homo sapiens mRNA for KIAA1263 protein,	19.9	19.9
411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	19.4	19.4
408040	AL266496	Hs.22305	ESTs, Weakly similar to RHG5, HUMAN RHO-G	19.4	19.4
435145	AL227259	Hs.116633	ESTs	18.5	2.8
407029	X03084	Hs.50319	gH-fusion protactin gene 5' region.	18.1	18.1
409263	AA069573	Hs.50319	ESTs	16.8	16.8
449078	AK001256	Hs.22975	KIAA1576 protein	16.1	16.1
426968	U07616	Hs.173034	amphiphysin (Shi Mann syndrome with br	15.3	15.3
432286	AL118812	Hs.274923	Homo sapiens mRNA, cDNA, DNFPpT61G11111 f	15.1	15.1
426645	NM_014682	Hs.151449	KIAA0535 gene product	15.1	15.1
450590	AI701507	Hs.273740	ESTs	14.9	3.8
417175	RA45508	Hs.94002	ESTs	14.6	8.9
423449	AB491900	Hs.33067	ESTs	14.5	14.5
441869	NM_003947	Hs.8304	huntingtin-associated protein interactin	14.4	14.9
405560	AW887701	Hs.20628	hypothetical protein FLJ20628	14.0	8.0
440209	H05049	Hs.247837	neurexin 3	13.9	18.7
439238	NM7305	Hs.302161	ESTs	13.9	5.3
452022	AW072330	Hs.263815	ESTs	13.8	13.8
459080	AW192083	Hs.290855	ESTs	13.5	13.5
425649	U03930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	13.4	38.6
413324	V00571	Hs.75294	serotonergic releasing hormone	13.2	13.2
443982	AW022228	Hs.322922	ESTs	13.1	13.1
410635	D58563	Hs.334372	chondric; somatomedinotropin hormone 1 (p	12.9	6.6
420156	AAW49258	Hs.6187	ESTs	12.5	12.5
416490	AF090116	Hs.75348	regulator of G-protein signalling 7	12.5	12.5
450757	B6081080	Hs.31578	ESTs, Weakly similar to KIAA1324 protein	12.2	3.2
418037	AB020725	Hs.58009	KIAA018 protein	12.2	12.2
433940	H05129	Hs.3830	cyclic AMP-regulated phosphoprotein, 21	12.0	12.0
434367	AB020700	Hs.3830	KIAA0893 protein	11.6	5.6
410657	AF063228	Hs.65248	dynactin, cytoplasmic, intermediate polype	11.5	11.5

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431988	AC002302	Has 77202	protein kinase C, beta 1	11.2	10.5
451783	R4254	Has 210662	T-box, brain, 1	11.2	11.2
453165	S74727	Has 32042	aspartacylase (aspartacylase 2, Canavan	10.7	10.7
452238	P01811	Has 345757	ESTs	10.6	3.8
417167	AW020437	Has 4290	ESTs	10.4	10.4
420333	D59502	Has 292590	ESTs	10.4	10.4
427224	AL135554	Has 101937	sine oculis homeobox (Drosophila) homolo	10.4	3.9
424153	AA451737	Has 141496	MAGE-like 2	10.3	5.1
413293	AL047463	Has 302498	GTP-binding protein homologous to Saccha	10.0	10.0
400438	AF 185611	Has 115362	Target	9.8	5.1
447750	AI422234	Has 143434	contactin 1	9.8	9.8
419347	C15844	Has 90005	superior cervical ganglia, neural speci	9.8	22.2
418207	C14685	Has 34772	ESTs	9.8	9.8
413409	AJ58418	Has 1440	DEAD-box (Asp-Glu-Ala-AspHis) box polypep	9.4	9.4
447746	AW015920	Has 161359	ESTs	9.2	9.9
406311		NM_021979	Homo sapiens heat shock 70MD	9.1	11.5
444330	AJ597655	Has 49265	ESTs	9.1	9.1
426355	AA378667	Has 10283	RNA binding motif protein 8B	9.0	4.1
427322	AK002017	Has 176227	hypothetical protein FLJ11155	8.9	8.9
439450	RS1613	Has 125304	ESTs	8.7	8.3
429096	AB011106	Has 196012	KIAA0534 protein	8.6	8.6
426652	AJ584272	Has 336224	transmembrane protein with EGF-like and	8.6	8.6
426814	NE2459	Has 176227	hypothetical protein FLJ11155	8.6	8.6
410309	BE043077	Has 278153	ESTs	8.5	8.5
408950	AA707814	Has 14945	long fatty acyl-CoA synthetase 2 gene	8.5	8.5
425814	AF038943	Has 172619	myelin transcription factor 1-like	8.5	14.2
416851	AW083501	Has 85618	ESTs	8.5	8.5
430004	U27768	Has 227517	regulator of G-protein signalling 4	8.4	15.7
412155	R38167	Has 12449	Homo sapiens transmembrane protein HTMP1	8.4	27.9
427061	AB032971	Has 173392	KAA1145 protein	8.4	8.4
412049	HS3437	Has 12636	adenylate kinase 5	8.3	10.7
425752	AW040458	Has 33578	KIAA0820 protein	8.2	13.4
414659	AI815523	Has 76330	syncytin, alpha (non A4 component of am	8.2	4.5
422756	AA441787	Has 119689	glycoprotein hormones, alpha polypeptide	8.1	5.8
435648	H24347	Has 27524	ESTs	8.1	8.1
425470	AI878501	Has 203862	guanine nucleotide binding protein (G pr	8.0	8.0
416133	NM_001683	Has 89512	ATPase, Ca transporting, plasma membrane	8.0	8.0
438208	AL041224	Has 65379	ESTs	7.9	5.8
426427	AI344378	Has 145339	ESTs	7.8	7.8
441005	ZA1335	Has 303172	Homo sapiens mRNA; cDNA DKFpZp547G133 (f	7.7	7.7
442023	AI187878	Has 144549	ESTs	7.7	5.6
444458	BE041526	Has 31746	hypothetical protein DKFpZp547F072	7.7	7.7
429033	NM_007374	Has 194756	sine oculis homeobox (Drosophila) homolo	7.6	5.5
426642	R59773	Has 7130	copine IV	7.6	5.6
445544	AI631932	Has 7047	ESTs, Weakly similar to Unknown [H.sapi	7.5	12.4
438283	AI458931	Has 37282	ESTs	7.5	7.5
437073	AI859008	Has 94122	ESTs	7.5	7.5
408577	HS0572	Has 19515	ESTs, Highly similar to NRG3_HUMAN PRQ-H	7.4	7.4
424264	D04020	Has 232308	Human DNA sequence from clone RP1-304B14	7.3	7.3
441264	AA927170	Has 23230	ESTs	7.3	7.3
450474	AW872844	Has 117494	ESTs	7.2	7.2
425352	NM_000939	Has 1897	proopiomelanocortin (adrenocorticotropin	7.2	6.1
450715	AD264584	Has 31570	ESTs, Weakly similar to KIAA1324 protein	7.2	7.2
450181	H85254	Has 201198	ESTs	7.2	7.2
415076	NM_000857	Has 77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
415318	AW969742	Has 291005	ESTs	7.1	3.1
423003	AL120377	Has 122967	hath (Drosophila)-like 2 (Mayven)	7.0	7.0
434460	AA478486	Has 3652	KIAA0568 protein	7.0	4.8
433921	AA618174	Has 146114	glnq1461.01 N1 NC1 CGAP_Thy1 Homo sapiens	7.0	7.0
418940	H17739	Has 288513	Human DNA sequence from clone RP5-899C14	7.0	7.0
410765	AF694372	Has 66180	nucleosome assembly protein 1-like 2	7.0	8.0
427012	RI1440	Has 302754	ESTs	6.9	6.9
416018	AW138239	Has 78977	proprotein convertase subtilisin/kexin 1	6.9	14.0
445898	AF070623	Has 13423	Homo sapiens clone 24465 mRNA sequence	6.9	6.9
415669	NM_005025	Has 78369	serine (or cysteine) proteinase inhibitor	6.9	10.2
433558	AA531751	Has 201789	ESTs, Weakly similar to T24435 hypotheti	6.9	6.9
429031	AA376836	Has 288555	ESTs	6.8	6.8
409339	AB020686	Has 54037	ectonucleotide pyrophosphatase/phosphodi	6.8	3.6
436568	H12049	Has 91564	ESTs	6.8	6.8
442953	R39894	Has 31961	ESTs	6.7	6.7
417948	AA772920	Has 303927	ESTs	6.7	6.7
412266	N99006	Has 26133	ESTs	6.6	30.9
422980	N46569	Has 76722	C/CAAT/enhancer binding protein (C/EBP),	6.6	45.2
442026	AI243749	Has 8074	brain-specific angiogenesis inhibitor 3	6.5	6.5
425946	RI6330	Has 284129	KIAA1678	6.4	6.4
445279	RI41900	Has 222425	ESTs	6.4	6.4
428414	AL049980	Has 184216	DKFZp564C152 protein	6.4	6.4
427868	NM_005050	Has 40637	proline-rich Glu (G-carboxyglutamic acid	6.4	3.3
434104	AF116601	Has 116458	hypothetical protein PRO2758	6.4	4.0
443244	AI457235	Has 165479	ESTs	6.3	10.0
442042	AI990506	Has 8077	Homo sapiens mRNA; cDNA DKFpZp547E184 (f	6.2	6.2
444783	AK001468	Has 62180	anilin (Drosophila Scraps homolog), act	6.2	43.2
426536	AI143139	Has 2288	visinin-like 1	6.0	22.1

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5	415114	D50468	Hs.94181	ESTs	6.0	6.0
	448958	AB020651	Hs.22653	KIA00844 protein	5.9	5.9
	431467	T1831	Hs.256398	Homo sapiens mRNA, cDNA DKF-Zp34E0528 (l)	5.9	6.0
	447138	AA39112	Hs.93028	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
	414545	AA149287	Hs.76505	ESTs	5.8	5.8
10	418202	N4821	Hs.26549	KIAA1709 protein	5.8	5.8
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PHU6B salivary	5.7	9.6
	444124	R43057	Hs.6818	ESTs	5.7	9.3
	408065	AW954272	Hs.13365	gHcEST366342 MAGE sequences, MAGEC Homo	5.6	5.6
	448533	AL119710	Hs.156244	nucleosome assembly protein 1-like 3	5.6	9.6
15	425523	AB000798	Hs.156244	KIAA0479 protein	5.6	36.0
	459697	AA405062	Hs.98002	ESTs	5.6	5.4
	408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, member	5.6	5.6
	420111	AF256522	Hs.132863	gHcEST366342 MAGE sequences, MAGEC Homo	5.5	5.2
	450149	AW969781	Hs.193039	Zic family member 2 (odd-paired Drosophila	5.4	5.4
20	424918	R13982	Hs.193039	myelin-associated oligodendrocyte basic	5.3	5.3
	438202	AW169287	Hs.22588	ESTs	5.3	5.3
	448605	AL109678	Hs.21597	Homo sapiens mRNA, full length insert cDNA	5.3	5.3
	425580	L11144	Hs.1907	gadinin	5.3	3.5
	418866	T65754	Hs.233023	gHcEST366342 MAGE sequences, MAGEC Homo	5.3	3.8
25	430091	AB032958	Hs.179075	Homo sapiens cDNA FLJ11981 f1, clone HE	5.2	5.2
	444785	BE408442	Hs.174165	ectonucleotide pyrophosphatase/phospho	5.2	3.0
	427283	AL119706	Hs.174165	gHcEST366342 MAGE sequences, MAGEC Homo	5.2	3.0
	415666	H72693	Hs.61289	synaptotagmin 2	5.2	4.6
	412840	AL157424	Hs.193470	putative receptor P2X, ligand-gated ion	5.2	7.7
30	428784	T12651	Hs.193470	Homo sapiens mRNA for KIAA1763 protein,	5.2	33.0
	446692	Z46514	Hs.184658	SEB131 protein	5.2	4.1
	426508	BE252383	Hs.153651	ESTs	5.1	5.1
	446353	A1290919	Hs.26411	ESTs	5.1	8.2
	433133	N67665	Hs.21719	hypothetical protein DKFZp71M03313	5.1	5.1
35	437331	AL335333	Hs.324784	glutamate decarboxylase 1 (brain, 67ND)	5.1	5.1
	429988	M81883	Hs.225952	protein tyrosine phosphatase, receptor I	5.1	5.1
	411379	AB16344	Hs.12554	ESTs, Weakly similar to NFPA_HUMAN NUCLE	5.0	11.2
	403038	AW148652	Hs.167358	ESTs	5.0	5.0
	415734	NM_014747	Hs.78748	KIAA0237 gene product	5.0	5.0
40	429747	BE405065	Hs.159460	ESTs	5.0	5.6
	425984	AW836277	Hs.155636	hypothetical protein DKFZp71C07121	4.9	29.3
	414631	AW970130	Hs.65408	ESTs	4.9	4.9
	437117	AL494256	Hs.122653	ESTs	4.9	3.8
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fs, clone H	4.9	4.9
45	425073	W39509	Hs.22003	solute carrier family 6 (neurotransmitter	4.9	4.9
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	4.9	4.9
	443150	A034467	Hs.34650	ESTs	4.9	7.6
	422411	AW748443	Hs.22511	ESTs	4.9	12.0
	414931	AK000342	Hs.77646	Homo sapiens mRNA: cDNA DKFZp71M0223 (l)	4.9	3.4
50	430456	AA314958	Hs.241503	hypothetical protein	4.8	4.7
	428186	AW504300	Hs.255605	memosin, alpha, class 2A, member 2	4.8	3.9
	433516	AA592802	Hs.33410	ESTs, Weakly similar to T172791 hypothetical	4.8	4.8
	427287	NM_014903	Hs.174188	KIAA0938 protein	4.8	4.8
	416101	R24854	Hs.268806	ESTs	4.8	3.3
55	447252	R90916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8	3.2
	452659	AA428403	Hs.106131	ESTs	4.7	3.9
	440105	AA694010	Hs.6932	Homo sapiens clone Z3805 mRNA sequence	4.7	8.2
	445102	AW204610	Hs.22270	ESTs	4.7	19.2
	419643	F06096	Hs.51791	chromosome 11 open reading frame 25	4.7	4.7
60	414849	C15314	Hs.323348	ESTs	4.7	3.8
	453534	NM_014796	Hs.33187	KIAA0748 gene product	4.7	4.7
	445729	H21066	Hs.13223	Homo sapiens mRNA, full length insert cDNA	4.7	4.0
	451032	W03992	Hs.323079	Homo sapiens mRNA, cDNA DKFZp754M0716 (fr	4.7	4.9
	434572	AA644253	Hs.132458	ESTs	4.7	3.8
65	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fs, clone NT	4.7	3.0
	435793	X62692	Hs.2593	phosphodiesterase 8B, cGMP-specific, rod	4.6	4.6
	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
	453502	NM_000638	Hs.32945	glutamate receptor, metabotropic 1	4.6	4.6
	422876	AB028977	Hs.222974	ESTs	4.6	4.6
70	451516	A1800515	Hs.12024	ESTs	4.6	6.3
	433670	AA604405	Hs.102131	gHcEST366342 MAGE sequences, MAGEC Homo	4.6	3.9
	437380	AL359577	Hs.112198	Homo sapiens mRNA: cDNA DKFZp754M0713 (fr	4.5	3.8
	410386	A267269	Hs.302689	hypothetical protein	4.5	10.4
	419191	U17195	Hs.68866	A kinase (PKA) anchor protein 6	4.5	4.5
75	429290	AF203532	Hs.198760	neurofilament, heavy polypeptide (200kD)	4.5	3.3
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fs, clone L	4.5	10.2
	432736	AA786898	Hs.179502	transposin-like protein	4.4	4.0
	427952	AK030900	Hs.68849	ESTs, Moderately similar to AF151111 H	4.4	3.2
	429663	AW382652	Hs.256208	Homo sapiens, clone MGC:15606, mRNA, com	4.3	3.3
80	435040	A1832360	Hs.152825	ESTs	4.3	4.7
	451301	AF169514	Hs.209690	EST	4.3	4.3
	452381	H23329	Hs.209690	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3	4.3
	410305	AF030409	Hs.62185	solute carrier family 9 (sodium/hydrogen	4.3	7.8
	433109	N68907	Hs.162430	EST	4.3	3.9
	431342	AW971018	Hs.21659	ESTs	4.3	8.0
	447163	AW222770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, member	4.3	3.4

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	429414	AW875237	Hs.13701	ESTs	4.2	5.3
	438274	AF086092	Hs.48372	ESTs	4.2	18.3
	423589	AA328082	Hs.209569	ESTs	4.2	4.2
	429556	AJ374851	Hs.22542	ESTs	4.2	3.2
5	427317	AQ28955	Hs.175780	KIAA1032 protein	4.2	5.3
	428847	ST8723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	4.1	7.9
	408206	AFO41853	Hs.43670	kinesin family member 3A	4.1	4.1
	433803	AIB22693	Hs.27688	ESTs	4.1	4.1
	413024	AF036268	Hs.75149	SH3-domain GRB2-like 2	4.1	4.0
10	440117	H49129	Hs.172982	ESTs	4.1	4.1
	450600	BE079478	Hs.24890	ESTs	4.1	3.9
	429550	AW293055	Hs.119357	ESTs	4.1	6.4
	448681	AL109781	Hs.21754	Human sapiens mRNA full length insert cDN	4.0	7.2
	458944	F12632	Hs.3610	ESTs	4.0	4.0
15	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.0	7.9
	426556	XQ5008	Hs.211584	neurofilament, light polypeptide (F84D)	4.0	13.1
	445523	NM_015239	Hs.21542	KOAA1035 protein	4.0	4.0
	419663	AW952951	Hs.53485	Human sapiens mRNA; cDNA DKF-Zp7610191 (f	3.9	21.4
20	424212	R77677	Hs.346644	ESTs	3.9	3.9
	424001	W67883	Hs.137476	potentially expressed 10	3.9	5.4
	440293	AK04193	Hs.22123	ESTs	3.9	3.9
	422690	Z43784		enkephalin 3, node of Ranvier (enkephalin G)	3.9	3.6
	429554	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.9
25	412949	AI471639	Hs.71913	ESTs	3.8	3.7
	427457	AW779106	Hs.164682	ESTs	3.8	11.1
	416530	UC3801	Hs.79381	neurexin 6 (neuroxin, zyme)	3.8	4.4
	424676	AI733585	Hs.130897	ESTs	3.8	3.8
30	434998	AW975157	Hs.26037	ESTs	3.7	3.7
	424945	AJ221919		hypothetical protein FLJ10582	3.7	30.5
	415257	F03016	Hs.27513	ESTs	3.7	4.6
	407886	AW959588	Hs.100426	ESTs	3.7	20.2
	406844		NM_003105	Human sapiens sortilin-related	3.7	3.1
35	456765	AI497900	Hs.33067	ESTs	3.7	3.7
	432087	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.6	7.6
	425667	BT7719	Hs.13219	ESTs	3.6	3.6
	436773	AW078629		PC4 and SFRS1 interacting protein 1	3.6	3.6
	424120	T86579	Hs.290270	ESTs	3.6	14.7
	446574	AJ301316	Hs.335933	ESTs	3.6	3.5
40	432453	AB88537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	3.6	3.9
	406119	W62123	Hs.101672	ESTs, Weakly similar to T00331 hypothe	3.6	3.6
	449093	AB036356	Hs.22998	neurexin 1	3.6	3.6
	439239	AI031540	Hs.235331	ESTs	3.6	49.5
	451625	R50753	Hs.106576	alanine-glyoxylate aminooxidase 2-II	3.6	4.1
45	435059	Z45270	Hs.235873	hypothetical protein FLJ22672	3.6	4.8
	423346	AE267577	Hs.127416	synaptotagmin 1	3.6	20.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	3.5	3.5
	442106	AF205681	Hs.326728	ESTs	3.5	3.2
	449117	AF449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.5
50	405819		NM_002578	Human sapiens p21 (CDKN1A)-acti	3.5	13.5
	452311	AW304029	Hs.252744	ESTs	3.5	3.5
	448902	Z45998	Hs.122543	Human sapiens mRNA; cDNA DKF-Zp7611912 (f	3.5	21.8
	410224	MS5513	Hs.150206	potassium voltage-gated channel, shaker-	3.4	3.4
	420098			Est, Control	3.4	3.4
55	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.4	5.9
	437288	AI754847	Hs.227571	regulator of G-protein signalling 4	3.4	14.0
	443682	AJ383661	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.4	3.3
	417417	F05745	Hs.89512	ATPase, Ca transporting, plasma membrane	3.3	17.1
60	419629	AB020695	Hs.31662	KIAA088 protein	3.3	13.4
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.3	4.1
	417063	N60515	Hs.45061	ESTs	3.3	3.3
	435071	D06883	Hs.39495	ESTs	3.3	3.3
	446377	AW014022	Hs.170553	ESTs	3.3	3.3
	412453	R20205	Hs.75236	ESTs	3.3	3.3
65	450561	R49674	Hs.25909	ESTs	3.3	3.3
	423829	R44107	Hs.240505	ESTs	3.3	4.4
	415327	F11624		ghHSC22D101 normalized infant brain cDN	3.3	3.3
	427386	AW836261	Hs.6727	ESTs	3.3	3.3
	425121	AI797511	Hs.154679	synaptotagmin 1	3.2	3.9
70	422856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor t	3.2	10.7
	442879	AF032922	Hs.8813	synapsin binding protein 3	3.2	3.2
	417284	N62889	Hs.107242	Human sapiens cDNA FLJ12955 fs, clone NT	3.2	3.2
	416805	F13271	Hs.79981	Human clone Z3560 mRNA sequence	3.2	6.7
	429477	AJ275514	Hs.6658	ESTs	3.2	3.2
75	453169	AB037815	Hs.32156	KIAA1394 protein	3.2	5.7
	408039	AA131424	Hs.336636	ESTs	3.2	3.2
	426269	H15302	Hs.168950	Human sapiens mRNA, cDNA DKF-Zp566A1046 (f	3.2	22.1
	409746	NM_004794	Hs.56294	RAS33A, member RAS oncogene family	3.2	10.6
	416874	H98752	Hs.42598	ESTs	3.2	6.0
80	433919	AW959912	Hs.70705	KU41705 protein	3.2	3.2
	444561	R46789	Hs.78118	ubiquitin carboxyl-terminal esterase L1	3.2	3.2
	433315	R96754	Hs.239706	GRB2-associated binding protein 1	3.2	3.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23003	3.2	8.4

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424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	3.2	56.0
421790	AWB56201	Hs.22654	sodium channel, voltage-gated, type I, a	3.2	4.1
432809	AA565509	Hs.131703	ESTs	3.1	9.9
445225	AQ16555	Hs.202398	ESTs	3.1	5.5
424087	AB5333	Hs.143454	consortin 1	3.1	3.1
437524	AI935344	Hs.164118	ESTs, Weakly similar to SL51_HUMAN SODIU	3.1	3.2
419583	AA248897	Hs.48784	ESTs	3.1	5.9
420173	AA256151	Hs.22959	ESTs	3.1	4.1
411665	AF106564	Hs.713445	neurofilament c (NFND medium)	3.1	6.6
416220	HA9776	Hs.170504	hypothetical protein MGC10946	3.1	4.5
425138	H08849	Hs.167464	glutamate receptor, ionotropic, N-methyl	3.1	4.2
422234	AF119818	Hs.113287	discs, large (Drosophila) homolog associ	3.1	3.1
445194	AQ75667	Hs.175944	ESTs	3.1	3.1
438054	AA176626	Hs.163909	ESTs	3.1	10.2
432145	AW514326	Hs.133483	ESTs, Weakly similar to T345450 probate	3.1	12.2
445725	AK000556	Hs.13209	hypothetical protein FLJ10094	3.0	3.0
414245	BE148072	Hs.75850	WAS protein family, member 1	3.0	11.7
447673	AB03987	Hs.182785	ESTs	3.0	3.0
428392	HI0233	Hs.2265	secretory granule, neuroendocrine protei	3.0	49.3
418410	AA811441	Hs.107393	chromosome 3 open reading frame 4	3.0	3.9
429024	A952297	Hs.119302	complement C1q tumor necrosis factor-rel	3.0	3.7
426195	AL041728	Hs.70887	ELAV (embryonic lethal, abnormal vision,	3.0	9.0
424724	T05532	Hs.287709	Human sapiens cDNA: FLJ22674 f6, clone H	3.0	3.0
410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	3.0	10.0
408947	AL080083	Hs.49117	Homo sapiens mRNA: cDNA DKFZ664N1562 (I	3.0	13.5
426325	D28114	Hs.169309	myelin associated oligodendrocyte basic	2.9	81.1
429005	AA43143	Hs.55029	hypothetical protein FLJ13942	2.9	6.6
410711	AB002316	Hs.65746	KAA0318 protein	2.9	6.1
415486	HI1214	Hs.13284	ESTs, Weakly similar to 2109260A B cell	2.9	15.7
424474	AA308883	Hs.148580	calcitonin, D1 dopamine receptor-interacti	2.9	3.6
442298	AA497044	Hs.70387	hypothetical protein FLJ10392	2.9	11.5
419518	U79289	Hs.50798	Human clone Z6395 mRNA sequence	2.9	3.6
426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	2.9	5.1
430347	NM_002039	Hs.239705	GRB2-associated binding protein 1	2.9	3.2
429401	AY026102	Hs.95972	ESTs, Weakly similar to S32657 A4 protein	2.9	6.1
450154	RI5991	Hs.281387	Human clone C1G-A4 mRNA sequence	2.9	5.9
434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.8	28.5
424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	2.8	23.1
416835	D54745	Hs.80247	phencycline	2.8	6.8
443277	AA011054	Hs.43620	ESTs	2.8	8.5
451952	AL120173	Hs.301653	ESTs	2.7	19.2
408554	AA36381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	2.7	3.7
413408	R51793	Hs.1440	DEADH (Asp-Glu-Ala-Asp/His) box polypep	2.7	3.0
416343	AA064273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	2.7	3.2
420489	AA815089	Hs.183613	ESTs	2.7	4.1
447359	NM_012093	Hs.18258	adenylate kinase 5	2.7	17.2
423731	T08814	Hs.1787	gtr:EST06708 Infant Brain, Benton Scores H	2.7	4.0
409953	AA332277	Hs.57691	cadherin 18, type 2	2.7	5.5
424481	RI9453	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	2.7	11.5
449714	AB033015	Hs.23541	KAA1189 protein	2.7	7.5
424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.7	3.7
423447	X92681	Hs.2998	contactin 2 (axonin)	2.7	4.1
420371	AB028985	Hs.54206	ATP-binding cassette, sub-family A (ABC1	2.7	5.1
438068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ23133 f6, clone L	2.6	5.1
418512	AW498974	Hs.19489	diacylglycerol kinase, zeta (104kD)	2.6	7.9
447791	AF051573	Hs.19489	procoxaderin 8	2.6	6.3
448743	AB023862	Hs.21856	KAA1136 protein	2.6	23.2
420547	AA674291	Hs.57837	ESTs	2.6	4.0
426580	AI291267	Hs.145950	ESTs	2.6	6.9
420688	AB002379	Hs.100113	KAA0381 protein	2.6	3.7
440357	AA373553	Hs.20950	phosphorylase phosphoridylase inorganic	2.6	3.7
424572	MI19650	Hs.10613	2',3'-cyclic nucleotide 3' phosphodiester	2.6	6.9
418338	NM_002522	Hs.84154	neuronal pentraun 1	2.5	6.1
427658	H61387	Hs.30868	nogo receptor	2.5	3.0
410359	R38624	Hs.106313	ESTs	2.5	6.3
449717	AB040535	Hs.23854	control cell adhesion molecule 5	2.5	2.5
424458	M29273	Hs.1780	myelin associated glycoprotein	2.5	10.1
450133	AW969769	Hs.105201	ESTs	2.5	40.5
428976	AL037824	Hs.194695	ras homolog gene family, member I	2.5	17.4
454293	HA9739	Hs.134013	ESTs, Moderately similar to H601_HUMAN H	2.5	9.5
405447	AK002689	Hs.45900	Homo sapiens cDNA FLJ11227 f6, clone PL	2.5	3.9
414683	S78256	Hs.76888	hypothetical protein MGC12102	2.5	7.1
422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.5	3.0
449648	AL157479	Hs.23740	KAA1598 protein	2.5	3.6
454053	AW023006	Hs.271172	ESTs, Moderately similar to PCA259 tem	2.5	3.6
426495	NM_013279	Hs.184640	hypothetical protein MGC10781	2.5	3.2
431096	AA324358	Hs.249227	Homo sapiens DNA, cosmid clones T162 and	2.4	3.6
452371	RA0950	Hs.21658	ESTs	2.4	3.3
424987	AL138167	Hs.96390	ESTs	2.4	6.7
452310	NE2341	Hs.941116	ESTs	2.4	3.6
452868	AA814497	Hs.78792	ESTs	2.4	3.9
436734	AB376162	Hs.273758	hypothetical protein FLJ23112	2.4	4.7
421931	NM_000814	Hs.1440	gamma-aminobutyric acid (GABA) A recepto	2.4	3.1

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	430428	AA358625	HE_190490	ESTs	2.4
	445255	NM_14841	HE_12677	synaptonemal-associated protein, 91 kDa	2.4
	436420	AA443966	HE_31595	ESTs	2.4
5	408822	AW005707	HE_51079	Homo sapiens cDNA FLJ13257 fs, clone OV	2.4
	451407	AA113376	HE_343039	Rhizopus stolonifer growth factor 12B	2.4
	419527	AA773620	HE_63870	ESTs	2.4
	446100	AW967109	HE_13804	hypothetical protein dJ46203.2	2.4
10	439199	R03773	HE_26299	ESTs	2.3
	427627	R07582	HE_179915	guanine nucleotide binding protein (G pr	2.3
	450408	HQ5626	HE_6921	ESTs	2.3
	412675	AA460716	HE_9798	hypothetical protein MGC10924 similar to	2.3
	434611	AW971205	HE_114260	ESTs	2.3
	431677	AK000496	HE_306959	hypothetical protein FLJ20489	2.3
15	451368	AB290606	HE_26334	spastic paraplegia 4 (autosomal dominant	2.3
	447328	AB73126	HE_161227	brain link protein-1	2.3
	451050	AW537420	HE_69662	ESTs	2.3
	437397	AA349847	HE_4221	hypothetical protein DKFZp761H039	2.3
	408538	AI695533	HE_43069	ESTs	2.3
	408777	U71204	HE_47626	Rc (Drosophila)-like, expressed in neur	2.3
	453024	RA0295	HE_24986	ESTs	2.3
20	427709	AA315331	HE_153485	ESTs	2.3
	438911	AF085481	HE_301920	ESTs	2.3
	459108	AW163034	HE_6467	synaplogyrin 3	2.2
	422267	AI628272	HE_88323	ESTs, Weakly similar to ALU1_HUMAN ALU.5	2.2
25	404619		NM_000589	homo sapiens peanut (Drosophila	2.2
	427544	AB018259	HE_118140	KIA0716 gene product	2.2
	433597	AA708205	HE_103043	ESTs	2.2
	440152	AB005676	HE_7006	KIAA0378 protein	2.2
30	413375	NM_003081	HE_84369	synaptonemal-associated protein, 29kD	2.2
	408582	AW956133	HE_7149	gB-EST368183 MAGE sequences, MAGD Homo	2.2
	425267	R82849	HE_155524	peanut (Drosophila)-like 2	2.2
	433657	AI244368	HE_8124	PH domain containing protein in retina 1	2.2
	438703	AI603373	HE_31595	ESTs	2.2
	428845	AK151758	HE_153610	KIA0716 gene product	2.2
35	417865	AW086059	HE_65229	ESTs, Weakly similar to 178855 semeth	2.2
	449034	AA930315	HE_48965	Homo sapiens cDNA: FLJ21693 fs, clone C	2.2
	419271	N14901	HE_238352	ESTs	2.2
	446544	R13209	HE_21143	adult cancer family 12, (potassium-chi	2.2
	439416	F05338	HE_4773	ESTs	2.2
	451570	RA4386	HE_164578	ESTs	2.2
	433641	AK137256	HE_130489	ATPase, aminophospholipid transporter-8	2.1
	427387	AB083676	HE_146383	ESTs	2.1
	452108	AW135982	HE_203013	hypothetical protein FLJ12748	2.1
40	429037	X01895	HE_194765	H sapiens GENX.5624 mRNA, 3' UTR	2.1
	418900	BE207337	HE_3454	KIAA1821 protein	2.1
	421268	AI126821	HE_305154	ESTs	2.1
	446372	AD026644	HE_14945	long fatty acyl-CoA synthetase 2 gene	2.1
	450214	AF052152	HE_159412	Homo sapiens clone 24631 mRNA sequence	2.1
45	450214	BE_433973	HE_227571	regulator of G-protein signalling 4	2.1
	452738	AK133900	HE_7086	hypothetical protein MGC12445	2.1
	417877	AI435184	HE_164252	ESTs	2.1
	424241	AA335158	HE_235873	hypothetical protein FLJ22672	2.1
	432882	NM_013267	HE_276959	phosphatidylinositol-regulated kinase-8	2.1
50	410631	AA086469	HE_41771	ESTs	2.1
	407808	AA663559	HE_279789	histone deacetylase 3	2.1
	424379	Z42034	HE_93597	cyclo-dipeptide kinase 5, regulatory su	2.1
	448410	AK000227	HE_21128	hypothetical protein FLJ20220	2.1
	433832	AB984999	HE_105330	neuronal protein	2.1
55	425130	AA448208	HE_99163	ESTs	2.1
	402027			Target Exon	2.1
	435191	RI15912	HE_4817	Homo sapiens clone 24461 mRNA sequence	2.0
	420547	AF155140	HE_99378	neuronal-regulated testicular RNA he	2.0
	404541			NM_007950 Homo sapiens stathmin-like 4 (2.0
60	420050	AI118615	HE_94563	neurorachnion	2.0
	417880	AO78534	HE_122592	ESTs	2.0
65	416602	NM_006159	HE_70389	net (chicken)-like 2	2.0
	438315	BE39513	HE_27335	hypothetical protein MGC4837	2.0
	439340	AB023246	HE_6535	brain-specific Na-dependent inorganic ph	2.0
70	429900	AA480421	HE_30875	ESTs	2.0
	431762	T78028	HE_154679	synaptotagmin 1	2.0
	425172	AA447729	HE_12714	ESTs	2.0
	425072	SE6207	HE_91343	gamma-aminobutyric acid (GABA) A recepto	2.0
	451734	NM_006176	HE_26944	Homo sapien protein kinase C substrate,	2.0
	428603	AB007880	HE_129863	Homo sapiens KNA0420 mRNA, complete c	2.0
75	432677	AD023236	HE_6139	synaptotagmin 1	2.0
	423767	HI8263	HE_132753	f box only protein 2	2.0
	434813	RI8095	HE_4276	KNA04701 protein	2.0
	426575	MR4626	HE_170068	glutamate decarboxylase 2 (pancreatic)	2.0

Key: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
408005	103646_1	AW954272 AI003154 AA059300 AA046911
5	415527	F11624 243212 H08385 RS6332 H09256 RS2303 R13075
415566	1536380_1	H72693 R08673 H12664 F20990 R08550
415572	1543492_1	AW408974 T09132 RS3460 AA350590 T33786 T30036 AA350595 T08592 T09274 AA242427 D64678 T08951 R15346 AW953188 AA350074
418866	179788_1	AW890649
420111	190535_1	T65754 AA229857 AA229598
422890	222707_1	AA255632 AA290011 A1696750 AA262684
10	424572	Z43784 F03383 AW627911 AA409303 H17037 R19603 A1632565 AW004030 BE502530 Z25032 AA063324 AA449241 A1651825 A1264863 AW196918
423731	231466_1	AA548267 A1953735 A263703 AA319159 AW664436 A1903440 AW554711 A1867447 AW204071 AW935510 C15616 D81142 H17038 AW162343
424572	24057_1	T87230 A13
15	424572	T06814 H19198 A1120536 AA330216 AW961552 N47159
424572	24057_1	A118650 R18180 F18172 AW895146 AW89520 AA152362 AA175814 F12085 BE255264 BE251303 T52548 AA380595 AA380465 BE406584
424572	24057_1	AA455037 AA459869 AA776107 BE274289 A45269 M61958 AA378818 AW663160 AW672958 H08611 M78164 BE30321 AA348660 R36303
424572	24057_1	AW498662 AA019090 AA001
424572	24057_1	A1221919 Z19967 AA348780 AW964077 AW166028 BE540193 N48800 AA452366 N95604 A1341345 AW268000 AA204961 AA531158 A1471227
424572	24057_1	A1806680 A1982625 D81263 D63637 D52496 A974487 AW043854 N50483 Z39997 AH92961 A1081526 F04032 AA452141 T23551 AH72555
20	426191	AL014228 D82004 D51361 A1140037 AW900295 A1018308 AW087473 AW183530 AA393346 H50055 AA356501
426191	273507_1	AA604405 BE062234 AA1748386
426191	273507_1	AA618174 A1114549 R36464 R36465
426191	273507_1	H05125 N52433 A1651050 AA084734 A1368716 N40915 A1989705 F99042 T03905 R88588 AF112220
426191	273507_1	AW078629 A1853735 N64357 AA731069
25	426191	Z44514 A1352097 A1803954 AW235923 AW196558 A1954637 A1336983

Pkey	Ref	Strand	NI_positon
402844	918605	Plus	24745-24872:23035-23204
402844	918605	Plus	51645-51685:52917-53005
404841	831859	Plus	103456-103694
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18251-18257,18443-18578
405560	183148	Plus	5495-5655,6077-6241,6495-6692
405819	4007557	Plus	2830-2957
408311	9211559	Minus	137114-159033

TABLE 19A. ABOUT 356 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLOBULINOSIA COMPARED TO NORMAL ADULT CNS

Pkey	Ref	Strand	NI_positon
402844	918605	Plus	24745-24872:23035-23204
402844	918605	Plus	51645-51685:52917-53005
404841	831859	Plus	103456-103694
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18251-18257,18443-18578
405560	183148	Plus	5495-5655,6077-6241,6495-6692
405819	4007557	Plus	2830-2957
408311	9211559	Minus	137114-159033

TABLE 19B. ABOUT 356 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLOBULINOSIA COMPARED TO NORMAL ADULT CNS

Pkey	Ref	Strand	NI_positon
402844	918605	Plus	24745-24872:23035-23204
402844	918605	Plus	51645-51685:52917-53005
404841	831859	Plus	103456-103694
404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18251-18257,18443-18578
405560	183148	Plus	5495-5655,6077-6241,6495-6692
405819	4007557	Plus	2830-2957
408311	9211559	Minus	137114-159033

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18207	C14685	Hs.34772	ESTs	9.8	9.8
417175	R44558	Hs.94002	ESTs	9.6	8.9
444330	A597655	Hs.49265	ESTs	9.1	9.1
427322	AK020217	Hs.176227	hypothetical protein FLJ11155	8.9	8.9
429396	AB011106	Hs.159812	KIAA0534 protein	8.6	8.6
428652	AA024272	Hs.336224	transmembrane protein with EGF-like and	8.6	8.6
419347	C15944	Hs.90005	superior cervical ganglia, neural specifi	5.6	22.2
10309	BE043077	Hs.278153	ESTs	8.5	8.5
415351	AW963951	Hs.85618	ESTs	8.5	8.5
427061	AK032971	Hs.173392	KIAA1145 protein	8.4	8.4
400438	AF185611	Hs.115352	Target	8.3	5.1
40209	H05049	Hs.247837	neurexin 3	8.2	18.7
422756	AA441757	Hs.119569	glycoprotein hormones, alpha polypeptide	8.1	5.8
435648	H24347	Hs.27524	ESTs	8.1	5.1
429470	A1878901	Hs.203662	guanine nucleotide binding protein (G-pr	8.0	8.0
416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	8.0	8.0
408814	N62499	Hs.176227	hypothetical protein FLJ11155	7.9	8.6
430004	U02768	Hs.227571	regulator of G-protein signalling 4	7.9	15.7
434027	A334378	Hs.143209	ESTs	7.8	7.8
434367	AB020700	Hs.3830	KIAA0853 protein	7.8	5.6
429876	AB028977	Hs.225974	KIAA1054 protein	7.8	16.8
441008	Z13105	Hs.303172	Homo sapiens mRNA; cDNA DKFZp47G133 (fr	7.7	7.7
442023	A1197878	Hs.144649	ESTs	7.7	5.6
429033	NM_007374	Hs.194756	sine oculis homeobox (Drosophila) homolo	7.5	5.5
450642	R39773	Hs.7130	copine IV	7.6	5.6
437073	AB85508	Hs.94122	ESTs	7.5	7.5
441264	AA927170	Hs.23290	ESTs	7.3	7.3
424153	AA451737	Hs.141456	MOGE-like 2	7.3	5.1
450474	AW872844	Hs.117494	ESTs	7.2	7.2
450715	A1265484	Hs.31570	ESTs. Weakly similar to KIAA1324 protein	7.2	7.2
419076	NM_006857	Hs.77890	guanylate cyclase 1, soluble, beta.3	7.1	4.8
423003	AL120077	Hs.122967	weid (Drosophila)-like 2 (Maven)	7.0	7.0
433921	AA518174	Hs.141456	gobm1/401.s1 NCL_GCAP_Thy1 Homo sapiens	7.0	7.0
423532	NM_009393	Hs.1897	promelanin (adrenocorticotropin	6.9	6.1
435012	AL14180	Hs.302754	ESTs	6.9	6.9
445898	AF070623	Hs.13474	Homo sapiens clone 24468 mRNA sequence	6.9	6.9
450855	AA833757	Hs.201769	ESTs. Weakly similar to T24635 hypotheti	6.9	6.9
490031	AA376836	Hs.288856	ESTs	6.8	6.8
453590	AF150278	Hs.33578	KIAA0820 protein	6.6	22.3
450181	H05254	Hs.201198	ESTs	6.6	7.2
425580	L11144	Hs.1907	galactin	6.5	3.5
452729	R41900	Hs.22245	ESTs	6.4	6.4
428414	AL049380	Hs.184216	DKFZP564C152 protein	6.4	6.4
434104	AF118691	Hs.118459	hypothetical protein PR02198	6.4	4.0
443244	A157235	Hs.168479	ESTs	6.3	3.0
447750	A1422234	Hs.143434	contactin 1	6.2	9.8
415114	D60458	Hs.94181	ESTs	6.0	6.0
450600	BE079478	Hs.24880	ESTs	5.9	3.9
444453	BE041526	Hs.37145	hypothetical protein DKFZp547F072	5.9	7.7
449556	AB020651	Hs.22553	KIAA0544 protein	5.9	5.9
447138	A143112	Hs.93828	ESTs. Weakly similar to 2109260A B cell	5.8	5.8
414545	AA149287	Hs.76605	ESTs	5.8	3.6
410389	AW9554049	Hs.8177	ESTs. Weakly similar to PINLU6 salivary	5.6	5.6
405990	A1701507	Hs.271340	ESTs	5.6	3.8
408428	NM_014787	Hs.44496	DnaJ (Hsp40) homolog, subfamily B, membe	5.6	5.6
442026	A1243749	Hs.8074	brain-specific angiogenesis inhibitor 3	5.5	6.5
450149	AW969781	Hs.132663	Zic family member 2 (zcd-paired Drosophi	5.4	5.4
414699	A1815523	Hs.76530	syncytin, alpha (non A4 component of sim	5.3	4.5
438202	AW159287	Hs.22508	ESTs	5.3	5.3
448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.3	5.3
418866	T65754	Hs.179075	gby-yc1107.s1 Strausberg lung (537210) H	5.3	3.8
446786	BE048642	Hs.179075	Homo sapiens cDNA FLJ11881 fs, clone HE	5.2	5.2
406311			NM_021979/Homo sapiens head shock 70kD	5.2	11.5
443682	A1383061	Hs.47248	ESTs. Highly similar to similar to Cdc14	5.2	3.3
415666	H72631	Hs.18656	gby-yc1107.s1 Soares fetal liver spleen	5.2	5.2
416101	R24854	Hs.268806	ESTs	5.2	3.3
428508	BE252383	Hs.186606	SBR031 protein	5.2	4.1
413318	AW969742	Hs.291005	ESTs	5.2	3.1
439238	N47305	Hs.302161	ESTs	5.1	5.3
446533	AF290919	Hs.153661	ESTs	5.1	5.1
412049	NS3437	Hs.18266	adenylate kinase 5	5.1	10.7
437331	AL353333	Hs.21710	hypothetical protein DKFZp61G0313	5.1	5.1
413988	M81883	Hs.324784	glutamate decarboxylase 1 (brain, 67kD)	5.1	5.1
408068	AW148652	Hs.167398	ESTs	5.0	5.0
414831	AW970130	Hs.65406	ESTs	4.9	4.9
418527	AA450386	Hs.71149	Homo sapiens cDNA: FLJ21950 fs, clone H	4.9	4.9
425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitter	4.9	4.9
427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	4.9	3.9
433516	AA958202	Hs.33410	ESTs. Weakly similar to T17279 hypotheti	4.8	4.8
427287	NM_014903	Hs.174188	KIAA0526 protein	4.8	4.8
447252	R30916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8	3.2
424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fs, clone L	4.7	10.2
419643	F06066	Hs.91791	chromosome 11 open reading frame 25	4.7	4.7

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	414949	C15314	Hs.323349	ESTs	4.7	3.8
	453534	NM_014796	Hs.33187	KIAA0768 gene product	4.7	4.7
	453537	X52652	Hs.25503	phosphodiesterase 8B, cGMP-specific, rod	4.6	4.6
5	453431	AF094754	Hs.32973	glycine receptor, beta	4.6	4.6
	453302	NM_000838	Hs.32945	glutamate receptor, metabotropic 1	4.6	4.6
	447104	R19085	Hs.210705	Homo sapiens cDNA FLJ13182 fs, clone NT	4.6	3.0
	418202	N48521	Hs.26549	KIAA1708 protein	4.6	5.8
	419191	U17195	Hs.89566	A kinase (PRKA) anchor protein 6	4.5	4.5
	453080	AW102083	Hs.200855	ESTs	4.5	13.5
10	451783	R42684	Hs.210862	T-tube, brain, 1	4.4	11.2
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	4.4	3.2
	451050	AW937420	Hs.65662	ESTs	4.4	4.4
	423728	AW891294	Hs.123736	solute carrier family 4, sodium bicarbon	4.4	7.9
	447746	AW015920	Hs.161359	ESTs	4.3	4.3
15	451301	A1765514	Hs.205890	EST	4.3	4.3
	452381	H23329	Hs.250880	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST	4.3	3.9
	412158	R28167	Hs.12446	Homo sapiens transmembrane protein HTMP1	4.3	27.9
20	426365	AA375567	Hs.10283	RNA binding motif protein 8B	4.3	4.1
	423585	AA328082	Hs.205569	ESTs	4.2	4.2
	423453	A885537	Hs.27172	ESTs, Moderately similar to PC4259 fem	4.2	3.9
	420489	AA815089	Hs.153513	ESTs	4.1	4.1
	427457	AW773105	Hs.164682	ESTs	4.1	11.1
	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	4.1
25	433803	AA23553	Hs.27688	ESTs	4.1	4.1
	407868	NM_005950	Hs.43637	proline-rich Glu (C-garboxyl)glutamic acid	4.1	3.3
	448117	H49129	Hs.172982	ESTs	4.1	4.1
	447106	AW205881	Hs.326728	ESTs	4.1	3.2
	450757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.0	3.2
30	442042	A1950506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp47E184 (fr	4.0	6.2
	458564	F1832	Hs.36110	ESTs	4.0	4.0
	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	448563	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
35	418490	H17730	Hs.288513	Human DNA sequence from clone RPS-89C14	3.9	7.0
	442412	R77877	Hs.34564	ESTs	3.9	3.9
	440253	AA004153	Hs.22123	ESTs	3.9	3.9
	433670	AA604405	gbm07705.s1 NCL_CGAP_AA1	Homo sapiens	3.9	3.9
	459597	AA406062	Hs.98002	ESTs	3.9	5.4
40	429250	AF703032	Hs.198760	neurofilament, heavy polypeptide (200kD)	3.9	3.3
	420554	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.5
	424001	W67883	Hs.137476	paternally expressed 10	3.8	5.4
	442676	A1733585	Hs.130857	ESTs	3.8	3.8
	410240	AL157424	Hs.61285	synaptotagmin 2	3.8	4.6
	423329	AB020696	Hs.54037	ectonucleotidase pyrophosphatase/phosphodi	3.7	3.6
45	434568	AW891257	Hs.26537	ESTs	3.7	3.7
	439460	RS1613	Hs.125304	ESTs	3.7	8.3
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.7	4.9
	400844			NM_003105* Homo sapiens sortilin-related	3.7	3.1
50	456765	AA497900	Hs.33067	ESTs	3.7	3.7
	452667	T87219	Hs.13219	ESTs	3.6	3.6
	436773	AW078629		PC4 and SFRS1 interacting protein 1	3.6	3.6
	453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.6	15.9
	422140	AW614326	Hs.133483	ESTs, Weakly similar to T34549 probable	3.6	12.2
55	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypocheli	3.6	3.6
	440933	AB035356	Hs.22558	neurexin 1	3.6	3.6
	429698	U07616	Hs.173034	anaphyphysin (S&H-Mann syndrome with br	3.6	15.3
	410211	AB020641	Hs.57856	PTP4IRE protein kinase 1	3.6	10.0
	447238	AW002370	Hs.131055	ESTs, Weakly similar to NFPM_HUMAN NUCLEO	3.5	3.5
60	451032	W03652	Hs.322073	Homo sapiens mRNA; cDNA DKFZp564P116 (fr	3.5	4.9
	445117	AW446310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.5
	416490	AF090116	Hs.73348	regulator of G-protein signaling 7	3.5	12.5
	412865	N52006	Hs.26133	ESTs	3.5	3.6
	452311	AW304029	Hs.252744	ESTs	3.5	3.5
65	425649	U30930	Hs.158540	UDP-glucosyltransferase 8 (UDP-glucosyl	3.5	38.6
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4	3.4
	451516	A1805515	Hs.12624	ESTs	3.4	6.3
	400098			Est Control	3.4	3.4
	424918	R13582	Hs.163039	myelin-associated oligodendrocyte basic	3.4	5.3
70	452238	F01811	Hs.345757	ESTs	3.3	3.8
	417063	N50515	Hs.45081	ESTs	3.3	3.3
	443692	AW022228	Hs.320922	ESTs	3.3	13.1
	412453	R26205	Hs.75236	ESTs	3.3	3.3
	450561	R45674	Hs.25909	ESTs	3.3	3.3
	415527	F11624		gh-HSC22D101 nonnormalized infant brain cDN	3.3	3.3
75	427386	AW836261	Hs.67277	ESTs	3.3	3.3
	423346	A1267577	Hs.127416	synaptotagmin 1	3.2	20.1
	431342	AW971018	Hs.21659	ESTs	3.2	8.0
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	3.2	9.6
80	442675	AF032522	Hs.88415	cystatin-binding protein 3	3.2	3.2
	417284	N62889	Hs.107242	Homo sapiens cDNA FLJ12965 fs, clone NT	3.2	3.2
	429477	A1755514	Hs.6658	ESTs	3.2	3.2
	410343	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	3.2	3.2
	427317	AB028955	Hs.175780	KIAA1032 protein	3.2	5.3

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	408039	AA131424	Hs.336636	ESTs	3.2	3.2
	428976	AL037824	Hs.194695	ras homolog gene family, member 1	3.2	17.4
	420297	AK628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.2	4.1
5	453919	AW959912	Hs.1076	KIAA1705 protein	3.2	3.2
	428963	AW362682	Hs.236208	Homo sapiens, clone MGC:15605, mRNA, com	3.2	3.3
	423829	RAA1017	Hs.240905	ESTs	3.1	4.4
	424087	N69333	Hs.143434	actin1	3.1	3.1
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	3.1	4.1
	444783	AK501468	Hs.62180	actin (Drosophila), Scaps homolog, act	3.1	43.2
10	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog, ascot	3.1	3.1
	446592	244514	Hs.	Homo sapiens mRNA for KIAA1763 protein,	3.1	33.0
	437117	AL049256	Hs.122593	ESTs	3.1	3.8
	405919			NM_002578:Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
	452752	AW044058	Hs.33578	KIAA0320 protein	3.1	13.4
15	416220	N49776	Hs.170994	hypothetical protein MGC10945	3.1	4.5
	437380	AL359577	Hs.112198	Homo sapiens mRNA; cDNA DKF3647M073 (t	3.0	3.8
	428091	H97428	Hs.219607	ESTs, Moderately similar to Transforming	3.0	5.9
	445725	AK000566	Hs.13209	hypothetical protein FLJ10094	3.0	3.0
	447673	AK023867	Hs.182285	ESTs	3.0	3.0
20	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.0	3.0
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fs, clone H	3.0	3.0
	408547	AA574291	Hs.57837	ESTs	3.0	4.0
	433315	R67644	Hs.239705	GRB2-associated binding protein 1	3.0	3.1
	438274	AF069092	Hs.48372	ESTs	3.0	16.3
25	410765	AA594972	Hs.66180	nucleosome assembly protein 1-like 2	3.0	8.0
	458208	AA428403	Hs.106131	ESTs	3.0	3.9
	424641	AB001106	Hs.151413	glu-maturation factor, beta	3.0	5.6
	441959	NM_003947	Hs.8004	huntingtin-associated protein interacti	3.0	14.9
	442593	R39804	Hs.31961	ESTs	2.9	6.7
30	426380	A1291267	Hs.149990	ESTs	2.9	6.9
	428536	AL143139	Hs.2268	vesilin-Ric 1	2.9	22.1
	417417	P05745	Hs.69512	ATPase, Ca transporting, plasma membrane	2.9	17.1
	411379	AB16344	Hs.12554	ESTs, Weakly similar to HPL4_HUMAN NUCLE	2.9	11.2
	422414	AW875237	Hs.13701	ESTs	2.9	5.3
35	426186	AW504300	Hs.236505	mannosidase, alpha, class 2A, member 2	2.9	3.9
	415518	U79269	Hs.50798	Human clone 23655 mRNA sequence	2.9	3.0
	426919	AL041228		ELAV (embryonic lethal, abnormal vision,	2.9	9.0
	446544	AK631932	Hs.7047	ESTs, Weakly similar to Unknown [Hsape	2.8	12.4
40	422411	AW749443	Hs.22511	ESTs	2.8	12.0
	416874	V98752	Hs.42568	ESTs	2.8	6.0
	440902	Z45998	Hs.22543	Homo sapiens mRNA, cDNA DKFZp76119192 (f	2.8	21.8
	430456	AA314958	Hs.241503	hypothetical protein	2.8	4.7
	429659	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.8	5.1
45	429656	X05505	Hs.211584	neurofilament, light polypeptide (NF-L)	2.8	13.1
	437948	AA177230	Hs.303227	ESTs	2.8	26.8
	440105	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	2.8	8.2
	414931	AK000342	Hs.77646	Homo sapiens mRNA; cDNA DKFZp761M0223 (f	2.8	3.4
	416830	U52851	Hs.79361	kallikrein 6 (neurosin, zyme)	2.8	4.4
	446574	A130136	Hs.335933	ESTs	2.8	3.5
50	422890	Z43784	Hs.	ankyrin 3, node of Ranvier (ankyrin G)	2.8	3.6
	410711	AB002316	Hs.65746	KIAA0318 protein	2.7	6.1
	422680	NA6669	Hs.76722	CCAAT/enhancer binding protein (CEBP),	2.7	45.2
	405554	AA836381	Hs.315111	nuclear receptor co-repressor/hRX3 comp	2.7	3.7
55	434460	AA478486	Hs.3852	KIAA0368 protein	2.7	4.8
	431988	AC002302	Hs.77202	protein kinase C, beta 1	2.7	10.5
	447163	AW292770	Hs.5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.7	3.4
	437924	AI935344	Hs.164118	ESTs, Weakly similar to SL51_HUMAN SODU	2.6	3.2
	424845	AI221019		hypothetical protein FLJ11562	2.6	30.5
60	425964	AW835277	Hs.165636	hypothetical protein DKFZp761C07121	2.6	29.3
	447761	AF061573	Hs.19492	protocadherin 8	2.6	6.3
	425138	H05849	Hs.167464	glutamate receptor, ionotropic, N-methyl	2.6	4.2
	436948	H12049	Hs.91564	ESTs	2.6	5.6
	406065	AW964272		gh EST3366342 IMAGE resequences, MAGC Homo	2.6	5.6
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.6	7.6
65	408777	U71204	Hs.47626	Ric (Drosophila), like, expressed in neur	2.6	38.7
	420713	AA264151	Hs.22899	ESTs	2.6	4.6
	429550	AW253055	Hs.119357	ESTs	2.6	6.4
	433068	AI927209	Hs.306210	Homo sapiens cDNA: FLJ21313 fs, clone L	2.6	5.1
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	2.6	7.3
70	428269	AA365609	Hs.131703	ESTs	2.6	9.9
	407886	AW909668	Hs.100626	ESTs	2.5	20.2
	445225	AI216555	Hs.202398	ESTs	2.5	5.5
	415257	F03016	Hs.27513	ESTs	2.5	8.6
75	423135	N67655	Hs.26411	ESTs	2.5	8.2
	134283	AA58931	Hs.37282	ESTs	2.5	7.5
	454053	AW023006	Hs.27172	ESTs, Moderately similar to PCA259 feni	2.4	3.6
	443190	AK034467	Hs.34650	ESTs	2.4	7.6
	429596	AI374681	Hs.22542	ESTs	2.4	3.2
	428392	H10233	Hs.2265	secretory granule, neuroendocrine prote	2.4	42.3
80	437288	AF54847	Hs.227571	regulator of G-protein signaling 4	2.4	14.0
	426529	AF090100	Hs.170241	Homo sapiens clone IMAGE 23915	2.4	5.1
	430347	NM_002039	Hs.239706	GRB2-associated binding protein 1	2.4	3.2
	422949	AA319435		gh EST21657 Adrenal gland tumor Homo sap	2.4	7.4

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451952	AL120173	Hs.301663	ESTs	2.4	19.2
434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	2.4	28.5
422927	AW247388	Hs.301423	calcium binding protein 1 (caltrans)	2.4	3.0
425121	AI797511	Hs.154679	synaptotagmin I	2.4	3.9
435959	Z45270	Hs.235673	hypothetical protein FLJ22672	2.4	4.2
446377	AW014222	Hs.170563	ESTs	2.4	3.3
452371	R40990	Hs.21658	ESTs	2.4	3.3
419103	Z40229	Hs.96423	hypothetical protein FLJ23033	2.4	8.4
427658	H61387	Hs.30868	ncgn receptor	2.3	3.0
445100	AW961109	Hs.13804	hypothetical protein U462023.2	2.3	3.4
439607	BE540565	Hs.159460	ESTs	2.3	5.6
412949	AI471639	Hs.71913	ESTs	2.3	3.7
419757	AA773820	Hs.63670	ESTs	2.3	3.3
410637	AB020725	Hs.58099	KIAA0918 protein	2.3	12.2
451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant)	2.3	3.1
409953	AA332277	Hs.57691	cadherin 18, type 2	2.3	5.5
419529	AB020695	Hs.91662	KIAA0688 protein	2.3	13.4
434792	AA649263	Hs.132468	ESTs	2.3	3.8
429006	AA441143	Hs.58929	hypothetical protein FLJ13842	2.3	6.6
445194	AI215967	Hs.175044	ESTs	2.3	3.1
422491	AA338548	Hs.117546	neuroxin	2.3	3.6
415734	NW_014747	Hs.78748	KIAA0237 gene product	2.3	27.4
434933	R91095	Hs.4276	KIAA1701 protein	2.2	6.1
424922	BE386547	Hs.217112	hypothetical protein MGC10825	2.2	3.7
426325	D28114	Hs.163309	myelin associated oligodendrocyte basic	2.2	81.1
424140	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	2.2	56.0
418410	AA511441	Hs.107350	chromosome 3 open reading frame 4	2.2	3.9
409746	NW_004794	Hs.56294	RAS33A, member RAS oncogene family	2.2	10.6
439239	AI031540	Hs.235331	ESTs	2.2	49.5
450310	NE2341	Hs.94116	ESTs	2.2	3.6
453924	RA9295	Hs.24886	ESTs	2.2	13.4
411666	AF106564	Hs.71346	neurofilament 3 (150kD medium)	2.2	6.6
404819			NM_002688: Homo sapiens pernat (Drosophi	2.2	5.8
449568	AL157479	Hs.23740	KIAA1598 protein	2.2	3.6
419271	N34901	Hs.238532	ESTs	2.2	7.5
424474	AA303883	Hs.148660	calypon; D1 dopamine receptor-interactin	2.2	12.5
432008	AL041224	Hs.65379	ESTs	2.2	5.8
424458	N029273	Hs.1790	myelin associated glycoprotein	2.2	10.1
421790	AW896201	Hs.22854	sodium channel, voltage-gated, type I, a	2.2	4.1
432682	NM_013257	Hs.27808	serum phosphocortisol regulated mouse l	2.1	4.2
419853	AW952691	Hs.93455	Homo sapiens mRNA cDNA DKF-Zp761D191 (tr	2.1	21.4
449277	AA001064	Hs.43670	ESTs	2.1	8.5
420156	AW449258	Hs.6187	ESTs	2.1	12.5
452738	AL133600	Hs.7089	hypothetical protein MGC12435	2.1	3.5
410366	J0267599	Hs.302669	hypothetical protein	2.1	10.4
452106	AI141031	Hs.21342	ESTs	2.1	3.4
413409	AI638418	Hs.1440	DEADH (Asp-Glu-Ala-Asp)like box polytyp	2.1	9.4
423641	AL137256	Hs.130439	ATPase, aminophospholipid transporter-4	2.1	6.2
410909	AW896161	Hs.53112	ESTs, Moderately similar to ALLU_HUMAN A	2.1	12.5
410531	AA008469	Hs.47171	ESTs	2.1	5.8
412675	AA460716	Hs.9788	hypothetical protein MGC10924 similar to	2.1	3.3
448299	AA497044	Hs.20687	hypothetical protein FLJ10392	2.1	11.5
444124	RA3307	Hs.6810	ESTs	2.1	9.3
403950	AA707814	Hs.14545	long fatty acyl-CoA synthetase 2 gene	2.1	8.5
432736	AA788898	Hs.179902	transporter-like protein	2.1	4.0
429924	AI652297	Hs.119302	complement-c1q tumor necrosis factor-rel	2.1	3.7
420071	AB026985	Hs.94306	ATP-binding cassette, sub-family A (ABC1	2.1	5.1
403522	AW500715	Hs.57079	Homo sapiens cDNA FLJ13257 fs, clone Ov	2.1	3.0
424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004398A chromos	2.1	23.1
426814	AF036543	Hs.172619	myelin transcription factor 1-like	2.1	14.2
425130	AA448208	Hs.99163	ESTs	2.1	3.1
449714	AB033015	Hs.22541	KIAA1189 protein	2.0	7.5
431918	AW103034	Hs.6467	synaptobrevin 3	2.0	6.9
415669	NM_065025	Hs.78589	serine (or cysteine) proteinase inhibito	2.0	10.2
435040	AB322350	Hs.152825	ESTs	2.0	4.7
440152	AB002376	Hs.7006	KIAA0378 protein	2.0	14.2
445102	AW294610	Hs.22720	ESTs	2.0	16.2
436734	AI937612	Hs.273758	hypothetical protein FLJ23112	2.0	4.7
437414	AW894071	Hs.48468	hypothetical protein DKFZp547C176	2.0	6.4
418512	AW496974	Hs.94306	disacetylglucosyl kinase, zeta (104MD)	2.0	7.9
433189	AB037815	Hs.32156	KIAA1354 protein	2.0	5.7
420050	AL118615	Hs.94563	neurochordin	2.0	6.5
429900	AA460421	Hs.30875	ESTs	2.0	4.2
423447	X52961	Hs.2998	contactin 2 (zonar)	2.0	4.1
431677	AK006496	Hs.306889	hypothetical protein FLJ20489	2.0	3.1
452656	AF034799	Hs.30881	protein tyrosine phosphatase, receptor 1	2.0	10.7
448681	AI109781	Hs.21754	Homo sapiens mRNA full length insert cDN	2.0	7.2
453754	AW972880	Hs.172753	ESTs	2.0	3.4
422544	AE010299	Hs.118140	KIAA0716 gene product	2.0	11.8
416836	DS4745	Hs.68247	chaperonin	2.0	6.8
454048	H5626	Hs.6921	ESTs	2.0	9.9
425741	AF052152	Hs.155412	Homo sapiens clone 24626 mRNA sequence	2.0	6.5

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5	TABLE 19B:	
	Play: CAT number: Accession:	Unique Eos probe/seq identifier number Gene cluster number Genbank accession numbers
10	Play	Accession
	408065	103646_1 AW954272 A003154 AA059300 AA046911
	415527	1539393_1 F11624 243212 H08536 R56332 H05256 R52303 R13075
	415666	1543492_1 H72693 R08673 H07332 R54694 AA350990 133786 T30936 AA350995 T08592 T09274 AA224297 U54678 T08961 R15336 AW953168 AA350074 418572 176394_1 AW890649 T65754 AA229857 AA229858 Z43784 R13382 AW972911 AA449369 H17037 R19603 AW52565 AW004030 BE502530 T25603 AA805324 AA449241 A051625 A264063 AW196918 AA449567 AW53735 AW53735 AA319155 AW964436 AG503440 AW594171 AB67447 AW204077 AW956110 C156116 D61142 H17038 AW152343 187230 A13 AA319435 N55456 AA319377 AW961532 T48452 AA894424 A021919 Z 19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 A0341435 AW238800 AA274961 AAG31158 A1741227 AB066667 AW96266 D81263 U53937 U52496 AA574487 AW043854 N56483 Z35987 AW492961 A0361526 F04002 AA452141 T23551 AW472655 A103667 A1341
20	426919	273507_1 AL041228 D62004 D61361 A1020314 A690307 AW000296 A018308 AW087473 AW183530 AA393346 H50055 AA393601
	433670	372721_1 AG604405 BE062234 AW748386
	433621	377350_1 AA618174 A114549 R36454 R36465
	433940	37787_1 H05129 H53433 A051350 AA394734 AA689716 N40915 AW98705 F00042 T03605 R88588 AF112220
25	437923	428857_1 AW076629 AW87375 N64357 AA731069
	446692	589523_1 Z44514 A1352097 A1030984 AW235923 AW196558 AW94637 A1336983

30	TABLE 19C:	
	Play: Ref: Strand: Nt position:	Unique number corresponding to an Eos probe/seq Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons.
35	Play	Ref
	400844	9188605 Plus
	404819	46140_1 Plus
	405560	183148 Plus
40	405819	4007559 Plus
	405311	9211557 Minus
		Nt position 24748-24872,25035-25204 16223-16219,16407-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 2830-2967 137114-139033

	TABLE 20A. ABOUT 328 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS	
45	Table 20A lists about 328 CNS-enriched genes significantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix HuU13 GeneChip array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2. The "average" normal CNS level was set to the 80 th percentile amongst various normal CNS tissues. The "average" LGG level was set to the 80 th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 80 th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95 th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10 th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.	
50	Play:	Unique Eos probe/seq identifier number
	Ex/Accession:	Exemplar Accession number, Genbank accession number
	UnigenID:	Unigene number
	Unigene title:	Unigene gene title
55	R1:	Ratio of CNS compared to LOWER GRADE GLIOBLASTOMA
	R2:	Ratio of CNS compared to NON-CNS NORMAL ADULT TISSUE

Play	Ex/Accession	UnigenID	Unigene Title	R1	R2
60	425580	L11144	Hs.1907 glutamin prolactin	33.1	3.5
	425489	MS5954	Hs.1905 differentiation-associated Na-dependent	24.7	10.5
	430538	AB032435	Hs.242821 parvalbumin	22.6	22.6
	417275	X63578	Hs.29449 calreticulin B (secretory granule 1)	22.4	6.0
65	425505	AL335461	Hs.2281 ESTs, Weakly similar to RHG6_HUMAN RHG-6	21.8	21.8
	408040	AI266496	Hs.22005 ESTs	19.4	19.4
	435145	AI277259	Hs.116031 ESTs	18.5	3.8
	407039	X00368	Hs.194605 gH Human prolactin gene 5' region.	18.1	18.1
70	428976	AL337624	Hs.194605 ras homolog gene family, member I	17.4	17.4
	425683	AA685673	Hs.50919 KIAA0353 gene product	16.8	16.8
	424645	NM_014682	Hs.151449 proprotein convertase subtilisin/kexin 1	15.1	15.1
	416018	AW138239	Hs.78977 hypothetical protein FLJ20628	14.0	14.0
75	405560	AW687701	Hs.159425 ESTs	13.9	8.0
	452622	AW072330	Hs.293875 cyclic AMP-regulated phosphoprotein, 21	13.8	13.8
	433940	H05129	Hs.75294 corticotropin releasing hormone	12.0	12.0
	413324	V00571	Hs.65248 dynen, cytoplasmic, intermediate polype	12.0	13.2
80	410657	AF063228	Hs.159425 ESTs	11.5	11.5
	410330	AW023630	Hs.159425 aspartate cytochrome 2, Cytosol	11.1	23.4
	453165	ST4727	Hs.32042 ESTs, Weakly similar to ALU1_HUMAN ALU 5	10.7	10.7
	425297	AI626272	Hs.68323 ESTs	10.5	4.1
	417167	AW206437	Hs.4290 ESTs	10.4	10.4
	420033	D95902	Hs.252590 ESTs	10.4	10.4
	413293	AL047483	Hs.302498 GTP-binding protein homologous to Saccha	10.0	10.0
	425380	AI291267	Hs.149990 ESTs	9.8	6.9
	410635	D68863	Hs.334372 chorionic somatomammotropin hormone 1(p	9.5	6.6
	427256	AA441787	Hs.119689 glycoprotein hormones, alpha polypeptide	9.1	5.8

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	444330	A1597655	Hs.49265	ESTs	9.1	9.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ111155	8.9	8.9
	421633	AF121860	Hs.106260	sorting nexin 10	8.6	6.7
5	429096	AB011106	Hs.196012	KIAA0534 protein	8.6	8.6
	428652	AAS84272	Hs.33624	transmembrane protein with EGF-like and	8.5	8.5
	410329	BE043077	Hs.278153	ESTs	8.5	8.5
	424932	R14070	Hs.315369	Homo sapiens cDNA: FLJ23075 fs, clone L	8.5	10.2
	417175	R44558	Hs.94002	ESTs	8.4	8.9
	427061	AB032571	Hs.173352	KIAA1145 protein	8.4	8.4
10	420438	AJ155611	Hs.115352	Target	8.3	5.1
	418207	C14685	Hs.34772	ESTs	8.2	9.8
	402029	H05949	Hs.247637	neurexin 3	8.1	18.7
	429876	AB028977	Hs.225874	KIAA1054 protein	8.1	16.8
	429470	A1878501	Hs.320362	guanine nucleotide binding protein (G pr	8.0	8.0
15	430004	U27768	Hs.227571	regulator of G-protein signalling 4	7.9	15.7
	436427	AG44378	Hs.143399	ESTs	7.8	7.8
	408814	N82499	Hs.176227	hypothetical protein FLJ111155	7.8	8.6
	434367	AB020090	Hs.3629	KIAA0893 protein	7.7	5.6
20	441005	Z41355	Hs.303172	Homo sapiens mRNA: cDNA DKFZp547G133 (fr	7.7	7.7
	416651	AW963951	Hs.85618	ESTs	7.7	8.5
	429033	NM_007374	Hs.154756	sine oculis homeobox (Drosophila) homolo	7.6	5.5
	437073	AB85908	Hs.94122	ESTs	7.5	7.5
	441264	AJ027170	Hs.23290	ESTs	7.3	7.3
25	450715	AZ56484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.2	7.2
	415076	NM_008557	Hs.77890	guanylate cyclase 1, soluble, beta 3	7.1	4.8
	410011	AB020041	Hs.87856	PTF1A2E protein kinase 1	7.1	10.0
	423003	AL122007	Hs.122967	actin (Drosophila)-like 2 (Mayen)	7.0	7.0
	433621	AA618174		gln-341401.1 NCL_CGAP_Thy1 Homo sapiens	7.0	7.0
	457012	R41480	Hs.302754	ESTs	6.9	6.9
30	445898	AF070623	Hs.13423	Homo sapiens clone 24458 mRNA sequence	6.9	6.9
	425352	NM_009529	Hs.1697	proopomelanocortin (adrenocorticotropin)	6.9	6.1
	433568	AA832572	Hs.201769	ESTs, Weakly similar to T24435 hypoph	6.9	6.9
	409031	AA376836	Hs.288656	ESTs	6.8	6.8
	419347	C15944	Hs.90005	superfornicovaginal ganglia, neural speci	6.5	22.2
35	445279	R19100	Hs.22245	ESTs	6.4	6.4
	437414	AJ094071	Hs.48448	hypothetical protein DKFZp564C176	6.4	6.4
	428414	AL049980	Hs.184216	DKFZP564C152 protein	6.4	6.4
	434104	AF116691	Hs.116459	hypothetical protein PRO2198	6.4	4.0
	443244	AJ457235	Hs.166479	ESTs	6.3	3.0
40	447761	AF051573	Hs.154952	protocadherin 8	6.3	6.3
	450900	BE075478	Hs.248980	ESTs	6.2	3.9
	427457	AW779105	Hs.164682	ESTs	6.2	11.1
	416133	NM_001683	Hs.89512	ATPase, Ca transporting, plasma membrane	6.1	8.0
45	432453	AB95537	Hs.27172	ESTs, Moderately similar to PC4259 lem	6.0	3.9
	432298	AL118912	Hs.274253	Homo sapiens mRNA: cDNA DKFZp51G1111 f	6.0	15.1
	415114	D60468	Hs.54181	ESTs	6.0	6.0
	416101	R24854	Hs.268805	ESTs	5.9	3.3
	448958	AB020051	Hs.22653	KIAA0844 protein	5.9	5.9
50	447138	AK39112	Hs.53826	ESTs, Weakly similar to 2109260A B cell	5.8	5.8
	414545	AA145287	Hs.76605	ESTs	5.8	3.6
	424153	AA451737	Hs.141456	MAGE-like 2	5.7	5.1
	424641	AB001106	Hs.151413	glia maturation factor, beta	5.6	5.6
	415289	AW954049	Hs.8177	ESTs, Weakly similar to PHU40B salivary	5.6	9.6
55	432149	AW814236	Hs.133483	ESTs, Weakly similar to T34549 probable	5.6	12.2
	408428	NM_014787	Hs.44896	Onaj1 (isp40) homolog, subfamily B, membe	5.6	5.6
	443912	R37325	Hs.184780	ESTs	5.5	6.1
	442023	A167878	Hs.144549	ESTs	5.5	5.6
	425642	R39773	Hs.7139	copine IV	5.4	5.6
60	439772	AL365406	Hs.107958	Homo sapiens mRNA full length insert cDN	5.4	9.8
	450149	AW965781	Hs.132863	Zic family member 2 (odd-paired Drosophi	5.4	5.4
	438202	AW169287	Hs.22588	ESTs	5.3	5.3
	448605	AL109678	Hs.21937	Homo sapiens mRNA full length insert cDN	5.3	5.3
	418866	T65754	Hs.184568	gbc-yc1c07.s1 Stratagene lung (53/210) H	5.3	3.8
65	448786	BE048942	Hs.179075	Homo sapiens cDNA FLJ11561 fs, clone HE	5.2	5.2
	443682	AI383061	Hs.47248	ESTs, Highly similar to Cdc14	5.2	3.2
	415666	H72693	Hs.184568	gln-341401.1 Sources fetal liver spleen	5.2	5.2
	428508	BC252383	Hs.184568	SRSF31 protein	5.2	5.2
	446353	AI290919	Hs.153661	ESTs	5.1	5.1
	442106	AW205881	Hs.326728	ESTs	5.1	3.2
70	437331	AL353933	Hs.21710	hypothetical protein DKFZp761G0313	5.1	5.1
	419318	AW969742	Hs.291005	ESTs	5.0	3.1
	408068	AW146652	Hs.167398	ESTs	5.0	5.0
	434149	Z43829	Hs.244624	hypothetical protein MGC5469	5.0	5.0
	439328	N47305	Hs.302161	ESTs	4.9	5.3
75	414631	AW970130	Hs.65406	ESTs	4.9	4.9
	447104	R15085	Hs.210705	Homo sapiens cDNA FLJ13182 fs, clone NT	4.9	3.0
	418527	AA450386	Hs.7149	Homo sapiens cDNA: FLJ21950 fs, clone H	4.9	4.9
	425073	W39609	Hs.22003	solute carrier family 6 (neurotransmitter	4.9	4.9
80	433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.8	4.8
	427287	NM_014903	Hs.174188	KIAA0838 protein	4.8	4.8
	447252	R09916	Hs.12449	Homo sapiens transmembrane protein HTMP1	4.8	3.2
	419643	F00666	Hs.91791	chromosome 11 open reading frame 25	4.7	4.7
	414949	C15314	Hs.323349	ESTs	4.7	3.8

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	429600	AA450421	Hs.30875	ESTs	4.7	4.2
	422949	AA319435		gb:EST21657 Adrenal gland tumor Homo sap	4.7	7.4
	430537	X62692	Hs.2593	phosphodiesterase 6B, cGMP-specific, rod	4.6	4.6
	419191	U17195	Hs.89866	A kinase (PRKA) anchor protein 6	4.5	4.5
5	421562	AA300900	Hs.89849	ESTs, Moderately similar to AF161511.1 H	4.4	3.2
	406311			NM_021979 Homo sapiens heat shock 70KD	4.4	11.5
	451050	AW537420	Hs.69662	ESTs	4.4	4.4
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	4.4	7.9
	411438	NM_014210	Hs.70499	eotopic viral integration site 2A	4.3	19.4
10	451301	A1709514	Hs.209090	EST	4.3	4.3
	452381	H23329	Hs.290890	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.3	4.3
	433109	N58907	Hs.162430	EST	4.3	3.9
	423589	AA326082	Hs.209569	ESTs	4.2	4.2
	427224	AL135554	Hs.101637	sine oculis homeobox (Drosophila) homolo	4.2	3.9
15	429489	AA615905	Hs.153513	ESTs	4.1	4.1
	408206	AF041853	Hs.43670	kinesin family member 3A	4.1	4.1
	418202	N48521	Hs.26549	KIAA1708 protein	4.1	5.8
	468117	H49129	Hs.172562	ESTs	4.1	4.1
	421158	R39187	Hs.12440	Homo sapiens transmembrane protein HTMP1	4.0	27.9
20	458994	F12832	Hs.3610	ESTs	4.0	4.0
	452197	AW023595	Hs.232048	ESTs	4.0	4.0
	408547	AA674291	Hs.57837	ESTs	4.0	4.0
	433447	U25186	Hs.3281	neuronal pentacin II	4.0	3.7
	448583	NM_015239	Hs.21542	KIAA1035 protein	4.0	4.0
25	442412	R77677	Hs.346644	ESTs	3.9	3.9
	440293	A1004193	Hs.22123	ESTs	3.9	3.9
	426365	AA376667	Hs.10283	RNA binding motif protein RB	3.9	4.1
	420844			NM_003105 Homo sapiens sortilin-related	3.9	3.1
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.9	3.9
30	429290	AF200332	Hs.198760	neurofilament, heavy polypeptide (200KD)	3.8	3.3
	408777	U171204	Hs.47626	Rc (Drosophila)-like, expressed in neur	3.8	3.8
	442876	AF133895	Hs.138907	ESTs	3.8	3.8
	414699	AB15523	Hs.76930	synuclein, alpha (non A4 component of am	3.8	4.5
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.8	3.3
35	434968	AW675157	Hs.26037	ESTs	3.7	3.7
	412049	N53437	Hs.18268	serine/threonine kinase 5	3.7	10.7
	416220	NA9776	Hs.170954	hypothetical protein MGC10946	3.7	4.5
	459697	AA406062	Hs.58002	ESTs	3.7	5.4
	439648	H24347	Hs.27524	ESTs	3.7	8.1
40	442042	A1969506	Hs.8077	Homo sapiens mRNA; cDNA DKFZp547E184 (t	3.7	6.2
	462765	AW67900	Hs.33967	ESTs	3.7	3.7
	434933	R91095	Hs.4276	KAA1701 protein	3.6	6.1
	419518	U75289	Hs.90758	Human clone 23695 mRNA sequence	3.6	3.6
	452667	T87219	Hs.13219	ESTs	3.6	3.6
45	436773	AW070629		PCNA and SFRS1 interacting protein 1	3.6	3.6
	408119	W62613	Hs.101672	ESTs, Weakly similar to T00331 hypothe	3.6	3.6
	453534	NM_014796	Hs.33187	KIAA0478 gene product	3.6	4.7
	449093	AB035356	Hs.22998	neurexin 1	3.6	3.6
50	442738	AW002370	Hs.131058	ESTs, Weakly similar to NFM_HUMAN NUCLEO	3.5	3.5
	447746	AW015920	Hs.101359	ESTs	3.5	9.9
	449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	3.5	3.5
	447750	AI422234	Hs.143434	contactin 1	3.5	9.8
	453990	AF150278	Hs.33378	RAA0820 protein	3.5	22.3
55	402339	AB023695	Hs.54037	actinucleotide pyrophosphatase/phosphodi	3.5	3.6
	410240	AL157424	Hs.61289	synaplanin 2	3.5	4.6
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.4	3.4
	400998			Eos Control	3.4	3.4
	450181	H65254	Hs.201198	ESTs	3.4	7.2
60	459080	AW152083	Hs.290855	ESTs	3.4	13.5
	417063	N50515	Hs.45051	ESTs	3.3	3.3
	424918	R13982	Hs.169309	myelin-associated oligodendrocyte basic	3.3	5.3
	453431	AF094754	Hs.32973	glycine receptor, beta	3.3	4.6
	412453	R20205	Hs.75726	ESTs	3.3	3.3
65	450561	R49674	Hs.29509	ESTs	3.3	3.3
	415527	F11624	Hs.29509	gb:HSCZD0101 normalized infant brain cDN	3.3	3.3
	429568	U07618	Hs.173034	amylphosphatase (S&M-Mann syndrome with br	3.3	15.3
	427386	AW836261	Hs.7177	ESTs	3.2	7.7
	424001	W57883	Hs.137476	paternally expressed 10	3.2	5.4
70	439450	R51613	Hs.125304	ESTs	3.2	8.3
	447879	AF103292	Hs.8813	synapsin binding protein 3	3.2	3.2
	417284	N62869	Hs.107242	Homo sapiens cDNA FLJ12965 fs, clone NT	3.2	3.2
	410343	AA054273	Hs.76581	ESTs, Weakly similar to S47072 finger pr	3.2	3.2
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	3.2	12.5
	453919	AW959912	Hs.7076	KIAA1705 protein	3.2	3.2
75	424087	N69333	Hs.143434	contactin 1	3.1	3.1
	425963	AW012642	Hs.286208	Homo sapiens, clone MGC-15606, mRNA, com	3.1	3.1
	419552	AW503756	Hs.286164	hypothetical protein dJ551D2.5	3.1	4.1
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog associ	3.1	3.1
80	423629	R44107	Hs.240905	ESTs	3.1	4.4
	443297	A049864	Hs.133029	ESTs	3.1	3.1
	453302	NM_009838	Hs.32545	glutamate receptor, metabotropic 1	3.1	4.6
	405319			NM_002578 Homo sapiens p21 (CDKN1A)-acti	3.1	13.5
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	3.0	3.0

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	447673	A1823987	Hs 182285	ESTs	3.0	3.0
	433670	AA604405	Hs 31570	glnr687M09.s1 NC1_CGAP_AA1 Homo sapiens	3.0	3.9
	450757	BE081050	Hs 31570	ESTs, Weakly similar to KIAA1324 protein	3.0	3.2
	424724	T06352	Hs 287709	Homo sapiens cDNA: FLJ22674 fls, clone H	3.0	3.0
	433315	R06754	Hs 237076	GRB2-associated binding protein 1	3.0	3.1
	451022	U03652	Hs 323075	Homo sapiens mRNA, cDNA DKFZ564P116 (f	3.0	4.9
	433346	A1267677	Hs 127416	synaptotagmin 1	3.0	20.1
	439274	AF086092	Hs 48372	ESTs	3.0	18.3
	426649	U03500	Hs 158540	UDP glycosyltransferase 6 (UDP-galactose	2.9	38.6
	44 1859	NM_003947	Hs 8009	huntingtin-associated protein interactin	2.9	14.9
	407868	NM_009550	Hs 40637	proline-rich Glu (C-carboxyglutamic acid	2.9	3.3
	410765	A1694972	Hs 66160	nucleosome assembly protein 1-like 2	2.9	8.0
	428001	H97428	Hs 219507	ESTs, Moderately similar to Transferrin	2.8	5.9
	446533	AL119710	Hs 21365	nucleosome assembly protein 1-like 3	2.8	3.6
	425130	AA448208	Hs 59163	ESTs	2.8	3.1
	408654	AA836381	Hs 315111	nuclear receptor co-repressor/NRAC3 comp	2.8	3.7
	452238	P18111	Hs 345757	ESTs	2.8	3.8
	445544	A1831532	Hs 7047	ESTs, Weakly similar to Unknown [H sapie	2.8	12.4
	433803	A1823593	Hs 27588	ESTs	2.8	4.1
	407728	AW071502	Hs 175831	ESTs	2.7	10.2
	414931	AK000342	Hs 77646	Homo sapiens mRNA, cDNA DKFZp761M0223 (f	2.7	3.4
	410711	A18002316	Hs 65746	KIAA0318 protein	2.7	6.1
	452728	AL133000	Hs 7086	hypothetical protein HGCI2435	2.7	3.5
	451516	A1800515	Hs 12024	ESTs	2.7	6.3
	454053	AW023006	Hs 27172	ESTs, Moderately similar to PC4259 feni	2.7	3.6
	454074	AW872844	Hs 117464	ESTs	2.7	7.2
	422414	AW875237	Hs 13701	ESTs	2.7	5.3
	428186	AW504300	Hs 255605	mannosidase, alpha, class 2A, member 2	2.7	3.9
	431342	AW971018	Hs 21659	ESTs	2.7	8.0
	423449	A1497900	Hs 33067	ESTs	2.6	14.5
	427283	AL119796	Hs 174185	neurofilament phosphoprotein/tau/tau/tau	2.6	3.0
	426919	AL041228	Hs 75426	ELAV (embryonic lethal, abnormal vision,	2.6	9.0
	437117	AL049256	Hs 122593	ESTs	2.6	3.8
	422491	AA338548	Hs 117546	neurofilament	2.6	3.6
	436068	A1827209	Hs 306210	Homo sapiens cDNA: FLJ23133 fls, clone L	2.6	5.1
	432809	AA565059	Hs 131703	ESTs	2.5	9.9
	433551	A1965544	Hs 12450	protocadherin 9	2.5	18.1
	444783	AK001468	Hs 62180	anillin (Drosophila Scraps homolog), act	2.5	43.2
	417417	P05745	Hs 89512	ATPase, Ca Transporting, plasma membrane	2.5	17.1
	415554	AA331946	Hs 75426	neurofilament II (neurofilament C)	2.5	5.7
	448902	Z45958	Hs 22543	Homo sapiens mRNA, cDNA DKFZp761H1912 (f	2.5	21.8
	422910	A1365130	Hs 11307	ESTs, Weakly similar to T19326 (hypothet	2.5	14.5
	423135	N67555	Hs 26411	ESTs	2.5	8.2
	452311	AKG04029	Hs 252744	ESTs	2.5	3.5
	418440	H17739	Hs 288813	human DNA sequence from clone RP5-899C14	2.5	7.0
	432882	NM_013267	Hs 279696	serum/glucocorticoid induced regulated kinase-II	2.5	4.2
	422411	AW749443	Hs 22511	ESTs	2.5	12.0
	451386	AB029006	Hs 26334	spastic paraplegia 4 (autosomal dominant	2.4	3.1
	404819			NM_305087 Homo sapiens (pseni) (Drosophi	2.4	5.8
	429656	X05608	Hs 211554	neurofilament, light polypeptide (E8K)	2.4	13.1
	431988	AC002302	Hs 77202	protein kinase C, beta 1	2.4	10.5
	411379	A1816344	Hs 12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.4	11.2
	422680	N45669	Hs 76722	CCAAT/enhancer-binding protein (CEBP),	2.4	45.2
	429859	NM_007050	Hs 225652	protein tyrosine phosphatase, receptor 1	2.4	5.1
	430287	AW182459	Hs 125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.4	7.6
	427890	Z43784	Hs 30668	ankyrin 3, node of Ranvier (ankyrin G)	2.4	3.6
	427658	H61387	Hs 30668	rogo receptor	2.4	3.8
	445100	AW671109	Hs 13804	hypothetical protein dJ462023.2	2.3	3.6
	412266	N69006	Hs 26133	ESTs	2.3	30.9
	435069	Z45270	Hs 233873	hypothetical protein FLJ22672	2.3	4.8
	420173	AA258151	Hs 22299	ESTs	2.3	4.1
	452371	RA0990	Hs 21658	ESTs	2.3	3.3
	430456	AA314998	Hs 241503	hypothetical protein	2.3	4.7
	409553	AA332277	Hs 57691	cadherin 18, type 2	2.3	5.5
	429006	AA443143	Hs 50929	hypothetical protein FLJ13842	2.3	6.6
	445194	A215667	Hs 175044	ESTs	2.3	3.1
	428392	H10213	Hs 2205	secretory granule, neuroendocrine protei	2.3	42.3
	434460	AA478486	Hs 3852	KIAA0368 protein	2.3	4.8
	416490	AF090116	Hs 73348	regulator of G-protein signalling 7	2.3	12.5
	437924	AB535344	Hs 164118	ESTs, Weakly similar to SL51_HUMAN SODU	2.3	3.2
	418738	AW388633	Hs 6582	zinc finger family 7, (zinc finger) smoo	2.2	16.5
	424945	A121919	Hs 78913	hypothetical protein FLJ10582	2.2	30.5
	416530	U62801	Hs 79361	kallikrein 6 (neurokin, zyme)	2.2	4.4
	422927	AW247388	Hs 301423	calcium binding protein 1 (caltrain)	2.2	3.0
	438831	BE263273	Hs 54339	synapsin II	2.2	3.4
	443078	AK001256	Hs 225975	KIAA1576 protein	2.2	16.1
	410631	AA086469	Hs 417171	ESTs	2.2	5.8
	419271	N34901	Hs 238532	ESTs	2.2	7.5
	452752	AW044088	Hs 33578	KIAA0820 protein	2.2	13.4
	446574	AI310135	Hs 330933	ESTs	2.2	3.6
	452106	AI141031	Hs 21342	ESTs	2.2	3.4
	415910	U02030	Hs 78913	chemokine (C-X3-C) receptor 1	2.2	28.9
	444458	BE041526	Hs 31746	hypothetical protein DKFZp547H072	2.2	7.7

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433658	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypothetical	4.0
429470	AIR78901	Hs.203862	guanine nucleotide binding protein (G pr	4.0
415666	H72653		gby03c11.1 f1 Soares fetal liver spleen	3.9
407988	N47760	Hs.285107	hypothetical protein FLJ13387	3.9
427061	AB532871	Hs.173393	KIAA1145 protein	3.9
430261	AA305127	Hs.237225	hypothetical protein HT023	3.9
440624	AF017587	Hs.7306	secreted fibroblast-related protein 1	3.8
431668	AW969610	Hs.151179	ESTs	3.8
446892	Z4614		Homo sapiens mRNA for KIAA1763 protein,	3.8
408739	W01556	Hs.238797	ESTs, Moderately similar to 18022 hypot	3.8
426716	NM_006379	Hs.173291	sera domain, immunoglobulin domain (Ig),	3.8
450103	R08665	Hs.17244	hypothetical protein FLJ13365	3.7
426775	AA384564	Hs.3628	ESTs	3.7
430469			Target Exon	3.7
450181	H05254	Hs.201198	ESTs	3.7
438202	AW165287	Hs.22888	ESTs	3.7
445278	R41900	Hs.22245	ESTs	3.7
422546	AB007569	Hs.301478	KIAA0500 protein	3.7
435712	AA654007	Hs.176556	ESTs	3.6
417620	RC2530	Hs.191198	ESTs	3.6
421952	AA306000	Hs.98849	ESTs, Moderately similar to AF161511 1 H	3.6
435365	AW950427	Hs.342874	transforming growth factor, beta receptor	3.6
426365	AA376567	Hs.10293	RNA binding motif protein 10	3.6
416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (parcom	3.6
438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	3.6
424704	A1263293	Hs.152656	cytochrome P450, subfamily 10 (arachido	3.6
414631	AW570130	Hs.65406	ESTs	3.6
463698	AA337615	Hs.42746	ESTs	3.6
438704	AA35060	Hs.23825	ESTs	3.5
437073	AIR85608	Hs.94122	ESTs	3.5
434460	AA478486	Hs.3852	KIAA0368 protein	3.5
414541	BE293116	Hs.76392	asialdehyde dehydrogenase 1 family, member	3.5
423665	BE167153	Hs.24380	ESTs	3.5
446390	AA233393	Hs.14892	hypothetical protein FLJ11511	3.5
441284	AA927170	Hs.23290	ESTs	3.5
433628	R13140	Hs.13359	ESTs	3.5
411811	AW864370		gb-PNM-SN0016-100500-004-h09 SN0016 Homo	3.5
410140	AL134435	Hs.247837	neurexin 3	3.4
415114	D60488	Hs.94181	ESTs	3.4
455945	BE96051		gb-RC1-CT0913-110500-017-c04 G10313 Homo	3.4
433670	AA604405		gb-m87809.s1 NCL_CGAP_AA1 Homo sapiens	3.4
417175	R44558	Hs.94002	ESTs	3.4
427176	AW381569	Hs.40334	ESTs	3.4
448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	3.4
457012	R41480	Hs.302754	ESTs	3.3
405354			CX000321.g3167579[NP_031518.1] ari	3.3
446872	A1681573	Hs.288671	Homo sapiens cDNA FLJ11997 f1, clone HE	3.3
433903	AIR23593	Hs.27888	ESTs	3.3
448017	AW002425	Hs.224142	ESTs	3.3
414545	AA145287	Hs.76905	ESTs	3.3
409010	A1648675	Hs.103441	Homo sapiens, similar to RIKEN cDNA 1700	3.3
426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.3
422411	AW748443	Hs.22511	ESTs	3.3
429850	AA534975	Hs.185078	ESTs	3.3
406822	S70284	Hs.119597	gb-aleanyl-CoA desaturase [human, adipo	3.2
429556	AW133059	Hs.98988	ESTs	3.2
434104	AF116891	Hs.115459	hypothetical protein PRO2198	3.2
427229	A1799751	Hs.5635	ESTs	3.2
444458	BE041526	Hs.31746	hypothetical protein DKFZp547F072	3.2
433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.2
412796	AW090654	Hs.285729	ESTs, Weakly similar to unnamed protein	3.2
446828	AK001339	Hs.74242	hypothetical protein FLJ104077	3.1
442117	AW664964	Hs.128699	ESTs, hypothetical protein for IMAGE:447	3.1
429876	AB028977	Hs.225974	KIAA1054 protein	3.1
4650757	BE081050	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.1
414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypothetical	3.1
459396	BE407712	Hs.153959	creatine kinase, mitochondrial 1 (ubiqui	3.1
433582	BE548749	Hs.148016	ESTs	3.1
452752	AW044058	Hs.33578	KIAA0820 protein	3.0
439165	AA028517	Hs.55162	KCNK1 overlapping transcript 1	3.0
439403	AA561224	Hs.56134	Homo sapiens cDNA: FLJ25247 f1, clone H	3.0
422414	AW875237	Hs.13701	ESTs	3.0
407173	T64349		gb-yc1008.s1 Stratagene lung (S37210) H	3.0
446583	NM_015239	Hs.21542	KIAA1035 protein	3.0
429943	AIR24977	Hs.145319	ESTs	3.0
452290	AA887428	Hs.246670	myogen-activated protein kinase kinase	3.0
412258	AA376768	Hs.324641	hypothetical protein FLJ22622	3.0
429968	AA322603	Hs.227011	G-substrate	3.0
434348	BE353191	Hs.181725	putative D-b-carotene 9',10'-dioxygenase	2.9
427115	AW972653	Hs.112037	ESTs	2.9
430538	AB032435	Hs.242621	differentiation-associated N-dependent	2.9
445951	A1022240	Hs.17524	ESTs, Moderately similar to ALU1_HUMAN A	2.9
405403			Target Exon	2.9

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	452197	AW022595	Hs.232048	ESTs	2.9
	437357	AL359559	Hs.313666	Homo sapiens mRNA, cDNA DKFZp76202215 (I	2.9
	436427	A1343378	Hs.143399	ESTs	2.9
5	417787	R14848	Hs.23863	ESTs	2.9
	438272	AA324474	Hs.25951	ESTs	2.9
	454247	AJ243950	Hs.46735	deafness locus associated putative guani	2.9
	415839	RA0611	Hs.94694	ESTs	2.9
	408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.9
10	408468	A1939712	Hs.93837	phosphatidylinositol transfer protein, m	2.9
	431304	BE157283	Hs.121840	gs-RC4-HT0373-130200-011-403 HT0373 Homo	2.9
	410240	AL151424	Hs.61289	synaptotagmin 2	2.9
	444783	AK001468	Hs.62180	arilin (Xrosophila Scorpis homolog), act	2.8
	408436	AB011180	Hs.100960	KIAA0609 protein	2.8
	450793	N80159	Hs.121840	microtubule-associated proteins 14TB II	2.8
15	429788	U87791	Hs.221040	HBS1 (S. cerevisiae)-like	2.8
	424254	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	2.8
	431019	N85907	Hs.162430	EST	2.8
	427974	BE033023	Hs.105767	ESTs	2.8
20	432266	AK000385	Hs.274222	hypothetical protein FLJ20378	2.8
	414754	AW013687	Hs.31522	ESTs	2.8
	411918	AW876354		gltPM4-PT0019-141299-009-F08 PT0019 Homo	2.8
	404663			Target Exon	2.8
	444469	A1755990	Hs.16341	MWWD binding protein	2.8
25	444755	AA431791	Hs.113823	Cpx (caseinolytic protease X, E. coli)	2.8
	445898	AFQ70623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.7
	427263	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	2.7
	400138			Est Control	2.7
	459676	A1892464	Hs.202263	ESTs	2.7
30	456957	AA404062	Hs.58002	ESTs	2.7
	444420	A1148157	Hs.146766	ESTs	2.7
	433371	D87466	Hs.240112	AA04276 protein	2.7
	444117	AW445310	Hs.210252	ESTs, Weakly similar to HSS2_HUMAN HEPAR	2.7
	424994	AW954525		gb:EST366595 MAGE resequences, MAGE Homo	2.7
35	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.7
	417494	AJ369484	Hs.222137	ESTs	2.7
	427166	AA431576	Hs.59154	ESTs	2.7
	404746			CX000138:cg7512767[pi][T12477 hypothe	2.7
	411361	AW839073		gs-CM2-LT0056-030100-109-006 LT0056 Homo	2.7
40	426158	AA593222	Hs.101915	Stargardt disease 3 (autosomal dominant)	2.7
	408625	Y13647	Hs.119507	stearoyl-CoA desaturase (delta-9-desatur	2.7
	416101	R24854	Hs.268806	ESTs	2.7
	404606			Target Exon	2.7
	433921	AA618174		gb:mq14001.c1 NC_01_CGAP_Thy1 Homo sapiens	2.7
45	414272	A1851803	Hs.46988	ESTs	2.7
	418047	R27633	Hs.4847	ESTs	2.7
	421089	AE037771	Hs.101799	KIAA1350 protein	2.7
	412244	AW548175		gs-RCD-MT0013-280300-021-c10 MT0013 Homo	2.7
50	424343	AL161977	Hs.2994	PCTAIRE protein kinase 3	2.6
	424153	AA451737	Hs.141496	MAGE-like 2	2.6
	427189	HE2453	Hs.5635	ESTs	2.6
	454454	AW612264	Hs.131705	ESTs	2.6
	426747	AA535210	Hs.171955	kallikrein 3, (prostate specific antigen	2.6
	456791	H05202	Hs.133968	FGF receptor activating protein 1	2.6
55	406715			ENSP0000000518P15162c kinase ML	2.6
	425494	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr	2.6
	430665	A1073424	Hs.5232	HSPC125 protein	2.6
	435787	H73505	Hs.117874	ESTs	2.6
	410119	F07841	Hs.13826	ESTs	2.6
60	432146	AW081072	Hs.115980	KIAA0539 protein	2.6
	448871	BE616709	Hs.159265	kruippel-related zinc finger protein hckr	2.6
	414516	A1307802	Hs.135660	ESTs, Weakly similar to T43458 hypothes	2.6
	429477	A125514	Hs.6655	ESTs	2.6
	400269			Est Control	2.6
	443992	AW022228	Hs.322922	ESTs	2.5
65	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FLB3816,	2.5
	453145	A0277259	Hs.119631	ESTs	2.5
	423009	AW043637	Hs.21768	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.5
	449709	BE410592	Hs.23918	hypothetical protein PP5395	2.5
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	2.5
70	411678	A1907114	Hs.71465	squalene epoxidase	2.5
	408119	W26213	Hs.101672	ESTs, Weakly similar to T00331 hypothes	2.5
	436624	T64237		fatty acid binding protein 1, liver	2.5
	459268	AA428403	Hs.106131	ESTs	2.5
	451336	A1264543	Hs.3610	ESTs	2.5
75	456924	A1631510	Hs.196996	ESTs, Highly similar to match to EST AA3	2.5
	455040	AW852286		gb:QV6CT0225-100400-157-008 CT0225 Homo	2.5
	420033	D59502	Hs.292590	ESTs	2.5
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fa, clone HE	2.5
	432261	AW972983	Hs.232165	polycomb target vasa 1, cell surface	2.5
80	405206	AF341853	Hs.43870	kinesin family member 3A	2.5
	440205	T86950	Hs.105448	ESTs, Weakly similar to B34087 hypothes	2.5
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fa, clone H	2.5
	420912	AW853196	Hs.90787	ESTs	2.4

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	439180	AI393742	Ha_195067	v-erb-b2avian erythroblastic leukemia v	2.4
	421025	AW958975	Ha_26397	Homo sapiens cDNA FLJ13226 fs, clone Ov	2.4
	439973	AI733308	Ha_124663	ESTs	2.4
5	445847	TS1454	Ha_82845	Homo sapiens cDNA:FLJ21930 fs, clone H	2.4
	414672	AJ216038	Ha_46504	ESTs, Moderately similar to ALUS_HUMAN A	2.4
	451522	BE565817	Ha_26498	hypothetical protein FLJ21657	2.4
	433058	NM_006455	Ha_288215	sialyltransferase	2.4
	445620	AA128808	Ha_179902	transporter-like protein	2.4
10	423863	NM_005709	Ha_132945	POZ-73 protein	2.4
	401978	AW385129	Ha_41717	phosphotransferase 1A, calmodulin-depende	2.4
	425907	AA365752	Ha_155965	ESTs	2.4
	433819	AW511097	Ha_112785	ESTs	2.4
	444395	AJ343931	Ha_145383	ESTs	2.4
	438573	AA144550	Ha_136245	ESTs	2.4
15	444952	R37558	Ha_21375	ESTs	2.4
	434975	AA657884	Ha_314413	ESTs	2.4
	458227	Z46670	Ha_181340	ESTs	2.4
	443244	AH57235	Ha_166479	ESTs	2.4
	433408	NC9127		ESTs, Weakly similar to A46010 X-linked	2.4
20	401600	BE247275		US snRNP-specific protein, 116 kD	2.3
	419066	Z98492	Ha_5975	PRO1073 protein	2.3
	424623	NM_006226	Ha_153322	phospholipase C, epsilon	2.3
	402124			NM_038591: Homo sapiens cadherin 20, type	2.3
25	419678	N80448	Ha_259106	ESTs	2.3
	444897	AW137088	Ha_144857	ESTs	2.3
	425111	BE018485	Ha_30977	ESTs, Weakly similar to B34087 hypothetical	2.3
	402536			NM_000811: Homo sapiens adrenergic, alph	2.3
	425544	AI761152	Ha_181400	ESTs, Weakly similar to 178885 serine/th	2.3
	429111	AI142379		gb:q64c01.1 Scores_test8, NHT Homo sap	2.3
30	415111	R39039	Ha_279041	EST	2.3
	433331	AI738815	Ha_117323	ESTs	2.3
	440263	AK004193	Ha_22123	ESTs	2.3
	411770	NM_014278	Ha_71952	heat shock protein (hsp110 family)	2.3
35	416964	D87467	Ha_80520	guanine nucleotide exchange factor for R	2.3
	415386	AA238667		ESTs, Weakly similar to I38022 hypoph	2.3
	402453	AI743250		mannosidase, alpha, class 1A, member 1	2.3
	401783			NM_003771: Homo sapiens keratin, hair, a	2.3
	420548	AA278246	Ha_920	ESTs	2.3
	419763	AI038691	Ha_121485	ESTs	2.3
40	421750	AK000758	Ha_107872	hypothetical protein FLJ20791	2.3
	406023			Target Exon	2.3
	454024	AA993527	Ha_293907	hypothetical protein FLJ23403	2.3
	401586			Target Exon	2.3
45	404091			Target Exon	2.3
	456773	AI038192	Ha_129764	EGF-like repeats and discoidin-like do	2.3
	414106	BE300325	Ha_77135	RNA binding protein	2.3
	454288	BE222548	Ha_241432	ESTs, Highly similar to c380A1.1b [h.sap	2.3
	441879	AI521536	Ha_107149	novel protein similar to archael, yeast	2.3
50	424724	T05532	Ha_267709	Homo sapiens cDNA: FLJ23574 fs, clone H	2.3
	415692	NE1935	Ha_47374	Homo sapiens cDNA FLJ13261 fs, clone PL	2.3
	415282	R66654	Ha_167257	brain linc protein-1	2.2
	404659			ENSP00000239997: HYPOTHETICAL 34.7 kDa P	2.2
	429956	AC374651	Ha_22542	ESTs	2.2
55	429570	L01087	Ha_211593	protein kinase C, theta	2.2
	429655	UA8959	Ha_211582	myosin, light polypeptide kinase	2.2
	458921	AA682058	Ha_79375	holocarboxylase synthetase (biotin-lipo	2.2
	436463	H05502	Ha_9555	ESTs	2.2
	408894	AW209520	Ha_43582	ESTs	2.2
60	413303	AW836130	Ha_75277	hypothetical protein FLJ13910	2.2
	418154	BE105865	Ha_84928	nuclear receptor subfamily 1, group 1, m	2.2
	418407	AL044818	Ha_77273	nuclear transcription factor Y, beta	2.2
	422907	AB79263	Ha_170953	Human glucose transporter pseudogene	2.2
	445377	AW014022	Ha_170953	ESTs	2.2
	429290	AF203032	Ha_198700	neurofilament, heavy polypeptide (200kD)	2.2
65	445914	AB033015	Ha_23941	KIAA1189 protein	2.2
	403460	AI355337	Ha_154558	thrombin growth factor 7 (keratinocyte	2.2
	410066	AL117654	Ha_58419	DKFZP588L2024 protein	2.2
	410912	AW810224		gb:WR4-ST0125-021199-017-ST0125 Homo	2.2
	447163	AW292770	Ha_5542	DnaJ (Hsp40) homolog, subfamily C, membe	2.2
70	421709	AA159394	Ha_107056	CED-5 protein	2.2
	453728			Target Exon	2.2
	453359	AA448787	Ha_24872	ESTs	2.2
	411379	AB15344	Ha_12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	2.2
	413427	U31120	Ha_845	interleukin 13	2.2
75	426028	AB014513	Ha_49998	Z band alternatively spliced POZ-motif	2.2
	413924	AL119964	Ha_75615	seafurin-1	2.2
	403463			Target Exon	2.2
	409068	AW148652	Ha_157398	ESTs	2.2
	407819	RA2195	Ha_102720	ESTs	2.2
80	414203	BE262710	Ha_78629	AI-Pase, Na ⁺ /transporting, beta 1 polypep	2.2
	448045	AJ297436	Ha_20155	prostate stem cell antigen	2.2
	449835	AW979300	Ha_293813	ESTs	2.2
	458547	AW204314	Ha_170784	ESTs	2.2

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447965	AI/292677	He 94445	ESTs	2.0
429073	BE252922	He 123119	MAD (mothers against decapentaplegic, D)	2.0
459256	AW967668	He 93821	hypothetical protein FLJ114547	2.0
411906	AW875765	He 83059	gq-QV2-P10012-020500-186-a08 FT0012 Homo	2.0
441584	AB037753	He 83059	synaptotagmin IV	2.0
437900	AI/53301	He 103331	ESTs	2.0
436092	AI345995	He 127383	ESTs	2.0
416529	AW009370	He 115772	ESTs	2.0
414320	U13616	He 75863	ankyrin 3, node of Ranvier (ankyrin G)	2.0
444749	AI109072	He 65026	ESTs	2.0
445277	AI284218	He 159204	ESTs	2.0
452550	AA026735	He 136049	Homo sapiens mRNA; cDNA DKFZp434M0420 [f]	2.0
445725	AK000956	He 13209	hypothetical protein FLJ10694	2.0
409265	U78237	He 321052	ESTs	2.0
426736	AA431615	He 130722	ESTs	2.0
447098	AI939409	He 157803	ESTs	2.0
403582			Target Exon	2.0

TABLE 21B:

Play	Unique Eos probest identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Play	CAT Number	Accession
25	409757	1154015_1 AW501470 AW502031 AW495900
	410705	1217235_1 BE004107 BE004105 AW591053 AK797879 AW930194 AW787881 AW797880 BE004108
	410912	1225545_1 AW810244 AW810337 AW810295 AW810303 AW810335 AW810296 AW810305
30	411361	1240511_1 AW853073 AW839324 AW8539230 AW878302 AW839109 AW843697
	411811	1259427_1 AW864370 AW864319 AW864504
	411906	1265204_1 AW875765 AW50294 AW875444
	411918	1265807_1 AW875354 AW875179 AW875318 AW875290 AW875234 AW875195 AW875199 AW875198
	412244	1284652_1 AW949175 AW947637 AW920669 AW947537 AW947531 AW947532 AW947530
	413607	1379911_1 T64741 BE158393 BE152805
35	414275	1432115_1 BE267852
	415666	1543482_1 HT7893 R08673 HT7694 F20990 R08580
	416338	1631178_1 AA190616 AA252564
	418154	17249_1 BE155896 BE165832 AA319621 AA401166 AB11501 H7857 X56199 R33797 AW896675 AA401072 AW374111 H52642 AW896685 AA348138
40		AJ399764 AA010244 W00159 N00874 AA339496 AW957136 W08705 AA029093 AW444647 BE175700 AV651556 AV651847 AA332039 AV648227
		AV649164 AV649491 N87556 AA332262 BE001661 HT5493 BE218742 AA333268 AA095633 AA091958 M76627 1165342 Y17094 AA126501
		AV374665 AA32905 AJ391690 AJ185090 AJ229528 A651843 AA082641 AB81019 AV651527 AV558133 BE044335 BE089545 AA308530 AA361376
		BE218739 AW207822 AA765340 AW512733 BE348741 AB060564 AB871563 AA808552 A050693 AA340232 AA147095
45	418866	179788_1 T55754 AA228857 AA229658
	419386	184355_1 AA236867 AA237066 AA354236 AW957759 H08961
	424994	245786_1 AW654525 AJ372685 AA345621 AJ372687 H10554
	427493	27561_2 H08337 AW674537 AA575521 H08138 H06513 H09016 AA404410 AA404454
	431304	331286_1 BE157283 BE157287 AA502438
	432408	346286_2 N39127 F20776 AI082691 AA865520 F36964 F33894
	433670	372721_1 AA604405 BE062234 AW748386
	433921	377350_1 T4518174 A114549 R236464 R36465
50	436624	4237_5 TA5297 AA694531 NM_001442 M10050 AW843109 AB698516 T53219 T48785 T64166 AA706930 R29613 T55913 T58518 T64679 R29666 M10617
		A7165956 AA101894 W90338 AT742193 AW752206 AA099433 T53220 AW082135 AA0272775 T29562 T55862 AJ343047 AJ345671 T68235 T68121
		AW842284
		Z44514 AJ352067 AB03984 AW235923 AW196558 A954637 AJ336983
55	446901	818996_1 AJ74072 BE26487
	454339	1122972_1 AW381590 BE152244 BE152235 BE152238 BE152232
	455040	1250028_1 AW852286 AW851934 AW852096 AW852274
	455545	1324514_1 AW994075 AW994386
	455649	1348708_1 BE085051 BE155165 BE054764 BE155231 BE064648 BE064671 BE064536
	456401	1944548_2 W28146 W28187
60	458480	58843_1 AJ792258 HT4121 AJ375113 AA960851 AA744592 AV648739 AI258360 AW293609

TABLE 21C:

Play	Unique number corresponding to an Eos probest
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al" refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NI_positon:	Indicates nucleotide positions of predicted exons.

	Play	Ref	Strand	NI_positon
70	400536	9797380	Minus	170994-172025
	400818	8569894	Plus	172644-172765,173085-173200
	401586	9838042	Minus	93974-94099
	401600	4388746	Minus	27363-27518,28727-28891,29526-29731
75	401783	7249190	Plus	139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283
	401929	3818670	Minus	3167-3285,4218-4310
	402124	4033980	Plus	164206-164459
	402493	9797970	Minus	205146-205240,205428-205542
80	403463	9929538	Plus	102596-102879
	403469	9929739	Minus	4831-7707
	403582	8101186	Plus	18308-18458
	403726	7534291	Minus	34481-34671
	404091	7684554	Minus	82121-83229
	404559	8748893	Minus	73499-73651,89575-89739

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5	404653	9838310	Plus	100136-100343
	404656	9212936	Minus	22310-23269
	404659	9797068	Minus	66026-67930
	404745	7219894	Minus	32543-32834
	405354	2642452	Plus	52713-53069
10	405403	6850244	Minus	37491-37670,40561-41031
	405502	9211311	Minus	50360-50584
	405715	4156209	Plus	26293-26706
	406023	8722681	Plus	25623-25936
	406475	5797684	Plus	125417-125563,128052-128180

TABLE 22A: ABOUT 301 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS

Table 22A lists about 301 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix U133A GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 55th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

20	Proy	Unique Ect probe set identifier number		
	ExAccn	Exemplar Accession number, Genbank accession number		
	UnigeneID	Unigene number		
	Unigene Title	Unigene gene title		
25	R1:	Ratio of CNS to GLIOBLASTOMA		
	Proy	ExAccn	UnigeneID	Unigene Title
				R1
30	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3
	445529	H14421	Hs.105613	ATP-binding cassette, sub-family A (ABC1)
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus
	417167	AW005437	Hs.4290	ESTs
	453165	S74727	Hs.33042	aspartoacylase (aminoacylase 2, Canavan
35	454076	AW204712	Hs.61957	ESTs
	417275	X55578	Hs.255449	perlecan
	412636	NM_004415	Hs.15692	desmoplakin (DPL, DPK)
	409743	N48721	Hs.163506	hypothetical protein FLJ114213
	424645	NM_014682	Hs.151449	KIAA0535 gene product
40	427322	AK000017	Hs.176227	hypothetical protein FLJ111155
	446380	AF233393	Hs.14592	hypothetical protein FLJ111151
	444409	A1752140	Hs.45265	ESTs
	409031	AA376836	Hs.288956	ESTs
	408428	NM_014787	Hs.44956	Deaf (hep40) homolog, subfamily B, membe
45	428414	AL049860	Hs.184216	DNFZP66AC152 protein
	428574	W32133	Hs.154365	transferrin (transferrin, amyloidosis t
	420605	BC381491	Hs.99291	HSPC156 protein
	445618	H79667	Hs.237542	Homo sapiens cDNA FLJ12052.6, clone HE
	450715	AE26484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein
50	428506	BC252383	Hs.184669	SBB131 protein
	434064	AL049045	Hs.180758	hypothetical protein PRO0802
	410330	AW023630	Hs.159425	ESTs
	426471	M22440	Hs.170009	transforming growth factor, alpha
	409231	AA446644	Hs.652	CD43-2 antigen; epithelial glycoprotein
55	448558	AB020651	Hs.22653	KIAA0844 protein
	428465	AW570676	Hs.253653	ESTs
	429470	A1878931	Hs.203862	guanine nucleotide binding protein (G pr
	432296	AL118112	Hs.214253	Homo sapiens mRNA, cDNA DKFZp761G11111 (f
	427061	AB020571	Hs.173392	KIAA1145 protein
60	430261	AA355127	Hs.237225	hypothetical protein HT023
	435145	A1727259	Hs.116631	ESTs
	416101	R24654	Hs.268903	ESTs
	428716	NM_006379	Hs.171021	sera domain, immunoglobulin domain (Ig)
	438202	AW169287	Hs.25688	ESTs
65	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24405 hypothes
	419566	AL137539	Hs.40096	ESTs
	430573	AA744550	Hs.136245	ESTs
	422546	AB007969	Hs.301478	KIAA0500 protein
	453344	BC349075	Hs.44571	ESTs
70	417620	R02530	Hs.191198	ESTs
	421952	AA303900	Hs.58689	ESTs, Moderately similar to AF161511.1 H
	414631	AW570130	Hs.65496	ESTs
	437073	A885808	Hs.94122	ESTs
	441264	AA327170	Hs.23280	ESTs
75	433629	R13140	Hs.13359	ESTs
	415114	D66468	Hs.94181	ESTs
	417770	NM_014278	Hs.71992	heat shock protein (hsp110 family)
	415665	H72693	Hs.302754	gb-yu03c11.1 f1 Scores fetal liver spleen
	416851	AW963951	Hs.85618	ESTs
80	433037	AW502305	Hs.8906	ginsenoside
	448511	AA361167	Hs.296261	guanine nucleotide binding protein (G pr
	427176	AW381569	Hs.40334	ESTs
	438704	AA33060	Hs.32825	ESTs
	417175	RA4558	Hs.94002	ESTs
85	430663	A073824	Hs.5232	HSPC125 protein
	450712	RA1480	Hs.302754	ESTs
	405354			CX000321.g6671579refNP_031518.1.1 ar
90	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyltransferase

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429676	AB028577	Hs.225974	KIA1054 protein	3.3
434348	BE393191	Hs.181795	putative b-carotene-9,10-dioxygenase	3.3
441071	D79550	Hs.7149	Homo sapiens cDNA: FLJ21950 fls, clone H	3.3
445275	RA1900	Hs.22245	ESTs	3.2
445451	BE293116	Hs.76352	aldolase dehydrogenase 1 family, member	3.2
448072	AA59306	Hs.42908	ESTs	3.2
402425			Target Exon	3.2
433328	AW298159	Hs.23644	ESTs, Weakly similar to S65824 reverse t	3.2
402138			Est Contral	3.1
441327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypothetical	3.1
459399	BE407712	Hs.153996	craline kinase, mitochondrial 1 (ubiqui	3.1
433582	BE548749	Hs.148016	ESTs	3.1
434104	AF116691	Hs.116459	hypothetical protein PRO2198	3.0
404506			Target Exon	3.0
407173	T64349		glycylidox06 s1 Skatogene lung (937210) H	3.0
415672	NS3097	Hs.193579	ESTs	3.0
446583	NM_015239	Hs.21542	KIA1035 protein	3.0
429643	AJ824977	Hs.145319	ESTs	3.0
439165	AA029517	Hs.95162	KCNQ1 overlapping transcript 1	2.9
445561	A1022240	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.9
436427	A1344378	Hs.143399	ESTs	2.9
425403			Target Exon	2.9
452197	AW023555	Hs.232048	ESTs	2.9
437357	AL355559	Hs.331666	Homo sapiens mRNA, cDNA DKFZp76202215 (I	2.9
439272	AAR32474	Hs.25851	ESTs	2.9
415839	RA0511	Hs.94954	ESTs	2.9
411596	AW875765		gh-CV2-PT00012-020500-186-a08 PT00012 Homo	2.9
409403	AA665224	Hs.6534	Homo sapiens cDNA: FLJ22547 fls, clone H	2.9
412258	AA376788	Hs.324841	hypothetical protein FLJ22622	2.8
435636	AW292532	Hs.343657	homolog of yeast long chain polyunsatura	2.8
433105	HE5907	Hs.162430	EST	2.8
404563			Target Exon	2.8
427974	BE093023	Hs.188767	ESTs	2.8
413324	VO0571	Hs.75294	corticotropin releasing hormone	2.7
405263	AA063673	Hs.50319	ESTs	2.7
464247	AJ243950	Hs.46785	deafness locus associated putative gnan	2.7
449150	AI633836	Hs.195649	ESTs	2.7
446004	D11650	Hs.295254	Homo sapiens cDNA: FLJ23557 fls, clone L	2.7
421694	AW564525		gh-EST136555 MAGE resequences, MAGE Homo	2.7
430371	DE0456	Hs.240112	KIAA0275 protein	2.7
445117	AW445310	Hs.210052	ESTs, Weakly similar to HSS2_HUMAN HEPAR	2.7
451007	H38106	Hs.32755	ESTs	2.7
414502	AL133721	Hs.224650	ESTs	2.7
485753	NC0159	Hs.121645	microtubule-associated proteins 1A/1B li	2.7
489053	AI807062	Hs.210361	ESTs	2.7
427229	AI799751	Hs.5635	ESTs	2.7
429649	U30530	Hs.155540	UDP glucosyltransferase 8 (UDP-galactose	2.7
444522	AJ521750	Hs.144971	Homo sapiens cDNA FLJ13752 fls, clone PL	2.7
433921	AA518174		gh-nw14801.s1 NC_CGAP_Thy1 Homo sapiens	2.7
414272	AI651603	Hs.46588	ESTs	2.7
416047	R37633	Hs.4647	ESTs	2.7
421089	AB037771	Hs.101799	KIAA1350 protein	2.7
416455	U33632	Hs.75351	potassium channel, subfamily K, member 1	2.6
414250	AI565891	Hs.71721	ESTs	2.6
433703	AA210653	Hs.3532	nemo-like kinase	2.6
406739	W01556	Hs.238797	ESTs, Moderately similar to B30022 hypot	2.6
414602	AW633086	Hs.76549	Homo sapiens mRNA; cDNA DKFZp56481264 (I	2.6
422137	A235885	Hs.112180	zinc finger protein 148 (pH2-52)	2.6
442023	A178787	Hs.144549	ESTs	2.6
421709	AA159394	Hs.107056	CEP-6 protein	2.6
426747	AA335210	Hs.171995	kallikrein 3, (prostate specific antigen	2.6
412244	AW548175		gh-RCO-M1013-280300-Q21-c10 M10013 Homo	2.6
413386	A236867		ESTs, Weakly similar to B30222 hypothet	2.6
423655	BE167153	Hs.24380	ESTs	2.6
430320	BE245290	Hs.235218	uncharacterized hypothalamus protein HCD	2.6
420468	AB09712	Hs.53837	phosphatidylcholine transfer protein, m	2.6
410657	AF063228	Hs.65348	dynam, cytoplasmic, intermediate polype	2.6
448871	BE516709	Hs.159265	kruppel-related zinc finger protein hckr	2.6
414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypothet	2.6
455080	AW152063	Hs.290655	ESTs	2.5
455940	AW652286		gh-CV2-CT0225-100406-167-a08 CT0225 Homo	2.5
435712	AA694607	Hs.176956	ESTs	2.5
431662	AA513405	Hs.152307	ESTs	2.5
435592	AA708767	Hs.257726	ESTs	2.5
435624	T64297		aryl acid binding protein 1, liver	2.5
443155	RS4465	Hs.23772	ESTs	2.5
439183	AW576060	Hs.300261	ESTs	2.5
426365	AA379567	Hs.10283	RNA binding motif protein 8B	2.5
429033	D59502	Hs.292390	ESTs	2.5
408436	AB011150	Hs.100560	KIAA0606 protein	2.5
440205	T86950	Hs.105448	ESTs, Weakly similar to B34087 hypothet	2.5
448786	BE048842	Hs.173075	Homo sapiens cDNA FLJ11861 fls, clone HE	2.5
432251	AW972563	Hs.232165	polycythemia rubra vera 1, cell surface	2.5

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5	427115	AW972853	Hs.112237	ESTs	2.4
	433670	AA604405	Hs.293875	ESTs	2.4
	452022	AW072330	Hs.176227	hypothetical protein FLJ11155	2.4
	408814	NC2499	Hs.63469	Target Exon	2.4
	403949	AA397540	Hs.60293	Homo sapiens clone 122462 unknown mRNA	2.4
10	451926	AW134519	Hs.36125	Homo sapiens. Similar to clone FLB3816,	2.4
	443622	AB11527	Hs.11805	ESTs	2.4
	456791	H05202	Hs.133968	EGF receptor activating protein 1	2.4
	414572	A074038	Hs.48504	ESTs. Moderately similar to ALLUS_HUMAN A	2.4
	451522	BE565817	Hs.26498	hypothetical protein FLJ21657	2.4
15	422414	AW875237	Hs.13701	ESTs	2.4
	425383	D83407	Hs.155057	Down syndrome critical region gene 1-lik	2.4
	438066	AA336519	Hs.33523	ESTs. Weakly similar to 2105950A B cell	2.4
	410240	AL157424	Hs.61289	synaptotagmin 2	2.4
	432408	N39127	Hs.181340	ESTs. Weakly similar to A46010 X-linked	2.4
20	458227	Z40670	Hs.181340	ESTs	2.4
	431325	AW028751	Hs.5794	ESTs. Weakly similar to 2105950A B cell	2.4
	401600	BE247275	Hs.146504	US c-mRNP-specific protein, 116 kd	2.3
	422963	M79141	Hs.13234	ESTs	2.3
	444897	AW137088	Hs.144857	ESTs	2.3
25	418207	C1685	Hs.34772	ESTs	2.3
	445071	A082046	Hs.146504	ESTs	2.3
	407868	NM_000950	Hs.40637	proline-rich Glu (G-carboxyglutamic acid	2.3
	433331	A0738815	Hs.117323	ESTs	2.3
	442293	A004193	Hs.22123	ESTs	2.3
30	428650	AA549475	Hs.163076	ESTs	2.3
	401783		NM_003771*	Homo sapiens keratin, hair, a,	2.3
	419763	A039691	Hs.127486	ESTs	2.3
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	2.3
	420912	AW651156	Hs.90787	ESTs	2.3
35	442097	AW015799	Hs.128474	ESTs	2.3
	425907	AA365752	Hs.159565	ESTs	2.3
	404091			Target Exon	2.3
	414106	BE300325	Hs.77135	RNA binding protein	2.3
	454286	BE222048	Hs.241432	ESTs. Highly similar to c380A1.1b [H.sap	2.3
40	441040	AW448782	Hs.178003	ESTs	2.3
	424724	T06532	Hs.287709	Homo sapiens cDNA: FLJ22674 fs, clone H	2.3
	441679	A021256	Hs.107149	novel protein similar to archaical, yeast	2.3
	407388	N41760	Hs.285107	hypothetical protein FLJ13307	2.2
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 [CDC31 yeast	2.2
45	458676	A082454	Hs.202263	ESTs	2.2
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.2
	453538	AF062669	Hs.36794	D-type cyclin-interacting protein 1	2.2
	407378	AW385129	Hs.41717	phosphodiesterase 1K, calmodulin-depende	2.2
	420548	AA276246	Hs.920	ESTs	2.2
50	422907	A079263	Hs.77273	Human glucose transporter pseudogene	2.2
	446351	AW444551	Hs.35380	x 001 protein	2.2
	442117	AW64064	Hs.128599	ESTs, hypothetical protein for IMAGE-447	2.2
	429598	AA811257	Hs.269710	ESTs	2.2
	408480	A1350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	2.2
55	411361	AW639073	Hs.98002	ESTs	2.2
	459897	AA402062	Hs.100660	gr-CM2-L100660-030100-109-006 L100660 Homo	2.2
	429856	AW802082	Hs.98002	gr-LH-HF-BR0p-sig-g-04-0-LH.r1 NH_MGC_5	2.2
	444760	A0796296	Hs.208062	ESTs	2.2
	443258	AF169301	Hs.9098	sulfate transporter 1	2.2
60	428206	AB620643	Hs.183306	NIAA0836 protein	2.2
	410719	F07841	Hs.13026	ESTs	2.2
	413427	U31120	Hs.845	interleukin 13	2.2
	438021	AV653790	Hs.324275	WW domain-containing protein 1	2.2
	428652	AA584272	Hs.336224	transmembrane protein with EGF-like and	2.2
65	428655	U48959	Hs.211582	myosin, light polypeptide kinase	2.2
	424153	AA451737	Hs.141496	MAGE-like 2	2.2
	413303	AW836130	Hs.75277	hypothetical protein FLJ13910	2.2
	427287	NM_014903	Hs.174188	NIAA0538 protein	2.2
	440658	AB64033	Hs.195730	ESTs. Weakly similar to CTXN RAT CORTEX	2.2
70	441994	AB037763	Hs.8059	synaptotagmin IV	2.2
	449709	BE410592	Hs.23918	hypothetical protein PPS395	2.2
	408068	AW148652	Hs.167398	ESTs	2.2
	407819	AB2185	Hs.102720	ESTs	2.2
	414203	BE262170	Hs.78629	ATPase, Na7 transporting, beta 1 polypep	2.2
75	454339	AW381980	Hs.20166	gr-QV4-HF0316-091199-028-d05 HF0316 Homo	2.2
	448045	AL0297436	Hs.20166	prostate stem cell antigen	2.2
	458480	A0792298	Hs.20166	p20 DBC protein	2.2
	445815	AW973300	Hs.293813	ESTs	2.2
	458547	AW0204314	Hs.170784	ESTs	2.2
80	411678	A0907114	Hs.71465	squalene epoxidase	2.1
	444783	AK001468	Hs.62180	anillin (Xenophila Scrops homolog), act	2.1
	424632	AB014523	Hs.151406	NIAA0623 gene product	2.1
	445901	AB74072	Hs.151406	gr-HFD01-x1 Scars, NFL_2_GBC_S1 Homo s	2.1
	431583	AL024613	Hs.262476	S-adenosylmethionine decarboxylase 1	2.1
	410538	AW531115	Hs.262476	gr-pMG-C10248-131099-001-h12 CT0248 Homo	2.1
	426775	AA384954	Hs.3628	ESTs	2.1

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433862	D86960	Hs.3610	KIAA0205 gene product	2.1
458694	F12832	Hs.3610	ESTs	2.1
417063	N50515	Hs.45061	ESTs	2.1
416935	AA190712	Hs.2954	gB:zp67093.r1 Stratagene HeLa cell s3 s93	2.1
439489	AJ172269	Hs.121429	zinc-binding protein Rfco728	2.1
431128	AJ203545	Hs.296169	S-phase response (cyclin-related)	2.1
442310	AF033199	Hs.8196	zinc finger protein 204	2.1
434344	AL161977	Hs.2954	PCTAIRE protein kinase 3	2.1
400338	Z57131	Hs.246209	H2A histone family, member F, pseudogene	2.1
432266	AK000385	Hs.274222	hypothetical protein FLJ20378	2.1
414759	AW295157	Hs.47587	ESTs	2.1
438219	AJ916151	Hs.257154	ESTs	2.1
451336	AJ284443	Hs.3610	ESTs	2.1
430338	AB032435	Hs.242821	differentiation-associated Na-dependent	2.1
413493	BE144444	Hs.141199-002-009	HT0168 Homo	2.1
428501	AL041162	Hs.98587	ESTs	2.1
431568	AW972316	Hs.283303	ESTs	2.1
456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	2.1
441976	AA428403	Hs.106131	ESTs	2.1
421311	N71848	Hs.283609	hypothetical protein PRO2032	2.1
428358	AA593222	Hs.101915	Stargardt disease 3 (autosomal dominant)	2.1
439973	AJ733368	Hs.124663	ESTs	2.1
445185	AJ279191	Hs.148454	ESTs, Weakly similar to DSR5_HUMAN DOWN	2.1
451606	AA018791	Hs.7345	AIE-75 binding protein protein	2.1
433516	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypothe	2.1
441987	AW452234	Hs.128293	ESTs	2.1
457140	AJ279960	Hs.178140	ESTs	2.1
414055	AW819587	Hs.5366	hypothetical protein FLJ21522	2.1
445066	BE178734	Hs.197422	ESTs	2.1
459265	AJ300316	Hs.914003616	Selected chromosome 21 cDNA	2.0
425337	AA355442	Hs.169564	ESTs	2.0
400339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi	2.0
453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.0
420065	AW961959	Hs.96540	ESTs	2.0
425308	AL046716	Hs.154387	KIAA0163 gene product	2.0
444700	NM_0018645	Hs.11725	olity acid Cysteine A ligase, very long-	2.0
424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.0
450103	R08665	Hs.17244	hypothetical protein FLJ13605	2.0
448519	AW175665	Hs.278955	Homo sapiens protein mRNA, complete cds	2.0
440808	AK001339	Hs.7452	hypothetical protein FLJ10477	2.0
429968	AA322503	Hs.227011	G-substrate	2.0
429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	2.0
433068	NM_006496	Hs.288215	sialyltransferase	2.0
416982	J06401	Hs.80891	creatine kinase, mitochondrial 2 (sarcom	2.0
423479	NM_014326	Hs.125208	death-associated protein kinase 2	2.0
407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
452625	AA724771	Hs.61425	ESTs	2.0
410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member	2.0
409767	AW501470	Hs.202341	gB:UAF-BPp-gB-s-03-s-U1.1 NH_MGC_5	2.0
415925	H09474	Hs.200341	Homo sapiens cDNA: FLJ23753, clone L, C2000627, p7[2034653]igB/A045951.1JAF22	2.0
408206	AF041853	Hs.43670	kinasin family member 3A	2.0
456660	AJ299739	Hs.99601	hypothetical protein FLJ12553	2.0
432278	AL137506	Hs.274258	hypothetical protein FLJ23563	2.0
404559			Target Exon	2.0
403728			Target Exon	2.0
413055	AJ655701	Hs.75183	cytochrome P450, subfamily 11E (ethanol-	2.0
407786	AA480738	Hs.38972	retrospan 1	2.0
413266	BE300352	Hs.600944231F1	NH_MGC_17 Homo sapiens c	2.0
453994	BE180964	Hs.165590	ribosomal protein S13	2.0
451583	AJ653797	Hs.24133	ESTs	2.0
443344	AJ457235	Hs.189479	ESTs	2.0
453396	AW162768	Hs.22620	ESTs	2.0
415954	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11	2.0
459511	AI142379	Hs.315970	gB:zg64c01 r1 Soares_westc_NHT Homo sap	2.0
450757	BE081050	Hs.315970	ESTs, Weakly similar to KIAA1324 protein	2.0
451032	WE0392	Hs.323079	Homo sapiens mRNA, cDNA DKFZp556P116 (t	2.0
440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypothe	2.0
446447	H14718	Hs.11506	Human clone Z35B9 mRNA sequence	2.0
447932	AA637474	Hs.20021	vesicle-associated membrane protein 1 (s	2.0
444749	AJ190572	Hs.65926	ESTs	2.0
446277	AI284218	Hs.159204	ESTs	2.0
452550	AA026735	Hs.326048	Homo sapiens mRNA, cDNA DKFZp434V0420 (f	2.0
453843	D25215	Hs.36804	hecl domain and RLD 3	2.0
445725	AA000565	Hs.13209	hypothetical protein FLJ10094	2.0
409255	T78737	Hs.321052	ESTs	2.0

TABLE 22B:

Phy: Unique Eos probe-set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Phy	CAT Number	Accession
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5	409757	1154015_1	AW61470 AW502931 AW489500
	409866	1156268_1	AW62302 AW502979 AW502907 AW501876
	410538	1207341_1	AW753115 AW753113 R45779
	411361	1240611_1	AW839073 AW839234 AW839230 AW878302 AW839109 AW843897
	411906	1262304_1	AW857955 AW50294 AW875444
10	412244	1284982_1	AW84175 AW847637 AW82689 AW847537 AW847531 AW847532 AW847530
	412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW575299 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361143
			AW456274 AW857139 AW793004 AW793009 BE007020 BE007017 BE185187 AW987196 BE156621 BE179915 BE060561 BE143155 AW830985
			BE002107 AW103521 AA857316 AW838133 BE011378 AW170253 BE185750 AW888476 BE160433 J05211 BE082676 BE032584 BE004047
			AW002238 AW377700 AK217999 BE082525 BE082905 BE082507 BE082514 AW170000 AW177933 AW95935 AW147877 AW748114 BE148516
15			AW855232 AW847673 AW847688 AW836511 AW365148 AW365153 AW365156 AW365175 AW365157 AW065840 AW065872 AW365145
			BE019125 BE12166 BE144243 BE001823 AW51766 AW434518 BE184820 BE184333 AL024090 BE184941 AW804074 BE184924 CO4715 W33488
			AW959515 BE184948 BE159646 AW065653 AW069891 AA131128 AA133720 AA340777 AW364371 AA352212 RS5704 AW365566 AW364959
			AW025851 AW025852 AW455100 AA179558 AW552200 AW552205 BE165351 BE073467 AA371727 AW892624 AW509730 AW391912 AW849690
			T07267 AW85312 AW822113 W74149 BE009090 AW856401 HS1011 AW838329 AW838207 C18467 AW854920 NS5716 AW024580 AW857657
20			H93284 AW063816 AW177787 AW026654 AW177786 BE092134 BE092136 AW177784 A1022962 BE091653 AW376811 AW848692
			AAQ40018 BE185331 BE182164 AA368584 AW951516 T29918 AA131077 W95048 AW250789 H08089 N20754 W32490 R20904 BE167181
			BE167155 AW47671 1027408 J03146 AW1190590 C03376 AW554405 AW026563 AA128470 AW829208 AF139855 AW370813 AK770827 AW758417
			AW793780 AW758583 AW795589 R33557 AA146150 C03329 AW177783 AW08886 AW370825 AA474565 BE002273 AW80816 AA439101 AW794541
			AW109563 AA451923 AL040326 AW50975 T48793 AW568096 AA142882 AW039975 AA470146 AW466936 BE067737 BE067786 W15287 AA644381
25			AA702424 AA17612 AL030554 AW86868 AW568892 AW190555 AW150705 AW020573 AW065627 AW1871874 A1304772 AW518728 AW515596 AW527833
			A1273345 AW021347 AW166807 AW105614 AW046078 AA552300 W95970 AW49083 AW11702 AA149181 AW026884 AW30049 AW87258 AW750435
			AW15434 AW489984 AW58282 AW078448 AW025532 AW850564 AW438978 AW020647 AW103322 D12082 AW152026 AW455814 AW514557 AW591892
			T07181 AA782066 AW243815 AW150038 AW268383 AW004633 A1827707 AA782109 AW342323 A1804485 AW168216 AW572659 AA002182
			AW015480 AW771865 A1270027 AA961816 AA263207 AW76592 AW84887 AW348053 AW183914 H44405 AW779118 AA126330 AA515500 AA918281
30			W02116 AW805927 AW022701 W038382 R20795 W77861 AW860878
			BE300352 BE299274 BE075351 BE297444
			BE14444 BE144430
			W72593 R06673 W72634 F20990 R08580
			AA190712 AA190665 AA252564
35			AA236857 AA237066 AA354238 AW957759 AW8961
			AW54525 A137205 AA354901 AD27887 H10564
			N39127 F20776 AW82691 AW855520 F35964 F33894
			AA604405 BE062234 AW748366
			AA618174 A114548 R36484 R36465
40			T64297 AW894331 NM_001443 AW841309 AW89816 T53219 T48795 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617
			AW76586 AA101894 W93038 AW742193 AW752206 AA099433 T53220 AW828135 AW72775 T29562 T55862 A134304 AW345671 T68235 T68121
			AW842294
			AW74072 BE268487
			AW81980 BE152244 BE152226 BE152236 BE152232
45			AW86226 AW051814 AW829066 AW62274
			A179228 H14121 A1375113 AW860851 AA744592 AW674839 AA296360 AW29605
			AJ003616 AJ003654 AJ003617
TABLE 22C:			
Ref: Unique number corresponding to an Eos probe			
Sequence source: The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA			
sequence of human chromosome 22" Dunham, et al. (1999) Nature 402: 489-495.			
Stand Indicates DNA strand from which exons were predicted.			
NI_position: Indicates nucleotide positions of predicted exons.			
	Play	Ref	Strand NI_position
55	401600	4389746	Minus 27363-27518.28727-28891.29526-29731
	401783	7249190	Minus 130569-136577.140509-140591.140834-140990.141496-141657.141757-141882.142063-142283
	402429	9796372	Minus 57622-57793.58249-59402.59624-59827
	403469	9929739	Minus 4831-7707
	403728	7534291	Minus 34481-34671
60	404091	7645454	Minus 62121-63229
	404559	8148953	Minus 73459-73651.89575-89739
	404563	9638310	Plus 100136-100343
	404806	9212936	Minus 22210-23269
	405354	2642452	Plus 52713-53089
65	405403	6650244	Plus 37491-37670.40951-41031
	405670	4662655	Plus 96543-96870
TABLE 23A: ABOUT 441 GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS			
Table 23A lists about 441 genes significantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from between 59680 probesets			
on the Affymetrix/Exon HuD1 GeneChip array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2.5. The "average" normal CNS level was set			
to the 75 th percentile amongst various normal CNS tissues. The "average" LGG level was set to the 95 th percentile amongst various tumor samples. In order to remove gene-specific			
background levels of non-specific hybridization, the 10 th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before			
the ratio was evaluated.			
	Play	Unique Eos probe identifier number	R1
75	Ex/Con:	Exemplar Accession number, Genbank accession number	R1
	UnigeneID:	Unigene number	10.1
	Unigene Title:	Unigene gene title	10.1
	RT:	Ratio of CNS to LOWER GRADE GLIOBLASTOMA	9.9
			7.8
80	Play	Ex/Con:	UnigeneID
	15388	U471801	Unigene Title
	18318	U47732	corigin, type XVII, alpha 1
	44529	H14421	transmembrane 4 superfamily member 3
	417433	BE270266	ATP-binding cassette, sub-family A (ABC) 1

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422745	NM_004484	Hs.119651	glypican 3	7.7
448362	AA641757	Hs.21015	hypothetical protein DKFZp564l0864 simil	7.7
430573	AA744550	Hs.136345	ESTs	7.6
415274	AF001546	Hs.78344	myosin, heavy polypeptide 11, smooth mus	7.5
419290	A1128114	Hs.112865	spinal cord-derived growth factor-8	7.4
424670	W61215	Hs.116651	epithelial V-IIIe antigen 1	7.3
417157	AW006437	Hs.4290	ESTs	7.3
416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	7.3
424632	AB014523	Hs.151406	KIAA0823 gene product	6.9
453165	574727	Hs.12042	aspartacylase (aspartacylase 2, Canavan	6.5
411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	6.5
435272	AA832474	Hs.25851	ESTs	6.3
414631	M01158	Hs.17439	protein kinase, cAMP-dependent, regulate	6.4
454075	AW004712	Hs.61567	ESTs	6.3
446390	AA233393	Hs.14992	hypothetical protein FLJ11151	6.3
430865	A073424	Hs.5232	HSPC125 protein	6.3
434064	AL049045	Hs.180758	hypothetical protein PRO00082	6.2
414158	NM_005555	Hs.62173	TGF-beta inducible early growth response	6.1
412636	NM_004415		desmoglein (DPI, DPII)	5.0
409743	N48721	Hs.183506	hypothetical protein FLJ14213	5.9
430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	5.8
434725	AK0020795	Hs.4104	hypothetical protein	5.6
417175	RA4558	Hs.94002	ESTs	5.6
417275	X63578	Hs.25449	parvalbumin	5.5
427322	AK002017	Hs.176227	hypothetical protein FLJ11155	5.5
431029	BE149762	Hs.40566	gap junction protein, beta 6 (connexin 3	5.4
420297	AF082272	Hs.98323	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.4
412472	AW575398	Hs.293836	ESTs	5.4
443258	AF169301	Hs.9098	sulfate transporter 1	5.3
427710	BE396263	Hs.173567	eukaryotic translation initiation factor	5.3
442694	AK220867	Hs.80694	ESTs	5.2
438858	AW246243	Hs.334900	hypothetical protein FLJ20974	5.2
444409	A1792140	Hs.49265	ESTs	5.2
442310	AF033159	Hs.8198	zinc finger protein 204	5.1
409031	AA378636	Hs.288955	ESTs	5.1
438460	AB020702	Hs.6224	KIAA0855 protein	5.1
411939	A1365585	Hs.146246	ESTs	5.0
448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	5.0
413293	AL047463	Hs.302498	GTP-binding protein homologous to Saccha	5.0
402668	BE52226	Hs.43376	hypothetical protein FLJ20544	5.0
443491	AW499655	Hs.9456	SWI/SNF related, matrix associated, acti	4.9
448950	AF005513	Hs.22670	chromodomain helicase DNA binding protei	4.9
416101	R24854	Hs.268605	ESTs	4.9
432559	A4632757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	4.9
424645	NM_014482	Hs.151449	KIAA0535 gene product	4.8
437679	NM_014214	Hs.5753	inositol(1myo)-[or (4)-]-monophosphatase 2	4.8
408428	NM_014787	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe	4.8
414502	AL133721	Hs.224680	ESTs	4.8
442572	A051922	Hs.136121	hypothetical protein FLJ22415	4.8
412700	BE222433	Hs.236208	ESTs, Weakly similar to B30222 hypotheti	4.8
422603	BE242587	Hs.118651	hematopoietically expressed homeobox	4.8
424605	BE391491	Hs.39251	HSPC156 protein	4.7
422482	A1439005	Hs.344476	ghb57g06.s1 NC2_CGAP_Lym12 Homo sapien	4.7
415639	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	4.7
409263	AA089573	Hs.50319	ESTs	4.7
410557	AF063228	Hs.85248	dyenin, cytoplasmic, intermediate polype	4.6
457216	AA452554	Hs.253697	ESTs, Weakly similar to A41796 neural re	4.6
434323	BE407127	Hs.8597	heat shock 70kD protein 1A	4.6
449091	A1674072		gh.wd1Sh01.x1 Soares_NFL_T_GBC_S1 Homo s	4.6
445518	H79657	Hs.237642	Homo sapiens cDNA FLJ120522 lis, clone HE	4.6
431582	F07136	Hs.261828	G protein-coupled receptor kinase 7	4.5
424675	NM_005512	Hs.151841	glycogenin A, repetitive predominant	4.5
449511	A1436187	Hs.292261	guanine nucleotide binding protein (G pr	4.5
401600	BE247275		US snRNP-specific protein, 116 kD	4.5
447135	T58148		ghy59g06.s1 Stratiogene lung (307270) H	4.5
422689	BE245650	Hs.171825	basic helix-loop-helix domain containing	4.4
429598	AA811257	Hs.269710	ESTs	4.4
428206	AB020643	Hs.183006	KIAA0836 protein	4.4
450715	A1269484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	4.4
426506	BE523363	Hs.184668	SBBT31 protein	4.4
435145	A277225	Hs.116631	ESTs	4.4
405670			C20005277.g112034653[gh]AAG45551.1AF22	4.4
442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (4.3
427670	BE512888	Hs.180224	myosin regulatory light chain	4.3
428465	AW970976	Hs.203653	ESTs	4.3
449180	AK633836	Hs.195649	ESTs	4.3
402354	AV553231		CCAA1/Enhancer binding protein (CEBP),	4.3
426471	M22440	Hs.170009	transforming growth factor, alpha	4.2
413386	AA239667		ESTs, Weakly similar to B30222 hypotheti	4.2
441408	A1733249	Hs.126897	ESTs	4.2
419631	AW188117	Hs.303154	popeye protein 3	4.2
406231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.2
448958	AB020651	Hs.22553	KIAA0844 protein	4.2

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421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fs, clone HE	4.2
422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	4.2
459053	A807052	Hs.210361	ESTs	4.1
459500	BE79478	Hs.24880	ESTs	4.1
415839	R40611	Hs.84694	ESTs	4.1
450374	AA397540	Hs.80293	Homo sapiens clone 122482 unknown mRNA	4.1
422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (predi	4.1
405674			NM_022775 Homo sapiens hypothetical prot	4.1
453908	AW444652	Hs.757054	ESTs	4.1
419319	AW969742	Hs.291005	ESTs	4.0
456382	NM_001126	Hs.90011	adenylosuccinate synthase	4.0
435902	A4701867	Hs.297726	ESTs	4.0
444843	AK001971	Hs.23507	hypothetical protein FLJ11189	4.0
434228	Z42047	Hs.283978	Homo sapiens PR02751 mRNA, complete cds	4.0
403890			C50C2036"gt[1024514]emb(CAC09416.1) (A	4.0
429470	A1878901	Hs.203862	guanine nucleotide binding protein (G pr	4.0
409856	AW502082		gb:U1-HF-6R0p-agg-g-04-0-UR.1 NIH_MGC_53	4.0
443692	A2353061	Hs.47248	ESTs, highly similar to similar to Cdc14	4.0
402230	AL034344	Hs.284186	forkhead box C1	4.0
410509	AW840743		gb:QV1-CN0002-080300-102-007 CN0002 Homo	4.0
428414	AL049880	Hs.184216	DKF2P564C152 protein	3.9
400138			Eos Control	3.9
451522	BE565817	Hs.26498	hypothetical protein FLJ21657	3.9
436521	AW203966	Hs.213003	ESTs	3.9
401507			C150C0810"gt[111312728]pP79331YAT52_B0	3.9
449785	A2252325	Hs.288300	hypothetical protein FLJ23231	3.9
434815	AF155992	Hs.46744	core1 UDP-galactose 4-epimerase/galactosamin	3.9
411906	AW807855		gb:QV2-PT00102-020500-185-a08 PT0012 Homo	3.9
440509	BE410132	Hs.134202	ESTs, Weakly similar to T12729 hypothet	3.9
420761	AB030291	Hs.173392	KIAA1145 protein	3.9
432021	AA351127	Hs.237225	hypothetical protein NT023	3.9
449658	AB640333	Hs.195730	ESTs, Weakly similar to CTXN RAT CORTEXI	3.9
429876	AB028977	Hs.225974	KIAA1054 protein	3.8
410330	AW023630	Hs.159425	ESTs	3.8
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (3.8
437659	AB007944	Hs.5737	KIAA0475 gene product	3.8
438171	AW976507	Hs.293515	ESTs	3.8
418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	3.8
405856			NM_000299 Homo sapiens pitagophilin 1 (cc	3.8
432298	AL118812	Hs.274293	Homo sapiens mRNA: cDNA DKF2p7615111 (f	3.8
426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.8
438202	AW169287	Hs.22568	ESTs	3.8
404606			Target Exon	3.8
425329	A1961644	Hs.145444	Homo sapiens cDNA FLJ11494 fs, clone HE	3.8
407604	AW191962	Hs.288061	collagen, type VIII, alpha 2	3.8
416498	U33632	Hs.79361	potassium channel, subfamily K, member 1	3.7
403868	W93178	Hs.5232	HSPC125 protein	3.7
457008	AA410448	Hs.112011	ESTs, Weakly similar to unknown (Hsapie	3.7
458660	A1299739	Hs.99021	hypothetical protein FLJ12553	3.7
408732	AL117490	Hs.47225	Ras-associated protein Rap1	3.7
436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.7
413493	BE144444		gb:MR04-H70168-141195-002-009 HT0165 Homo	3.7
418407	AL244818	Hs.84928	nuclear transcription factor Y, beta	3.7
454797	A253414	Hs.180513	gb:aa140L.v1 Stanley Frontal NS pool 2	3.7
457121	A1743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	3.6
417620	RD2530	Hs.191196	ESTs	3.6
421952	AA302902	Hs.58849	ESTs, Moderately similar to AF161511.1 H	3.6
454247	AJ243950	Hs.467195	death locus associated putative guani	3.6
431662	AA513406	Hs.152307	ESTs	3.6
426908	AW815163	Hs.172851	arginase, type II	3.6
438519	A1186033	Hs.147025	ESTs, Weakly similar to CS7785 zinc fing	3.6
415606	W73022		gb:aa5140L.v1 Soares_tetal_hear_hn19W	3.6
444859	AW449137	Hs.157487	ESTs	3.6
414631	AW970130	Hs.65406	ESTs	3.6
428897	AJ245719	Hs.194385	hypothetical protein FLJ20234	3.5
437073	AB858608	Hs.94122	ESTs	3.5
477287	NM_014903	Hs.174168	KIAA0938 protein	3.5
415927	AL120168	Hs.78919	Kell blood group precursor (McLeod pheno	3.5
450235	AA007512	Hs.17538	ESTs	3.5
447263	AW985667	Hs.324706	hypothetical protein FLJ11494	3.5
419440	AB500389	Hs.59019	KIAA0882 protein	3.5
427754	AL121523	Hs.97774	ESTs	3.5
434348	BE393191	Hs.181795	putative b3-carotene 9',10'-dioxygenase	3.5
441264	AA927170	Hs.23290	ESTs	3.5
433629	R13140	Hs.133938	ESTs	3.5
446494	AA463276	Hs.288906	WW Domain-Containing Gene	3.5
441585	A1760755	Hs.202283	ESTs	3.5
438704	AA135060	Hs.32825	ESTs	3.4
445279	RA1960	Hs.227245	ESTs	3.4
415114	D60468	Hs.94183	ESTs	3.4
449561	A1022240	Hs.17924	ESTs, Moderately similar to ALLU1_HUMAN A	3.4
452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.4
416517	AA775987	Hs.79357	proteasome (prosome, macropain) 26S subu	3.4

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5	441134	W79052	Hs.348550	cellular retinoic acid-binding protein 1	3.4
	427176	AW381569	Hs.40334	ESTs	3.4
	415668	AW957684	Hs.306814	hypothetical protein FLJ21889	3.4
	450928	A0744417		gb t10h12.x1 NC1_CGAP_Ov23 Homo sapiens	3.4
	457072	R41480	Hs.302754	ESTs	3.3
10	405354			CX000321:gb6671573yallNP_031518.1) ori	3.3
	408855	T83061	Hs.319546	Homo sapiens mRNA for KIAA1727 protein,	3.3
	418525	AW450369	Hs.86637	ESTs	3.3
	420174	A824144	Hs.23612	ESTs	3.3
	437124	AA554458	Hs.27860	KIAA0566 protein	3.3
15	419211	BE270817	Hs.37617	ESTs, Weakly similar to A53833 myosin I	3.3
	424335	AW021508	Hs.28170	ESTs	3.3
	453344	BE434975	Hs.44571	ESTs	3.3
	428965	A6524046	Hs.157133	ESTs	3.3
	417248	AA329446	Hs.247302	twisted gastrulation	3.3
20	429415	NM_002553	Hs.202097	procollagen C-endopeptidase enhancer	3.3
	411393	AW579437	Hs.69771	B-factor, properdin	3.3
	406576	M60296		gb Human alpha-1 collagen type II gene,	3.3
	441071	D75550	Hs.7148	Homo sapiens cDNA: FLJ21550 fs, clone H	3.3
	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypothei	3.3
25	433703	AA210863	Hs.3532	nemo-like kinase	3.3
	418880	N87353	Hs.89421	CBF1 interacting repressor	3.3
	445947	AW612084	Hs.266494	ESTs	3.3
	437334	AL353547	Hs.283780	hypothetical protein DKFZp761N1814	3.2
	434795	BE620794	Hs.4147	translocating chain-associating membrane	3.2
30	400127			Eos Control	3.2
	414602	AW630088	Hs.76550	Homo sapiens mRNA: cDNA DKFZp564B1264 (f	3.2
	402429			Target Exon	3.2
	428595	A1355647	Hs.189999	putative receptor (family A group 5)	3.2
	427659	AW955076	Hs.180378	hypothetical protein 669	3.2
35	403442			Target Exon	3.2
	419272	AA663304	Hs.88962	THNFRSF1a-associated via death domain	3.2
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	3.2
	407581	R48402	Hs.173508	P3ECSL	3.2
	412633	AF001891	Hs.74304	periplakin	3.2
40	433328	AW298159	Hs.23644	ESTs, Weakly similar to S55824 reverse 1	3.2
	445294	A6517786	Hs.155045	ESTs	3.1
	442799	A1564739	Hs.68505	ESTs	3.1
	434045	AJ055133	Hs.152316	hypothetical protein PRO0971	3.1
	429403	AA686224	Hs.66314	Homo sapiens cDNA: FLJ22547 fs, clone H	3.1
45	420033	D65502	Hs.292590	ESTs	3.1
	422137	AJ236685	Hs.112180	zinc finger protein 148 (pH2-52)	3.1
	444760	A1799296	Hs.208062	ESTs	3.1
	404486			ENSPO00000201948:KARYOPHERIN BETA2E HOMOL	3.1
	411359	H86088	Hs.22635	ESTs	3.1
50	443037	AW500305	Hs.8906	syntaphin 7	3.1
	407127	R45970	Hs.236349	EST	3.1
	416851	AW963951	Hs.85618	ESTs	3.1
	416838	DB4109	Hs.80248	RNA-binding protein gene with multiple s	3.1
	443030	R68048	Hs.5238	hypothetical protein FLJ23516	3.1
55	410389	AW554049	Hs.8177	ESTs, Weakly similar to PIH1B6 salivary	3.1
	459399	BE407712	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.1
	433582	BE548749	Hs.148016	ESTs	3.1
	431128	A203545	Hs.296169	S-phase response (cyclin-related)	3.1
	420411	A1581085	Hs.24678	sphingosine-1-phosphatase	3.1
60	455584	AB108884	Hs.345429	ESTs	3.1
	443983	A0004464	AA341158	gb c55646.61 Scarsc_testis_3MT Homo sap	3.1
	445320	AA503397	Hs.167011	Homo sapiens cDNA: FLJ21362 fs, clone C	3.1
	410786	AW803340		gb U2-UM0079-090300-050-D02-UM0079 Homo	3.1
	418207	C14685	Hs.34772	ESTs	3.0
65	426521	AF191534	Hs.87258	ESTs	3.0
	425980	IG4530	Hs.273294	hypothetical protein FLJ20069	3.0
	416749	AW068550.comp1a	Hs.75732	ubitin 1	3.0
	412558	AA378798	Hs.324841	hypothetical protein FLJ26222	3.0
	407173	T54345	Hs.193575	gb y1008.s1 Sitatagene lung (637210) H	3.0
70	415672	NS3057	Hs.193575	ESTs	3.0
	446883	NM_015239	Hs.21542	KIAA1035 protein	3.0
	429043	AB245777	Hs.145319	Target Exon	3.0
	430451			Target Exon	3.0
	406085	BE327427	Hs.79853	ESTs	3.0
75	457441	BE467737	Hs.146125	ESTs	3.0
	403512			C3000579:gp 2643308:gp Q29Y4K1A MI1_HUM	3.0
	415866	AA297356	Hs.80324	serine/threonine protein phosphatase cat	3.0
	438977	I05845	Hs.250700	hyaluronate beta 1	3.0
	441984	AB037763	Hs.8055	synaptotagmin IV	3.0
80	436765	AB028952	Hs.5307	synaptotagmin	3.0
	445071	A1280246	Hs.149504	ESTs	3.0
	404333			C7001725:gp 7768636:gb BA095483.1) (AB	3.0
	427907	A187263	Hs.77273	Human glucose transporter pseudogene	3.0
	413266	BE300352	Hs.193575	gb 600944231F1 NH1_MGC_17 Homo sapiens c	3.0
	425393	AA383024	Hs.201603	Homo sapiens mRNA: cDNA DKFZp434D0917 (f	3.0
	415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bndi	3.0

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415044	AA419108	Hs.77840	amnesin A4	2.9
403469			Target Exon	2.9
416928	AA190573	Hs.85902	ESTs, Weakly similar to MCHU calmodulin	2.9
430195	AW969308	Hs.108594	ESTs	2.9
458544	AK531335	Hs.196843	ESTs	2.9
440567	BE070669	Hs.7337	hypothetical protein FLJ10036	2.9
424541	AB001106	Hs.151413	glu maturation factor, beta	2.9
428820	AA436187	Hs.172631	integrin, alpha M (complement component	2.9
404503			Target Exon	2.9
457197	AW023595	Hs.232048	ESTs	2.9
437357	AL359559	Hs.331666	Homo sapiens mRNA; cDNA DKF7p76202215 (f	2.9
423479	NM_014326	Hs.125208	death-associated protein kinase 2	2.9
404559			Target Exon	2.9
406270			Target Exon	2.9
422190	H17359	Hs.115056	Human clone 23589 mRNA sequence	2.9
431300	AA502346		gb:ne26003.s1 NC1_CCA_Co3 Homo sapiens	2.9
402086	AT796395	Hs.111377	ESTs	2.9
422664	AW439476	Hs.250655	ESTs	2.9
431583	AL040613	Hs.262476	Sadenosylmethionine decarboxylase 1	2.9
428595	AB037795	Hs.166547	KIAA1374 protein	2.9
402198			NM_024323 Homo sapiens hypothetical prot	2.9
416246	U47413	Hs.79101	cyclin G1	2.9
427593	AK001132	Hs.179752	Homo sapiens cDNA FLJ10270 fls, clone HE	2.9
446351	AW444551	Hs.35380	x 001 protein	2.9
440432	AI239637	Hs.202653	ESTs, Weakly similar to T14267 Xln prote	2.9
446525	AW967069	Hs.211556	hypothetical protein M3C5487	2.8
402665			CT10021907.gi12732794exp_012163.1j	2.8
435489	AJ272269	Hs.121429	zinc-binding protein Rboc720	2.8
458793	N80159	Hs.121849	microtubule-associated proteins 1A1B b1	2.8
406810	U82275	Hs.94498	leukocyte immunoglobulin-like receptor,	2.8
445577	NC0036	Hs.137054	cytoplasmic polyanylation element bind	2.8
428874	YQ22133	Hs.194366	transferrin (transferrin, amyloidosis 1	2.8
418745	AW982645	Hs.88044	sprouty (Drosophila) homolog 1 (antagoni	2.8
433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fls, clone HE	2.8
425580	L11144	Hs.1907	galanin	2.8
416233	AA176633	Hs.257194	gb:ap13p01.s1 Stratagene fetal retina 93	2.8
438219	AT916151		ESTs	2.8
404661			C8000306.gi12737280jexp_006682.2jk	2.8
435836	AW292532	Hs.343667	homolog of yeast long chain polyunsatura	2.8
423665	BE167153	Hs.170261	ESTs	2.8
435520	BE245290	Hs.239218	uncharacterized hypothetical protein HCD	2.8
401783			NM_003771 Homo sapiens keratin, hair, a	2.8
428337	AW937063	Hs.275150	gb:PM3-DT0037-231295-001.g11 DT0037 Homo	2.8
447271	AL041747	Hs.170261	ESTs	2.8
438913	AB084429	Hs.172445	ESTs	2.8
441962	AW972542	Hs.289009	Homo sapiens cDNA: FLJ21814 fls, clone H	2.8
444385	BE278964	Hs.11085	CGI-111 protein	2.8
432278	AL137506	Hs.274258	hypothetical protein FLJ23563	2.8
415656	H72693	Hs.274258	gb:ac03111.1 Scores fetal liver spleen	2.8
452345	AA263279	Hs.29173	hypothetical protein FLJ20515	2.8
445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.8
439556	AB237552	Hs.163603	ESTs	2.8
405474			NM_001093 Homo sapiens acetyl-Coenzyme	2.8
426208	A130739	Hs.132216	ESTs	2.8
419481	A1452601	Hs.288699	nuclear receptor subfamily 2, group f, m	2.8
428501	AL041162	Hs.98387	ESTs	2.8
413427	U31120	Hs.845	interleukin 13	2.8
433109	N51907	Hs.153430	EST	2.8
427974	BE053023	Hs.188767	ESTs	2.8
455040	AW852286		gb:QV0-CT0225-100400-187-d06 CT0225 Homo	2.8
453994	BE180964	Hs.165590	ribosomal protein S13	2.8
459171	AW967801	Hs.64783	ESTs, Weakly similar to T42705 hypothet	2.8
404845			C22000163.gi10242166gb:MAAG15318.1JAF2	2.8
403182	AA047854		gb:z49404.1 Scores retina N264HR Homo	2.8
427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibitor	2.7
414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.7
423815	Z30045	Hs.293676	ESTs	2.7
404036			Target Exon	2.7
418157	W99382	Hs.283709	Ippopolysaccharide specific response-7 p	2.7
426403	NM_000261	Hs.2030	thrombomodulin	2.7
429659	AW970760	Hs.58463	Homo sapiens cDNA FLJ114471 fls, clone MA	2.7
443932	AW888222	Hs.9973	tenascin	2.7
444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	2.7
419269	AA235838		gb:z41b04.s1 Scores NIH-MPc, S1 Homo sapi	2.7
416204	D11880	Hs.298254	Homo sapiens cDNA: FLJ23597 fls, clone L	2.7
430371	D87466	Hs.240112	KIAA0276 protein	2.7
449117	AW449310	Hs.210262	ESTs, Weakly similar to HSS2_HUMAN HEPAR	2.7
451007	H38108	Hs.32759	ESTs	2.7
421262	AF193339	Hs.102506	eukaryotic translation initiation factor	2.7
405308			NM_025192 Homo sapiens hypothetical prot	2.7
413208	BE071799	Hs.87040	gb:FC0-8T0522-071299-011-b10T0522 Homo	2.7
421420	A024236	Hs.123296	ESTs, Weakly similar to PEC1_HUMAN PLATE	2.7
445663	AW800444	Hs.76507	LPS-induced TNF-alpha factor	2.7

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	452051	AA025647		gb:ze5d01r1 Soares_fetal_heart_NBHH19W	2.7
	410538	AW573115		gb:PMO-CT0268-131099-001-k12 CT0248 Homo	2.7
	448072	AI459306	Hs 24908	ESTs	2.7
5	420912	AW853156	Hs 50787	ESTs	2.7
	453830	AA542266	Hs 20563	ESTs	2.7
	457791	AW117431	Hs 191906	ESTs	2.7
	417735	AA188175	Hs 82506	KIAA1254 protein	2.7
	411773	NM_005799	Hs 72026	protease, serine, 21 (testis)	2.7
	417076	AW573454	Hs 238493	ESTs, Moderately similar to ALU7_HUMAN	2.7
10	436476	AA326108	Hs 33329	bHLH protein DEC2	2.7
	440945	AW505345	Hs 7540	fbox and leucine-rich repeat protein 3A	2.7
	425826	U97698		mucin 6, gastric	2.7
	422795	AB033169	Hs 120866	KIAA1263 protein	2.7
	433321	AA418174	gb:cd40t.s1 NCI_CCAP_Thy1 Homo sapiens	2.7	
15	414272	AI051603	Hs 46988	ESTs	2.7
	418047	R37633	Hs 4847	ESTs	2.7
	421089	AB037771	Hs 101799	KIAA1350 protein	2.7
	419763	AJ039811	Hs 127466	ESTs	2.7
20	450265	AJ003616	gb:AJ003616 Selected chromosome 21 cDNA	2.7	
	410870	AW812151	gb:RCS-ST0178-081099-011-A06 ST0178 Homo	2.7	
	401925	N88378	Hs 85335	sialyltransferase 1 (beta-galactoside al	2.7
	418504	BE159718	Hs 85335	Homo sapiens mRNA, cDNA DKFZp564D1482 (f	2.7
	433789	AA220977	gb:zd1a0B.1 Stargazin N12 neuronal pr	2.7	
	418308	AA215738	Hs 182514	ESTs, Weakly similar to A64010 X-linked	2.7
25	444618	AV653785	Hs 173334	ELL-RELATED RNA POLYMERASE I ELONGATIO	2.6
	405299			Target Exon	2.6
	422963	M79141	Hs 13234	ESTs	2.6
	441244	BE612935	Hs 184052	PP1201 protein	2.6
30	439954	AL046748	Hs 6790	DnaJ (Hsp40) homolog, subfamily B, membe	2.6
	450588			Target Exon	2.6
	424741			Target Exon	2.6
	451927	AL355687	Hs 27261	Homo sapiens mRNA full length insert cDN	2.6
	439103	AF085959	Hs 38705	ESTs	2.6
35	437241	AL137318	Hs 306450	Homo sapiens mRNA: cDNA DKFZp434L171 (f	2.6
	442279	NM_004613	Hs 8265	transglutaminase 2 (C polypeptide, prote	2.6
	457394	M86023	Hs 266802	neurotrophin 5 (neurotrophin 45)	2.6
	427229	U1799751	Hs 5635	ESTs	2.6
	414630	BE410857	Hs 16064	gb:601301177F1 NIH_MGC_21 Homo sapiens c	2.6
40	406744	AA545482	Hs 273960	tumor protein, translationally-controlled	2.6
	442394	AK24415	Hs 143719	ESTs	2.6
	421221	AW276914	Hs 326714	Homo sapiens clone IMAGE 713177, mRNA se	2.6
	421709	AA159394	Hs 107056	OED-6 protein	2.6
	426747	AA355210	Hs 171995	kallikrein 3, (prostate specific antigen	2.6
45	439480	AL038511	Hs 125316	ESTs, Weakly similar to S33990 finger pr	2.6
	419567	AW335890	Hs 128187	ESTs	2.6
	421922	AW295043	Hs 109590	genethonin 1	2.6
	421859	AA366620	Hs 108947	NIAA0050 gene product	2.6
	431441	U81961	Hs 2794	sodium channel, nonvoltage-gated 1 alpha	2.6
	444843	AA400172		gb:zu600.01 Soares_fetal_liver_NHT Homo sap	2.6
50	416729	U46165	Hs 1027	Ras-related associated with diabetes	2.6
	439238	N47305	Hs 302161	ESTs	2.6
	439183	AW970600	Hs 303261	ESTs	2.6
	408739	W01556	Hs 259797	ESTs, Moderately similar to I38022 hypot	2.6
55	412061	AA833763	Hs 330211	ESTs	2.6
	432114	AL036021	Hs 8934	ESTs	2.6
	425337	AA355442	Hs 169054	ESTs	2.6
	424259	AK000377	Hs 82294	homolog of mouse C2PA	2.6
	444871	BE516709	Hs 155265	knuppel-related zinc finger protein hcf	2.6
60	414516	AI307802	Hs 135650	ESTs, Weakly similar to T43458 hypothe	2.6
	456235	AA203637	Hs 63657	gb:zu5Bb12 r1 Soares_fetal_liver_spleen	2.6
	419429	AA310600	Hs 63657	peptide-H-glycanase similar to yeast PNG	2.6
	440251	AW151660	Hs 31444	ESTs	2.6
	436546	AW023329	Hs 132743	ESTs	2.6
	450546	AA010200	Hs 175551	ESTs	2.6
65	437255	R58970	Hs 5887	ESTs	2.6
	430841	AB033825	Hs 50081	Hypothetical protein_XP_051860 (KIAA119	2.5
	427983	M17706	Hs 2233	colony stimulating factor 3 (granulocyte	2.5
	413341	H78472	Hs 191325	ESTs, Weakly similar to T18967 hypothe	2.5
	423763	R98203	Hs 132724	nuclear transcription factor Y, alpha	2.5
70	413282	BE078159	Hs 170081	gb:CM6-810615-140200-175-406 BT0615 Homo	2.5
	415590	T74086	Hs 170081	gb:cd1307.41 Soares_infant brain IN1B H	2.5
	406215			Target Exon	2.5
	453338	AF082969	Hs 36794	D-type cyclin-interacting protein 1	2.5
75	424310	AA338648	Hs 50334	testes development-related HYD-SP22	2.5
	424297	AW015799	Hs 128474	ESTs	2.5
	456650	AA620501	Hs 106773	ESTs, Weakly similar to T42689 hypothe	2.5
	413231	D87461	Hs 75244	BCL2-like 2	2.5
	457297	AW68188		gb:EST380383 IMAGE_resequences, MAGU Homo	2.5
80	444942	AW293458	Hs 28387	chromosome 11 open reading frame 16	2.5
	425764	AW696009	Hs 112672	Homo sapiens cDNA FLJ14139 f6, clone MA	2.5
	435712	AA694607	Hs 179956	ESTs	2.5
	436624	T64297		latty acid binding protein 1, liver	2.5
	443155	R54485	Hs 23772	ESTs	2.5

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5	425907	AA355752	Hs.155965	ESTs	2.5
	414759	AW295157	Hs.47587	ESTs	2.5
	414699	AB15523	Hs.76930	synuclein, alpha (non A4 component of am	2.5
	411426	BE141714		gq-QWB-H10101 gq-106109-032-034 H10101 Homo	2.5
	404942			CR0003677 gq104324039[hum]CAC10290.1(A	2.5
10	425153	AW023193	Hs.27046	ESTs	2.5
	26372	BE304680	Hs.159531	DEAD/HD (Asp-Glu-Ala-AspHis) box polypept	2.5
	343603	AW574640	Hs.303413	ESTs	2.5
	425694	US15333	Hs.159237	histone kinase 3 (white cell)	2.5
	433069	X76332	Hs.3164	nucleobindin 2	2.5
15	428054	AI548688	Hs.266619	ESTs	2.5
	424823	NM_006226	Hs.153322	phospholipase C, epsilon	2.5
	456972	A054347	Hs.2017	ribosomal protein L38	2.5
	431405	AI470895	Hs.32495	ribosomal protein L10a	2.5
	427982	NM_016156	Hs.181326	KIAA1073 protein	2.5
20	412831	AA121352	Hs.143314	ESTs	2.5
	437114	AA836541	Hs.163085	ESTs	2.5
	426157	AA370977	Hs.345736	STAT induced STAT inhibitor 3	2.5
	448786	BE048842	Hs.179075	Homo sapiens cDNA FLJ11881 fs, clone HE	2.5
	432251	AW572583	Hs.232165	polycythemia rubra vera 1; cell surface	2.5
	449239	T24653	Hs.23360	likely ortholog of yeast ARV1	2.5
	453572	AA362290	Hs.46365	KIAA0948 protein	2.5

TABLE 23b:

Play: Unique Eos preblast identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Play	CAT number	Accession
30	408182	104479.1 AA247854 AW057506 AA053841
	409585	1155285.1 AWP52062 AW025795 AW028087 AW501876
	410500	1206699.1 AW840743 AW254004 HA3469
	410538	1207341.1 AW753115 AW753113 RA5779
	410786	1221063.1 AW803340 AW803280 AW803275 AW803415 AW803343 AW803422
35	410970	1223131.1 AW512151 AW512166 AW812166
	411426	1245515.1 BE141714 AW845993 AW845989
	411906	1265204.1 AW757565 H50294 AW875494
	412636	13165.1 NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW375817 AW376699 AW848371 AW376762 AW348789 AW361413
		AW8493074 AW971139 AW793004 AW793009 BE077020 BE077017 BE105167 AW867196 BE156621 BE179915 BE030651 BE143155 AW809885
40		BE021087 AW021081 AA08715 BEA020133 BE011378 AW170253 BE105750 AW886475 BE104043 J05291 BE082576 BE082584 BE084047
		AW5607238 AW477700 AW377699 BE082526 BE082505 BE082514 AW178000 AW177923 AA05935 AW747877 AW748114 BE148516
		AW655328 AW847678 AW847688 AW365151 AW365148 AW365156 AW365175 AW365157 AW353154 AW068840 BE052572 AW365145
		BE010925 BE182166 BE144243 BE001923 A951766 AW343518 BE184280 BE184533 A284020 BE184941 AW040474 BE184924 C04715 AW9488
		AW895615 BE184940 BE159646 AW802653 AA028981 AA131128 AA332720 AA300777 AW834371 AA352212 T58704 AW365566 AW364699
45		AA025851 BE025852 AA025850 AA179588 AW365220 AW986245 BE165351 BE012457 AA377127 AW798026 AW069750 AW391912 AW948499
		H87267 AW653812 AA282213 W74149 BE009090 AA056401 H10111 AW368829 AW300272 C18467 AW514920 N51776 AW025480 AW576787
		H53284 AA028683 AW177787 AA026654 AW177786 BE082134 BE092137 BE092136 AW177784 A022662 BE091653 AW379811 AW848592
		AA040010 BE165331 BE182164 AA386554 AW951576 T29918 AA131077 W95048 H25458 AW205789 H50399 N29754 W332480 R20804 BE167181
		BE171651 H84761 H27408 H30746 A1395250 C03376 A1554403 A205263 AA118470 A152928 AF133065 AW030813 AW030827 AW798477
50		AW798780 AW798883 AW798569 R33557 AA149190 C03025 AW177783 AA088866 AW370825 AA247965 BE002273 J176016 A143910 AW79451
		A1700963 AA151923 A1340325 A1500975 T48793 A1559096 A1142882 A1033975 A140470 AA546936 BE067373 BE077676 W19287 AA64381
		AA1702424 AA176162 A1063654 A868689 A558892 AW190555 A571075 A120673 A0565527 AW187184 A130472 AW517828 A915596 AW827383
		A1270345 AW021347 AW166807 AW105514 A246078 A4532200 W50700 AW040803 A911702 AA149101 A1025654 A1833049 A837258 AW130435
		A1910434 A1879884 A1582882 A1078449 A0225932 A1580584 A6135878 A0206047 AW10733212 D10052 AW125085 AA658154 AA649217 AW5691892
55		T87181 AA105266 AW243815 AW150038 AW268383 AA004633 A5927207 AA782109 AW043233 A1801485 A91169216 A157269 AW514051
		AW015480 AW071865 A4270027 AA961816 AA283207 A0709652 AW494887 A348603 A1839314 H44405 AW799116 AA128330 AA515500 AA910281
		W02156 A1806527 A0227001 W18392 R20795 177861 AW860878
		BE071799 BE071804 BE071798
		BE300352 BE299274 BE075351 BE297444
60		BE078159 BE078276 BE078163 BE078277 BE078279 BE078158
		BE144444 BE144430
		W07002 R25201 F12763 T74725 H63485 Z45782 H61125
		H72693 R08673 H72694 F20990 R0580
		AA176633 AW961842 AA309418
65		AA235938 BE180775
		A0238687 A0237096 AA354236 AW957759 H08961
		U91698 AW561294 A1791566 A1732669 AA588236 A1521662 A0816760 A1955717 AW292169 A468222 A1420463 A043459 A1688225 A9119551
		AA502346 BE159853
		A0220977 AF091025 AA701227
70		AA618174 A114549 R23644 H34645
		T54287 AA84531 NM_001443 MW0020 AW841309 A1695516 T53219 T48785 T64166 AA1709330 R20613 T55913 T56518 T64769 R20686 M10617
		A765856 AA101894 W90338 A142193 AW752206 AA099433 T53220 AW082135 AW277755 T29562 T55862 A143047 A1345671 T68235 T68121
		AW842284
		AA400172 AA400146 AV651691
75		A253414 A365014 F04822
		T58148 AW516579 AW055603
		A1674072 BE268487
		A1744417 R91614 H77365
		A1025647 H45716 AW753786
80		AW652286 AW651934 AW652036 AW852274
		AA203637 AA383266 H67452
		AW968188 AA468196 AA468269 AA468298
		AJ003616 AJ003654 AJ003517
		454265 965690.1

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TABLE 23C:

	Play:	Unique number corresponding to an Ecos probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495		
	Strand:	Indicates DNA strand from which exons were predicted.		
	N_position	Indicates nucleotide positions of predicted exons.		
10	Play	Ref	Strand	N_position
	400965	7770576	Minus	173043-173554
	401507	7534110	Plus	71055-71259
	401600	438746	Plus	27363-27518,28727-28891,29526-29731
	401783	7249190	Plus	13369-13827,140509-140591,140834-140990,141496-141657,141757-141882,142053-142263
	401925	3892083	Minus	139252-139465,140239-140364,140437-140598,141037-141193,141925-142007,142787-143230
15	402798	8575116	Plus	79041-79191
	402934	9404515	Minus	54983-55240,56507-56785,56982-57365
	402429	9796372	Minus	57622-57793,59282-59402,59624-59827
	403442	7210003	Plus	174560-175270
20	403469	9525739	Minus	4051-7707
	403488	9586615	Minus	12450-12753
	403512	7556757	Minus	114487-114610
	403890	7710561	Plus	83165-83350
	404036	9567760	Minus	62247-61229,112537-114663
	404091	7694554	Minus	62121-83229
25	404333	9802821	Minus	137948-138024,138111-138300
	404492	8123400	Minus	130612-138903
	404559	8748893	Minus	73459-73951,86575-89739
	404606	9212536	Minus	22310-23265
	404661	8797073	Plus	33374-33675,33769-34008
30	404741	8574139	Plus	143025-143467
	404845	7958980	Minus	47174-47226,52928-53146,53312-53602
	405088	8072518	Minus	116580-117621
	405354	7642452	Plus	52213-53069
	405403	6850244	Minus	37491-37670,40951-41031
35	405474	8439781	Plus	172055-172175
	405596	5002511	Plus	38810-39017
	405670	4662655	Plus	9654-96870
	405674	4559984	Plus	68302-68429
	406085	9123888	Plus	16665-16843
40	406215	7342161	Plus	310-432
	406270	7534217	Plus	13136-13591
	406299	9585278	Minus	35655-36119
	406308	9211532	Plus	356408-358651

TABLE 24A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 24A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/HuEco Hu3 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Play	ExAccn	UnigenID	Unigene Title	RI	
55	431917	D16181	Hs.2858	peripherin myelin protein 2	75.2
	427343	A0880044	Hs.179977	protein kinase C binding protein 2	74.6
	455601	A0368680	Hs.816	SRY (sex determining region Y)-box 2	74.2
	428321	A0999994	Hs.2886	peripherin myelin protein 2	74.0
	412719	AW019810	Hs.129911	ESTs	70.7
	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fls, clone L	66.3
65	415817	U89967	Hs.78857	protein tyrosine phosphatase, receptor-t	64.3
	413472	BE242870	Hs.75379	scute carrier family 1 (glial high alt)	60.1
	426769	BE285150	Hs.127752	delta (Drosophila)-like 3	52.3
	435147	AL133731	Hs.4774	Homo sapiens mRNA, cDNA DKFZp751C1712 (f	46.7
	425842	A057490	Hs.159623	NK-2 (Drosophila) homolog B	40.1
70	412733	AA984472	Hs.74554	KIAA0080 protein	39.0
	418375	NA_003081	Hs.84369	synaptosomal-associated protein, 29kD	38.7
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	37.2
	423849	AL157425	Hs.133315	Homo sapiens mRNA, cDNA DKFZp761J1324 (f	36.8
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	32.8
75	416829	A013805	Hs.80220	cristin (cathelin-associated protein), d	31.8
	431941	AK006106	Hs.272227	Homo sapiens cDNA FLJ20055 fls, clone CO	31.8
	438878	BE465204	Hs.47448	ESTs	31.4
	426325	C26114	Hs.109309	myelin-associated oligodendrocyte basic	30.9
	425057	AA264534	Hs.16119	achute-scute complex (Drosophila) homol	30.4
	446711	A7169692	Hs.129450	protocadherin 9	30.2
	439415	F05538	Hs.12825	ESTs	28.3
	430838	N46664	Hs.160395	hypothetical protein FLJ12015	26.9
	429466	M85835	Hs.12827	ESTs	25.9

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447004	AW290959	Hs.157539	ESTs	25.3
424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	24.8
452744	A1267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (r	24.8
441285	NM_002374	Hs.167	microtubule-associated protein 2	24.3
433642	A1070536	Hs.24074	disphylipinase VI	24.2
423440	Z48051	Hs.141308	myelin oligodendrocyte glycoprotein	24.2
450133	AW969769	Hs.105201	ESTs	24.2
408562	A106323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	23.3
448672	A1953111	Hs.225106	ESTs	22.7
432704	A1062049	Hs.75169	ESTs	22.0
407304	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	21.9
407168	R45175	Hs.117183	ESTs	21.7
431019	NM_005249	Hs.2714	linkhead box G16	21.5
430849	AW23132	Hs.146343	ESTs	21.4
433896	AW294729	Hs.274461	ESTs	21.1
445041	T64183	Hs.282982	solute carrier	21.0
410738	AW389633	Hs.6962	solute carrier family 7, (cationic amino	20.4
444378	R41339	Hs.12569	ESTs	20.0
411305	BE241595	Hs.69547	myelin basic protein	19.9
437414	AW894071	Hs.48448	hypothetical protein DKFZp547C176	19.8
441016	AW138653	Hs.25845	ESTs	19.6
440435	AL042021	Hs.21273	transcription factor NYD-ap10	18.5
433209	AL120659	Hs.6111	arylhydrocarbon receptor nuclear transd	18.4
452461	N78223	Hs.108106	transcription factor	18.1
409395	U46745	Hs.54435	dystrobrevin, alpha	18.1
417183	R52080	Hs.172717	ESTs	18.0
409538	AW453430	Hs.21326	ESTs	18.0
428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	18.0
449611	A1970394	Hs.197075	ESTs	17.0
444692	Z44514	Hs.156229	Homo sapiens mRNA for KIAA1763 protein,	16.9
425088	A1463372	Hs.109359	hypothetical protein FLJ12015	16.8
444471	AB020584	Hs.11217	KIAA0877 protein	16.8
421659	NM_014459	Hs.106511	protocadherin 17	16.7
431725	X55724	Hs.2839	Horrie disease (psoriasis/glioma)	16.6
429276	AF105085	Hs.198612	G-protein-coupled receptor 51	16.6
416892	L24468	Hs.80409	growth arrest and DNA-damage-inducible,	16.5
441440	AB07981	Hs.30495	ESTs	15.7
449433	A1672096	Hs.8012	ESTs, Weakly similar to S26650 DNA-bind	15.7
421264	AL035123	Hs.103042	microtubule-associated protein 18	15.5
415910	U20330	Hs.78913	chemokine (C-X3-C) receptor 1	15.3
413597	AW02885	Hs.117183	ESTs	15.1
424845	A221919	Hs.173438	hypothetical protein FLJ10582	14.9
447414	D62343	Hs.18551	neuroblastoma (nerve tissue) protein	14.9
426269	H13382	Hs.169849	Homo sapiens mRNA; cDNA DKFZp566A1046 (I	14.8
416857	AA188775	Hs.292453	ESTs	14.7
419721	NM_001650	Hs.286590	aquaporin 4	14.6
411078	A222020	Hs.182364	Coccolitrop	14.4
453024	R49296	Hs.24896	ESTs	14.4
403089	A2007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific	14.3
430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (14.1
410909	AW888161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN A	14.0
412266	N69006	Hs.26133	ESTs	14.0
412966	X81120	Hs.75110	cannabinoid receptor 1 (brain)	14.0
424790	AL119344	Hs.13326	ESTs, Weakly similar to 2004399A chromos	14.0
439239	A031540	Hs.235331	ESTs	14.0
441487	R51064	Hs.23172	ESTs	14.0
445495	BE022541	Hs.38408	ESTs, Weakly similar to 138022 hypotheti	14.0
414245	BE148072	Hs.75480	WAS protein family, member 1	13.7
429900	AA402421	Hs.30875	ESTs	13.6
448595	AB014544	Hs.21572	KIAA0644 gene product	13.6
449005	AW139381	Hs.198416	ESTs	13.6
425226	W34837	Hs.280740	hypothetical protein MG23040	13.3
420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA, ho	13.3
441390	AE020690	Hs.7782	paraneoplastic antigen MA2	13.3
420077	AW512260	Hs.87767	ESTs	13.2
424120	T80579	Hs.290270	ESTs	13.2
456965	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	13.2
423361	AW170055	Hs.47628	ESTs	13.1
428409	AW117207	Hs.98523	ESTs	12.9
417160	N16497	Hs.1787	proteolipid protein 1 (Pellegrini-Merzbac	12.6
451621	AB79148	Hs.28770	fatty acid binding protein 7, brain	12.6
411379	AB183434	Hs.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	12.5
436954	AA740151	Hs.130425	ESTs	12.4
430691	C14167	Hs.103538	ESTs	12.4
433551	A195544	Hs.12450	protocadherin 9	12.4
422544	AB018259	Hs.118140	KIAA0716 gene product	12.2
427540	R12614	Hs.20976	ESTs	12.1
435624	AF218542	Hs.24889	frnmin 2	12.1
415849	R20529	Hs.0806	ESTs	12.1
428445	AL115579	Hs.163610	KIAA0751 gene product	11.9
442671	A005668	Hs.134779	EST	11.9
444396	165213	Hs.4257	ESTs	11.8
452752	AW040058	Hs.33578	KIAA0820 protein	11.8

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425523	AB007948	Hs.158244	KIAA0479 protein	11.8
419072	AL110370	Hs.79000	growth associated protein 43	11.7
440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	11.7
428976	AL037824	Hs.194595	ras homolog gene family, member 1	11.6
444783	AB001468	Hs.52180	arilin (Drosophila Serape homolog), act	11.6
446299	AA467044	Hs.20807	hypothetical protein FLJ10382	11.6
414214	D45958	Hs.75819	glycoprotein M6A	11.5
428982	NM_005097	Hs.194704	leucine-rich, glioma inactivated 1	11.5
405236				11.4
420382	U79734	Hs.97208	huntingtin interacting protein 1	11.4
422980	N46589	Hs.76722	CCAAT/hennessy binding protein (CCEBP)	11.4
424918	R13982	Hs.195309	myosin associated oligodendrocyte basic	11.4
434277	X77748	Hs.3786	glutamate receptor, metabotropic 3	11.4
451952	AL120173	Hs.301653	ESTs	11.3
408829	NM_005042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfat	11.3
424278	AK000723	Hs.144517	hypothetical protein FLJ29716	11.3
429418	AL381028	Hs.118769	ESTs	11.3
429918	AB075986	Hs.119383	ESTs	11.3
433912	F37267	Hs.194789	ESTs	11.3
448743	AB032962	Hs.21896	KIAA1136 protein	11.3
420092	AA814043	Hs.88045	ESTs	11.2
406081	AW451937	Hs.167409	ESTs	11.2
411642	NM_014932	Hs.71132	neuroigin 1	10.9
415170	R44386	Hs.164578	ESTs	10.9
426320	W47596	Hs.169300	transforming growth factor, beta 2	10.8
425568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fts, clone NT	10.8
425789	TGB133	Hs.182099	Homo sapiens mRNA for KIAA1872 protein,	10.8
423853	AB011537	Hs.133466	sit (Drosophila) homolog 1	10.7
400293	NS1002	Hs.306490	Homo sapiens mRNA; cDNA DKFZp761E1212 f1	10.7
447773	AA423800	Hs.36790	ESTs, Weakly similar to putative p150 f1	10.7
448321	NM_005883	Hs.20912	adenomatous polyposis coli like	10.5
448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	10.5
449684	AU253123	Hs.127356	ESTs, Highly similar to S21424 neslin f1	10.3
444017	UC04840	Hs.214	neuro-oncological ventral antigen 1	10.3
438380	TG6430	Hs.6194	chondroitin sulfate proteoglycan BEHAAb	10.3
440471	AA485146	Hs.307944	ESTs	10.2
413063	AL035737	Hs.75194	chitinase 3-like 1 (canilage glycoprote	10.1
439978	BE130460	Hs.124673	Homo sapiens cDNA FLJ11477 fts, clone HE	10.1
448902	Z45958	Hs.22543	Homo sapiens mRNA; cDNA DKFZp7611912 f1	10.1
424932	R14070	Hs.316369	Homo sapiens cDNA: FLJ23075 fts, clone L	9.9
431721	AB032996	Hs.268044	KIAA1170 protein	9.9
419088	AI538323	Hs.52620	integrin, beta 8	9.8
420602	AF060877	Hs.99236	regulator of G-protein signaling 20	9.8
406511	AA721252	Hs.291502	ESTs	9.8
414696	AF002020	Hs.76718	Niemann-Pick disease, type C1	9.7
449639	W93063	Hs.58446	ESTs	9.7
412969	D87468	Hs.75090	KIAA0282 protein	9.6
412811	H06382	Hs.21400	ESTs	9.6
449300	AB56969	Hs.222165	ESTs	9.6
426344	H41821	Hs.322489	transcriptional activator of the c-fos p	9.5
419271	N04901	Hs.238532	ESTs	9.5
419078	M31119	Hs.89664	insulinoma-associated 1	9.4
451916	AI802515	Hs.17024	ESTs	9.4
422666	AB70436	Hs.1569	LIM homeobox protein 2	9.3
449318	AW236021	Hs.78531	Homo sapiens, Similar to Riken cDNA 5730	9.3
414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	9.3
452579	F04237	Hs.1447	glut thiolary acidic protein	9.2
428784	Y12851	Hs.193470	putative receptor P2K, ligand-gated ion	9.2
425903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.2
424641	AB001106	Hs.151413	glia maturation factor, beta	9.1
417435	NM_005181	Hs.82729	carbonic anhydrase III, muscle specific	9.1
445448	D60730	Hs.51471	ESTs	9.1
408508	AB05109	Hs.137336	KIAA1580 protein	9.0
452785	AL359942	Hs.296434	erythroid differentiation and demulcati	9.0
448966	H42169	Hs.18653	hypothetical protein FLJ14627	8.9
447072	D61584	Hs.17279	tyrosinprotein sulfotransferase 1	8.9
423800	AC34361	Hs.135100	lung type-I cell membrane-associated gly	8.9
426926	AF217525	Hs.45002	Dowm syndrome cell adhesion molecule	8.8
446925	NM_014253	Hs.23795	odt (odd Outlen-m, Drosophila) homolog 1	8.7
400292	AA250737	Hs.72472	ESTs	8.7
417404	NM_007350	Hs.82101	pleckstrin homology-like domain, famly	8.7
420345	AW285230	Hs.25231	ESTs	8.7
429827	NM_001115	Hs.2822	adenylate cyclase 8 (brain)	8.7
437528	N59646	Hs.169745	crumbs (Drosophila) homolog 1	8.7
440152	AB002376	Hs.7006	KIAA0376 protein	8.7
451099	R52796	Hs.29564	interleukin 13 receptor, alpha 2	8.6
407080				8.5
434891	AA814309	Hs.123883	ESTs	8.5
449277	AA301064	Hs.172976	ESTs	8.5
415709	AA649850	Hs.278658	ESTs	8.5
439547	AB006527	Hs.6788	astrotactin	8.5
447197	R36075		gby88b01.s1 Scores placenta Nb2HP Homo	8.5
433042	AW193334	Hs.281895	Homo sapiens cDNA FLJ11560 fts, clone HE	8.4

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1	416370	N90470	Hs.202697	ESTs, Weakly similar to 138022 hypothetical	8.4
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypothetical	8.4
	415796	R87548	Hs.78854	ATPase, Na+/K+-transporting, beta 2 poly	8.3
5	426271	AF026547	Hs.108407	chondroitin sulfate proteoglycan 3 (neur	8.3
	405947	AI080963	Hs.491117	Homo sapiens mRNA, cDNA DKF_Zp564M1652 (f	8.3
	419863	AW952691	Hs.156945	Homo sapiens mRNA, cDNA DKF_Zp761D191 (f	8.3
	433447	U29195	Hs.32981	neuronal pentraxin II	8.3
	431467	N71831	Hs.250298	Homo sapiens mRNA, cDNA DKF_Zp34E0528 (f	8.3
10	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.3
	414300	AI304870	Hs.188680	ESTs	8.2
	407728	AW071502	Hs.175931	ESTs	8.2
	427298	R93247	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.2
	419704	AA429104	Hs.45057	ESTs	8.2
	423507	D85642	gi.HUM082E090	Human fetal brain (TFajwa	8.1
15	442710	AI015631	Hs.23210	ESTs	8.1
	425048	HC0568	Hs.164902	ESTs	8.1
	429149	AW193360	Hs.179762	ESTs, Weakly similar to 138022 hypothetical	8.0
	445740	T76281	Hs.13226	Homo sapiens clone Z5181 mRNA sequence	8.0
20	418771	AA807881	Hs.25329	ESTs	7.9
	427228	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.9
	425984	AW938277	Hs.165636	hypothetical protein DKF_Zp761C07121	7.9
	448408	AA322866	Hs.21107	neurigin	7.9
	455354	HT2176	Hs.42773	hypothetical protein FLJ13159	7.9
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (postoponin,	7.9
25	435501	AW051819	Hs.129508	KIAA0591	7.8
	425860	AS533559	Hs.310359	ESTs	7.8
	459525	AW970107	gi.EST382188	MAGE resequences, MAGK Homo	7.8
	415314	N88802	Hs.5422	glycoprotein M6B	7.7
	420036	R60336	Hs.52792	Homo sapiens mRNA, cDNA DKF_Zp5681823 (f	7.7
30	427687	AW003367	Hs.1510	histamine receptor H1	7.7
	445328	AF924503	Hs.159747	ESTs	7.7
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recept	7.7
	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	7.7
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	7.6
35	438779	NM_003787	Hs.6414	nuclear protein 4	7.6
	433532	AV975367	gi.EST387475	MAGE resequences, MAGN Homo	7.6
	448555	AV536697	Hs.159863	ESTs	7.5
	439662	H97552	Hs.263960	ESTs	7.5
40	448643	AW897741	Hs.21360	Homo sapiens mRNA, cDNA DKF_Zp568P1124 (f	7.5
	410059	AA591530	Hs.190333	KIAA0036 gene product	7.5
	431592	R69016	Hs.213194	hypothetical protein MGC10695	7.4
	409731	AA125885	Hs.56145	thymosin, beta, identified in neuroblast	7.4
	405819				7.4
45	407886	AW969688	Hs.100826	ESTs	7.4
	437416	AL159605	Hs.283851	Homo sapiens mRNA, cDNA DKF_Zp547G036 (f	7.4
	437698	R61837	Hs.7990	ESTs, Moderately similar to B54505 catc	7.4
	408604	D51408	Hs.21925	ESTs	7.4
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	7.3
50	447459	AW262580	Hs.147674	procalcitonin beta 16	7.3
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	7.3
	409746	NM_004794	Hs.56294	RAB33A, member RAS oncogene family	7.2
	410037	AB020726	Hs.58009	KIAA0918 protein	7.2
	415018	AV9909742	Hs.291005	ESTs	7.2
55	424051	AL110203	Hs.139411	Homo sapiens mRNA, cDNA DKF_Zp566J1922 (f	7.2
	442026	A243749	Hs.8074	brain-specific angiogenesis inhibitor 3	7.2
	448243	AW399771	Hs.52620	integrin, beta 8	7.2
	436261	AA411194	Hs.85195	myeloid leukemia factor 1	7.2
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	7.2
60	407182	AA312581	Hs.230157	ESTs	7.1
	415293	RA4962	Hs.106541	ESTs	7.1
	427264	AI767727	Hs.47522	ESTs	7.1
	451592	AB05416	Hs.213897	ESTs	7.1
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating,	7.0
65	415734	NM_014747	Hs.78748	KIAA0237 gene product	7.0
	434149	Z43829	Hs.19574	hypothetical protein MGC53469	7.0
	436726	AA324975	Hs.128963	ESTs, Weakly similar to T00079 hypotheti	7.0
	417632	R20856	Hs.5422	glycoprotein M6B	7.0
	422421	AA325138	Hs.235873	hypothetical protein FLJ22672	6.9
	435267	N23797	Hs.110114	ESTs	6.9
70	431117	AL049286	Hs.125583	ESTs	6.9
	445523	Z30118	Hs.263788	ESTs, Moderately similar to unnamed prot	6.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.9
	445745	AB007924	Hs.13245	KIAA0455 gene product	6.9
	424085	NM_002914	Hs.135226	replication factor C (activator 1) 2 (40	6.9
75	426598	P12161	Hs.195703	Homo sapiens mRNA, full length insert cDN	6.8
	427123	AA620400	Hs.306717	sodium channel, voltage-gated, type III,	6.8
	447342	AI199258	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.7
	443297	AI049864	Hs.130029	ESTs	6.7
	443982	AW022228	Hs.322922	ESTs	6.7
80	453096	AW294631	Hs.11325	ESTs	6.7
	453857	AI080235	Hs.35861	DKF_ZP586E1621 protein	6.7
	443761	AS25743	Hs.180603	ESTs	6.6
	429509	AF002246	Hs.210863	cell adhesion molecule with homology to	6.6

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5	435056	AW023337	Hs.5422	glycoprotein M6B	6.5
	453431	AF094754	Hs.32973	glycine receptor, beta	6.5
	444190	AB78918	Hs.10526	cysteine and glycine-rich protein 2	6.5
	418110	R43523	Hs.217754	hypothetical protein FLJ22202	6.4
	413988	MB1583	Hs.324784	glutamate decarboxylase 1 (brain, 67KD)	6.4
	420805	I10333	Hs.59947	reticulon 1	6.4
	429125	AA446854	Hs.271004	ESTs, Weakly similar to 138022 hypothetical	6.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	6.4
10	407865	AW088232	Hs.85956	paired box gene 6 (antidia, heratilis)	6.3
	440700	AW552281	Hs.296184	quantine nucleotide binding protein (C pr	6.3
	427701	AA411101	Hs.243866	nuclear autoantigenic sperm protein (hs	6.3
	422949	AA319435	gb.EST121657	Adrenal gland tumor Homo sap	6.2
	445102	AW004610	Hs.22270	ESTs	6.2
	453401	NM_007115	Hs.29352	lunar necrosis factor, alpha-induced pro	6.2
15	435638	AB011540	Hs.4930	low density lipoprotein receptor-related	6.2
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fs, clone HE	6.2
	416871	H98716	gb.13x038.s1	Soares melanocyte 2ND-IM Ho	6.1
	416702	AA186428	Hs.85591	ESTs	6.1
	415347	I15944	Hs.90005	superficial convoluted ganglia, neural speci	6.1
20	424997	AL138167	Hs.96920	ESTs	6.1
	438660	U85740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	6.1
	453649	Y07494	Hs.34114	ATPase, Na+K+ transporting, alpha 2 (+)	6.1
	453444	AW618436	Hs.23590	solute carrier family 16 (monocarboxyl	6.1
	414117	W88559	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	6.0
25	426517	AF121173	gb.AF121173	Homo sapiens liver (Chang L-	6.0
	427457	AW779105	Hs.164682	ESTs	6.0
	437034	AAC42643	gb.97401.s1	NCI_GCAP_GCB1 Homo sapiens	6.0
	444170	AW613879	Hs.102408	ESTs	6.0
	457183	H91882	Hs.118569	Dlx-binding protein IDAX (inhibition of	6.0
30	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	6.0
	454048	H55626	Hs.6621	ESTs	6.0
	439772	AL365408	Hs.102058	Homo sapiens mRNA full length insert cDN	5.9
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.9
	410011	AB020641	Hs.57856	PTEFAIRE protein kinase 1	5.9
35	415486	HT2214	Hs.133284	ESTs, Weakly similar to 2105260A B cell	5.9
	438993	AA428626	gb.77066.s1	NCI_GCAP_Ov2 Homo sapiens	5.9
	447350	AI375572	Hs.172634	ESTs	5.9
	451783	R42554	Hs.210862	T-box, brain, 1	5.9
	447101	NT2185	Hs.441489	ESTs	5.9
40	446982	R39127	Hs.21433	hypothetical protein DKFZ547J035	5.9
	446274	R24595	Hs.7122	scrapie responsive protein 1	5.9
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	5.9
	418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	5.8
	437036	AI571514	Hs.133022	ESTs	5.7
45	412225	AW020042	gb.U00-NN1022-170400-193-c02	NN1022 Homo	5.7
	425342	AF033419	Hs.169378	multiple PDZ domain protein	5.7
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	5.7
	445828	F05802	Hs.81907	ESTs	5.7
	447198	DE1523	Hs.283436	ESTs	5.7
50	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	5.7
	448499	BE613280	Hs.77550	hypothetical protein MGC1780	5.7
	443672	AA323362	Hs.9667	butyrobetaine (gamma), 2-oxoglutarate d-	5.6
	412155	R38167	Hs.12649	Homo sapiens transmembrane protein HTMP1	5.6
	435718	R65669	Hs.269534	ESTs	5.6
55	449340	AW255786	Hs.193539	hypothetical protein MGC10954	5.6
	424481	R19483	Hs.1787	proteolipid protein 1 (Pelizaeus-Merzbac	5.6
	451996	AW614021	Hs.245510	ESTs	5.6
	422411	AW745943	Hs.225311	ESTs	5.6
	438328	AI492261	Hs.324550	ESTs	5.6
60	433244	AB040943	Hs.271285	KIAA1510 protein	5.6
	435191	R19912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	5.5
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	5.5
	400859				5.5
	413625	AW451103	Hs.71371	ESTs	5.5
65	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp34P228 (h	5.5
	434933	R91095	Hs.4276	KIAA1701 protein	5.5
	438702	AB79454	Hs.54618	ESTs	5.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10958	5.5
	430979	AI479355	Hs.129010	ESTs	5.5
70	412709	AL022327	Hs.74518	KIAA0027 protein	5.5
	439520	H55430	Hs.288433	neurokinin	5.5
	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	5.4
	407846	AA428202	Hs.40403	Cbp/p300-interacting transactivator, wii	5.4
	419235	AW470411	Hs.288433	neurokinin	5.4
75	416830	BE201573	Hs.83321	neurokinin B	5.4
	410330	AW023630	Hs.46786	ESTs	5.4
	410781	AI375672	Hs.165028	ESTs	5.4
	420658	AW965215	Hs.336656	ESTs	5.4
	421308	AA687322	Hs.192043	leucine zipper protein FKSG14	5.4
80	443740	R56434	Hs.21602	ESTs	5.4
	426457	AW894667	Hs.169965	chimerin (chimerin) 1	5.4
	450375	AA029647	Hs.8850	a draligin and metalloproteinase doma	5.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	5.4

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429600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	5.4
424432	AB037821	Hs.146588	protocadherin 10	5.4
429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
434785	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	5.4
436282	RS1913	Hs.272104	ESTs, Moderately similar to ALUT1_HUMAN A	5.4
404584				5.3
430091	AB032958	Hs.233023	KIAA1132 protein	5.3
439845	AL355743	Hs.56663	Homo sapiens EST from clone 41214, full	5.3
424001	YK7883	Hs.137416	patently expressed 10	5.3
425073	W39509	Hs.22003	soluble carrier family 5 (neuronal/immune)	5.3
426625	778300	Hs.300642	serologically defined colon cancer antigen	5.3
428137	AA421792	Hs.170999	ESTs	5.3
428679	AA431765		glrxz003.01 Soares_testis_NHT Homo sap	5.3
438176	AW138570	Hs.122113	ESTs	5.3
440138	AB033023	Hs.318127	hypothetical protein FLJ12021	5.3
451018	AW565699	Hs.247324	mitochondrial ribosomal protein S14	5.3
416340	N31772	Hs.79226	translocation and elongation protein zot	5.3
435444	NT7221	Hs.187824	ESTs	5.3
446035	NM_005598	Hs.13565	Sam68 like phosphotyrosine protein, T-ST	5.3
424624	AB032947	Hs.151301	Ca2+-dependent activator protein for sec	5.3
407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillator	5.3
430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 ts, clone PL	5.3
414625	X05370	Hs.77432	epidermal growth factor receptor (avian)	5.2
453941	U39817	Hs.36820	Bloom syndrome	5.2
424998	U58515	Hs.154138	chitinase 3-like 2	5.2
423419	RS5336	Hs.23539	ESTs	5.2
424922	BE365547	Hs.217112	hypothetical protein MGC10825	5.2
447359	NM_012093	Hs.16268	adenylylate kinase 5	5.2
408206	AF041853	Hs.43570	kinesin family member 3A	5.2
421013	M52387	Hs.1345	mutated in colorectal cancers	5.2
429443	AB022967	Hs.202587	potassium voltage-gated channel, Shal-re	5.2
434367	AB000700	Hs.36330	KIAA0953 protein	5.2
444851	R46789	Hs.76118	ubiquitin carboxyl-terminal esterase L1	5.2
448142	AI754593	Hs.145968	ESTs	5.2
448816	AB033052	Hs.22151	KIAA1226 protein	5.2
451050	AW527420	Hs.59852	ESTs	5.2
451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral related	5.2
439285	AL133916	Hs.172572	hypothetical protein FLJ20093	5.2
415737	AF154335	Hs.79591	LM domain protein	5.2
424880	AL035588	Hs.153200	NfyD family inhibitor	5.2
434656	AW204099	Hs.337720	ESTs, Weakly similar to AF126780.1 retin	5.2
415257	FC0315	Hs.27513	ESTs	5.2
433929	AI375499	Hs.27379	ESTs	5.1
415651	AI207162	Hs.3815	strabismus-like protein RB3	5.1
451027	AW515204	Hs.40898	ESTs	5.1
409172	Z99399	Hs.118145	ESTs	5.1
423343	AA324643	Hs.246106	ESTs	5.1
429172	AA447417	Hs.285491	ESTs	5.1
427268	AF154647	Hs.227571	regulator of G-protein signalling 4	5.1
451270	AW341392	Hs.235795	ESTs	5.1
452904	AL157581	Hs.30957	Homo sapiens mRNA; cDNA DKFZp434E052 ff	5.1
420550	AW207748	Hs.59115	ESTs	5.1
418037	RA5137	Hs.21868	ESTs	5.1
442910	AL365130	Hs.11307	ESTs, Weakly similar to T19326 hypothetical	5.1
434849	AW292755	Hs.8053	ESTs	5.1
413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	5.1
414217	A3305298	Hs.279698	Homo sapiens cDNA: FLJ23165 ts, clone L	5.1
412268	ST2943	Hs.73133	metallothionein 3 (growth inhibitory fac	5.0
413627	BE128082	Hs.246973	ESTs	5.0
418661	NM_001949	Hs.11189	E2F transcription factor 3	5.0
422438	AA445925	Hs.270896	ESTs, Moderately similar to Z195_HUMAN Z	5.0
423728	ABN51294	Hs.132136	soluble carrier family 4, sodium bicarbonate	5.0
431431	AL096711	Hs.252953	Human DNA sequence from clone RPS-403A15	5.0
435067	AW975241	Hs.23567	ESTs	5.0
452097	AB002364	Hs.27915	a disintegrin-like and metalloprotease (5.0
410434	AF051152	Hs.63658	Kil-like receptor 2	4.9
488552	AL040127	Hs.340874	dephosphorylase VI	4.9
407806	AA663559	Hs.279789	histone deacetylase 3	4.9
418940	HI1739	Hs.288513	Human DNA sequence from clone RPS-899C14	4.9
429977	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	4.9
426814	AF030943	Hs.172619	myelin transcription factor 1-like	4.9
447112	HI17800	Hs.7154	ESTs	4.9
449574	F05048	Hs.175373	ESTs	4.9
435652	AW009640	Hs.26368	ESTs, Moderately similar to S05657 alpha	4.9
423889	BE4069301	Hs.134012	C1g-related factor	4.9
413248	T64658	Hs.21433	hypothetical protein DKFZp574J036	4.9
449176	AI633545	Hs.193072	ESTs	4.9
448451	AW015994		gh UI-H-Blog-abn-g-09-0-ULS1 NCL_GCAP_5	4.8
428694				4.8
435039	AW023323	Hs.121070	ESTs	4.8
448769	N66037	Hs.38173	ESTs	4.8
423678	AW963357	Hs.7847	ESTs	4.8
439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.8

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425870	R13406	Hs.56782	ESTs	4.8
408777	U71204	Hs.47626	Ric (Drosophila)-like, expressed in neur	4.8
413409	A1638418	Hs.78580	DEAD/Hi (Asp-Glu-Ala-AspHis) box polypep	4.8
413623	AA25271	Hs.24873	ESTs	4.8
417246	A1760096	Hs.21411	ESTs	4.8
420900	AL045633	Hs.44269	ESTs	4.8
424153	AA451737	Hs.141496	MAGE-like 2	4.8
435339	A076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	4.8
448750	U55220	Hs.21953	calcium channel, voltage-dependent, beta	4.8
454020	JW021429	Hs.231980	ESTs	4.8
424458	M25273	Hs.1780	myelin associated glycoprotein	4.8
444119	R41231	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	4.8
407792	A1077715	Hs.19364	putative secreted ligand homologous to f	4.7
413462	AWS36672	Hs.256311	granin-like neurosecretory peptide precu	4.7
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.7
429956	A1374651	Hs.22542	ESTs	4.7
430560	A1422719	Hs.233349	ESTs, Weakly similar to fork head the p	4.7
436203	BE364882	Hs.5076	Homo sapiens cDNA: FLJ22128 fls, clone H	4.7
448475	BE613134	Hs.247474	hypothetical protein FLJ21037	4.7
422222	A169372	Hs.193247	hypothetical protein DKFZp434A171	4.7
431733	AW928410	Hs.21475	ESTs	4.7
449353	AA001220	Hs.271369	ESTs	4.7
452222	JW022330	Hs.263875	ESTs	4.7
454269	A1961060	Hs.129508	KIAA0591 protein	4.7
404541				4.7
428189	AA424030	Hs.46627	ESTs	4.7
420125	R17289	Hs.255873	axonal transport of synaptic vesicles	4.7
458435	AA181718	Hs.144121	ESTs, Weakly similar to T40516 hypotheti	4.6
425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fls, clone H	4.6
413492	D87470	Hs.75400	KIAA0280 protein	4.6
415629	A3020695	Hs.51662	KIAA088 protein	4.6
407638	A1404672	Hs.334483	hypothetical protein FLJ23571	4.6
436140	W87355	Hs.269587	ESTs	4.6
439169	AB12122	Hs.41095	ESTs	4.6
443150	AD04467	Hs.34650	ESTs	4.6
451071	A175805	Hs.208963	ESTs	4.6
451659	BE379761	Hs.14248	ESTs	4.6
452106	A141031	Hs.21342	ESTs	4.6
451407	AA131376	Hs.328401	fibroblast growth factor 12b	4.6
446765	R5337	Hs.21956	Homo sapiens mRNA: cDNA DKFZp470006 (fr	4.6
430147	R62704	Hs.234343	hair/tenases-of-spli related with YRP	4.6
437204	AL110216	Hs.12285	ESTs, Weakly similar to I55214 ciliary	4.6
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.6
422175	N7885	Hs.6382	ESTs, Highly similar to T00381 hypotheti	4.5
407889	R34556	Hs.30040	ESTs, Weakly similar to S65657 alpha-1C-	4.5
419343	AA456245	Hs.85603	down-regulated by Cimb1, a	4.5
421790	A/H86201	Hs.22654	sodium channel, voltage-gated, type I, a	4.5
428399	AA452244	Hs.16727	ESTs	4.5
450149	AW962781	Hs.132863	Zic family member 2 (odd-paired Drosophi	4.5
453118	AW195849	Hs.252757	ESTs	4.5
443455	AB001025	Hs.9349	ryanodine receptor 3	4.4
442613	A1004002	Hs.130522	Kv channel-interacting protein 1	4.4
429543	AA455889	Hs.167273	PYYC-finger-containing Rad5-effector pro	4.4
416209	AA236776	Hs.75078	MAO2 (maleic anhydride deficient, yeast, h	4.4
418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila) HP1 alpha	4.4
435202	A971313	Hs.170204	KIAA0591 protein	4.4
437496	AA452378	Hs.170144	Homo sapiens mRNA: cDNA DKFZp471125 (fr	4.4
451264	A1571616	Hs.172967	ESTs	4.4
439039	A1656707	Hs.48713	ESTs	4.4
439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.4
424963	AF742434	Hs.169911	ESTs	4.4
410611	AW954134	Hs.20924	KIAA1628 protein	4.4
402605				4.4
409248	AB033035	Hs.51965	KIAA1209 protein	4.4
442222	AB51301	Hs.164723	ESTs	4.4
454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	4.4
454293	H49739	Hs.134013	ESTs, Moderately similar to HK01_HUMAN H	4.4
442832	AW206560	Hs.253569	ESTs	4.4
407304	AA565832	Hs.209043	gln-32603.s1 NCX_CGAP_AA1 Homo sapiens	4.4
423279	AW959861	Hs.250835	ESTs	4.3
427194	AA399018	Hs.250835	ESTs	4.3
419723	AL120193	Hs.92614	longevity assurance (LAG1, S. cerevisiae	4.3
445810	AW265700	Hs.156660	ESTs	4.3
409734	BE161664	Hs.56155	hypothetical protein	4.3
410389	AW554049	Hs.8177	ESTs, Weakly similar to P1HUB6 tubulin	4.3
411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.3
433024	AA573847	Hs.26549	KIAA1706 protein	4.3
453202	AW085781	Hs.26270	hypothetical protein FLJ11568	4.3
425284	AA353953	Hs.203369	ESTs, Weakly similar to gonadotropin ind	4.3
416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	4.3
431789	H19500	Hs.269222	mitogen-activated protein kinase 4	4.3
444600	R41398	Hs.6996	ESTs	4.3

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454042	H22570	Hs.172572	hypothetical protein FLJ20953	4.3
441859	A132588	Hs.8022	T13A protein	4.3
425266	BE297611	Hs.155392	collapsin response mediator protein 1	4.3
410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	4.2
430291	AV660545	Hs.236126	CGI-49 protein	4.2
423597	AA708205	Hs.100343	ESTs	4.2
444127	N63620	Hs.13281	ESTs	4.2
448507	AL133109	Hs.21333	Homo sapiens mRNA, cDNA DKFZ569N1047 (f	4.2
113989	AW452631	Hs.313603	ESTs, Highly similar to AF159033.1 (non)	4.2
426577	H55672	Hs.195115	ESTs, Highly similar to NR022_HUMAN PRO-N	4.2
407919	AI069160	Hs.108581	Homo sapiens brain tumor associated prot	4.2
428536	AI143139	Hs.2288	vismin-like 1	4.2
429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	4.2
423665	AI573109	Hs.152484	ESTs, Weakly similar to I38022 hypothetical	4.2
447138	AA93112	Hs.33828	ESTs, Weakly similar to 210526A.6 cell	4.2
450648	AI703366	Hs.26766	ESTs	4.2
451459	AI797515	Hs.270560	ESTs, Moderately similar to ALUT_HUMAN A	4.2
421686	AB011156	Hs.106794	KIAA0584 protein	4.2
422776	AA194540	Hs.13322	ESTs, Weakly similar to I38022 hypothetical	4.2
346421	AI678031	Hs.122813	ESTs, Weakly similar to ZH22_HUMAN ZINC	4.2
423858	AL137326	Hs.133483	Homo sapiens mRNA, cDNA DKFZ43480650 (f	4.2
344001	AW950505	Hs.36597	serine (or cysteine) proteinase inhibitor	4.2
421380	AL335577	Hs.112198	Homo sapiens mRNA, cDNA DKFZ47474M073 (f	4.2
423239	AI572735	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.1
349607	BE540565	Hs.153460	ESTs	4.1
424028	AF055394	Hs.153692	Homo sapiens cDNA FLJ14354 fts, clone Y7	4.1
446936	H10287	Hs.47314	ESTs	4.1
424240	AB923185	Hs.143535	calcium/calmodulin-dependent protein kin	4.1
412446	AI768015	Hs.92127	ESTs	4.1
409953	AA332277	Hs.57691	cadherin 18, type 2	4.1
416220	N49776	Hs.170594	hypothetical protein MGC10546	4.1
415683	AA249897	Hs.48784	ESTs	4.1
426071	AW138057	Hs.163835	ESTs	4.1
428743	AL080050	Hs.301549	Homo sapiens mRNA, cDNA DKFZ564H172 (f	4.1
342809	AA365509	Hs.131703	ESTs	4.1
440105	AA594210	Hs.5592	Homo sapiens clone Z3809 mRNA sequence	4.1
452039	AI922988	Hs.172510	ESTs	4.1
425905	AB032959	Hs.318594	novel C2HC4 type Zinc finger (ring finger	4.1
457561	AA331517	Hs.286055	chimerin (chimaerin) 2	4.1
429038	AL022613	Hs.194766	solitaire related gene 5 (mouse)-like	4.1
423932	AW944556	Hs.165330	neuronal protein	4.1
436637	AI783629	Hs.26766	ESTs	4.1
439231	AW581935	Hs.141480	Homo sapiens mRNA, cDNA DKFZ434N079 (f	4.1
450530	NM_006668	Hs.25121	cytochrome P450, subfamily 46 (cholester	4.1
427721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	4.1
427881	AW012003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfat	4.1
410486	AW235094	Hs.69233	zinc finger protein	4.0
413916	N49813	Hs.75615	apolipoprotein C-II	4.0
438703	AB03373	Hs.31599	ESTs	4.0
424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fts, clone HE	4.0
405771				4.0
118841	NM_002332	Hs.89137	low density lipoprotein-related protein	4.0
421754	AB611535	Hs.148135	sarasin/threonine kinase 33	4.0
424175	AL137273	Hs.142307	hypothetical protein	4.0
425773	N12129	Hs.237749	ESTs	4.0
427304	AA761526	Hs.163853	ESTs	4.0
428682	AA436915	Hs.131748	ESTs, Moderately similar to ALUT_HUMAN A	4.0
452834	AE338627	Hs.105685	KIAA1688 protein	4.0
453745	AA952989	Hs.635908	hypothetical protein MGC14726	4.0
405239	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	4.0
413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	4.0
429558	AA685086	Hs.26339	ESTs, Weakly similar to S21348 probable	4.0
435854	AJ278120	Hs.4096	putative ankyrin-repeat containing prote	4.0
439199	R40373	Hs.26299	ESTs	4.0
439450	RS1613	Hs.125304	ESTs	4.0
446782	AB53048	Hs.144006	ESTs	4.0
419687	AB538859	Hs.227659	ESTs, Weakly similar to T202_HUMAN TRANS	3.9
420408				3.9
453362	H14988	Hs.107375	ESTs	3.9
414219	W20010	Hs.75823	ALL-1-kras gene from chromosome 1q	3.9
420578	AA813546	Hs.59034	GTP-binding protein Rho?	3.9
425010	T16837	Hs.4241	ESTs	3.9
444230	H95537	Hs.146067	ESTs	3.9
411736	AW282779	Hs.165979	ESTs	3.9
418551	F07809	Hs.83505	paired box gene 6 (aniridia, keratitis)	3.9
405311				3.9
408460	AA054726	Hs.285574	ESTs	3.9
410638	AW105231	Hs.192035	ESTs	3.9
414699	AB15523	Hs.76920	synuclein, alpha (non A4 component of am	3.9
418849	AA745447	Hs.53565	Homo sapiens PIG-M mRNA for mannose-6-ph	3.9
429477	AJ275514	Hs.66568	ESTs	3.9
433766	AA609234	Hs.112669	ESTs	3.9
436190	AK001059		gb1 homo sapiens cDNA FLJ10197 fts, clone	3.9

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	447891	R41754	Hs.6496	ESTs	3.9
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	3.9
	404283				3.9
5	453191	AW659912	Hs.7076	KIAA 1705 protein	3.9
	423666	XG5060	Hs.211584	neurofilament, light polypeptide (58kD)	3.9
	417754	AW160375	Hs.74565	amyloid beta (A β) precursor-like protein	3.9
	445314	AJ589948	Hs.65489	Homo sapiens cDNA: FLJ21517 f1s, clone C	3.9
	435652	N32388	Hs.334370	uncharacterized hypothalamic protein HBE	3.9
	407078	AA292264	Hs.57776	ESTs, Moderately similar to D38022 hypot	3.9
10	430564	AA179626	Hs.82183	ESTs	3.9
	436420	AA443896	Hs.31595	ESTs	3.9
	445133	AW157645	Hs.153505	ESTs	3.9
	432590	AJ609273	Hs.110783	ESTs	3.9
	453331	AJ240695	Hs.8095	ESTs	3.9
15	410227	AB009284	Hs.61152	exozucases (multiple)-like 2	3.8
	424535	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 f1s, clone PL	3.8
	451489	NM_005503	Hs.26468	amyloid beta (A β) precursor protein bind	3.8
	447247	AW365351	Hs.287555	Homo sapiens cDNA FLJ13880 f1s, clone NT	3.8
20	448302	AJ480288	Hs.182956	Homo sapiens mRNA for KIAA1672 protein,	3.8
	415659	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibit	3.8
	417365	D13168	Hs.82002	endothelin receptor type B	3.8
	446727	AB011895	Hs.16032	KIAA0523 protein	3.8
	424340	AA339036	Hs.7033	ESTs	3.8
	423346	AJ257677	Hs.127415	synaptotagmin 1	3.8
25	412788	AA120960	Hs.198416	ESTs	3.8
	404593				3.8
	416955	N27833	Hs.259028	ESTs, Weakly similar to D38022 hypot	3.8
	426956	AA450367	Hs.224223	ESTs, Moderately similar to D38022 hypot	3.8
30	439619	AW975998	Hs.58595	ESTs, Weakly similar to D38022 hypot	3.8
	436634	WV5377	Hs.157	microtubule-associated protein 2	3.8
	446322	AA879430	Hs.19492	grip118k: s1 Scores_NFL_T_C8C_S1 Homo s	3.8
	447751	AP861573	Hs.19492	protocadherin 8	3.8
	452453	AJ902519	Hs.61009-101198-051 BT009 Homo sapien	3.8	
	430671	AW162840	Hs.5541	kinase family member 5C	3.8
35	447937	AL109716	Hs.20034	Homo sapiens cDNA: FLJ22486 f1s, clone H	3.8
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22486 f1s, clone H	3.8
	447028	AW193128	Hs.157257	brain lipid protein-1	3.8
	446458	AJ805078	Hs.208251	ESTs	3.8
40	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	3.8
	407385	AA501019	Hs.272072	ESTs, Weakly similar to D38022 hypot	3.8
	428841	AJ418430	Hs.104935	ESTs	3.8
	430643	AW970055	Hs.287425	MEGF10 protein	3.8
	422263	AA307539	Hs.129908	KIAA0591 protein	3.8
	451625	R56793	Hs.105575	alanine-glyoxylate aminotransferase 2-B	3.8
	436236	BE165952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN1	3.8
	441928	AJ370188	Hs.211454	ESTs	3.8
	441797	AJ936933	Hs.214536	ESTs	3.7
	414922	D00723	Hs.77531	glycine cleavage system protein H (amino	3.7
	425589	F07396	Hs.49715	ESTs	3.7
50	437007	AA741300	Hs.262599	ESTs, Weakly similar to D38022 hypot	3.7
	435793	AB037734	Hs.4993	KIAA1313 protein	3.7
	443682	AJ363061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.7
	425741	AF032152	Hs.158412	Homo sapiens clone 24638 mRNA sequence	3.7
55	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	3.7
	440980	AW051597	Hs.143707	ESTs	3.7
	452898	AA814497	Hs.78792	ESTs	3.7
	436575	AF213457	Hs.44234	tingering receptor expressed on myeloid	3.7
	429334	AJ879418	Hs.27205	ESTs	3.7
60	420489	AA815089	Hs.193513	ESTs	3.7
	426890	AA363157	Hs.41284	ESTs	3.7
	438849	W08948	Hs.10762	ESTs	3.7
	441869	NM_003947	Hs.8004	huntingtin-associated protein interactin	3.7
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced	3.7
	459318	NM_000038		glt-Homo sapiens adenomatous polyposis c	3.7
65	459518	AB374119	Hs.294069	Homo sapiens cDNA FLJ13384 f1s, clone PL	3.7
	434444	AJ755278	Hs.101257	hypothetical protein MGC3295	3.7
	421183	AL138240	Hs.102447	TSC-22-like	3.7
	410555	U92649	Hs.64311	α disintegrin and metalloproteinase doma	3.7
70	421637	AF036290	Hs.105300	Homo sapiens clone 23556 mRNA sequence	3.7
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21956 f1s, clone H	3.7
	420807	AA206217	Hs.57946	ESTs	3.7
	449951	AW265634	Hs.133100	ESTs	3.7
	422634	NM_016010	Hs.118821	CG-62 protein	3.7
75	421030	AW161357	Hs.101174	microtubule-associated protein tau	3.7
	427099	AB032653	Hs.173560	odd Ozten m homolog 2 (Drosophila, mous	3.7
	452355	N64926	Hs.25002	G-protein-coupled receptor 34	3.7
	404483	AJ206836	Hs.150386	ESTs	3.7
	429597	NM_003816	Hs.2442	α disintegrin and metalloproteinase doma	3.7
	423756	AA828125	Hs.7149	glt-cd71a9:s1 NC1_CGAP_Ov2 Homo sapiens	3.6
80	425187	AW014486	Hs.22609	ESTs	3.6
	434959	BE255080	Hs.299315	collapse response mediator protein-5; C	3.6
	413199	M62843	Hs.75235	ELAV (embryonic lethal, abnormal vision,	3.6
	445729	H21066	Hs.13223	Homo sapiens mRNA full length insert cDN	3.6

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5	448758	AB018311	Hs.21917	KIAA0768 protein	3.4
	432613	AW081698	Hs.80712	KIAA0202 protein	3.4
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.4
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	3.4
	410108	AA081658	Hs.318775	ASBP-related protein 6	3.4
10	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferase	3.4
	402855				3.3
	422170	A1791949	Hs.112432	anti-Müllerian hormone	3.3
	445034	AW203376	Hs.143659	ESTs	3.3
	424278	W26020	Hs.167888	neural cell adhesion molecule 1	3.3
15	423611	AB011163	Hs.125908	KIAA0591 protein	3.3
	435593	R88872	Hs.4964	DKF ZP586J1624 protein	3.3
	404819				3.3
	439507	AW661783	Hs.211061	ESTs	3.3
	427315	AA179549	Hs.175563	Homo sapiens mRNA, cDNA DKF Zp564N0763 (f	3.3
20	426593	T79153	Hs.48589	zinc finger protein 228	3.3
	454996	AW650180		gb:U.3.C10219-271099-022-009.C10219 Homo	3.3
	409227	M26460		gb:Homo sapiens (clone 104) retinolact	3.3
	409045	AA635062	Hs.50094	Homo sapiens mRNA, cDNA DKF Zp540C0515 (f	3.3
	415238	R37780	Hs.21422	ESTs	3.3
25	417845	AI117461	Hs.82719	Homo sapiens mRNA, cDNA DKF Zp56F1822 (f	3.3
	421192	AA833718	Hs.204529	KIAA1806 protein	3.3
	425695	AW118191	Hs.112229	ESTs	3.3
	438885	A1886558	Hs.194907	ESTs	3.3
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	3.3
30	452103	R42764	Hs.339554	ESTs, Weakly similar to CB022 hypophel	3.3
	435590	AF150278	Hs.33578	KIAA0820 protein	3.3
	453616	NM_003462	Hs.33346	dynein, axonemal, light intermediate pol	3.3
	457285	A1038858	Hs.130522	Kv channel-interacting protein 1	3.3
	436045	AB037723	Hs.5028	DKF ZP564D0423 protein	3.3
35	437470	AL390147	Hs.134742	hypothetical protein DKF Zp547D0665	3.3
	446520	AB002567	Hs.21355	desiccatorin and CaM kinase-like 1	3.3
	436480	A1271643	Hs.87469	putative acid-sensing ion channel	3.3
	432656	NM_000246	Hs.3076	MHC class II transactivator	3.3
	414369	AW604296	Hs.9550	Sec1 gamma	3.3
40	423582	BE200831	Hs.23837	Homo sapiens cDNA FLJ11812 fs, clone HE	3.3
	445953	A1612775	Hs.145710	ESTs	3.3
	427940	AA417812	Hs.38775	ESTs	3.3
	414683	S78296	Hs.78888	hypothetical protein MGIC12702	3.3
	429484	AF104332	Hs.154501	soluble carrier family 7 (soluble amino	3.3
45	420649	A1866964	Hs.124704	ESTs, Moderately similar to S65557 alpha	3.3
	419498	AL036591	Hs.20887	hypothetical protein FLJ10392	3.3
	457579	AB030816	Hs.36761	HRAS-like suppressor	3.3
	436556	AC64497	Hs.7572	ESTs	3.3
	424369	R87622	Hs.26714	KIAA1831 protein	3.2
50	457065	A1476318	Hs.192480	ESTs	3.2
	440210	AW674562	Hs.125296	ESTs	3.2
	444513	AL120214	Hs.7117	glutamate receptor, ionotropic, AMPA 1	3.2
	434353	AA530693	Hs.131375	ESTs, Moderately similar to ALLU_HUMAN1	3.2
	414430	AC346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.2
55	439924	A1965897	Hs.125293	ESTs	3.2
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.2
	423175	W27595	Hs.16653	hypothetical protein FLJ14627	3.2
	415115	AA214228	Hs.127751	hypothetical protein	3.2
	407878	D87468	Hs.40888	activity-regulated cytoskeleton-associat	3.2
60	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.2
	437162	T78028	Hs.154679	synaptogamin 1	3.2
	439644	AA302517	Hs.92732	KIAA1444 protein	3.2
	450313	AC138989	Hs.332533	Bardet-Biedl syndrome 2	3.2
	409459	D86407	Hs.54481	low density lipoprotein receptor-related	3.2
65	410933	AW811706	Hs.334858	hypothetical protein MGIC12250	3.2
	418527	AA450396	Hs.71449	Homo sapiens cDNA, FLJ21950 fs, clone H	3.2
	420081	AW510776	Hs.54558	tubulin tyrosine ligase-1	3.2
	429496	AA453800	Hs.192793	ESTs	3.2
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	3.2
70	434928	AW015955	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	3.2
	433532	AW291486	Hs.117305	Homo sapiens, clone IMACE.3582908, mRNA	3.2
	438306	AW188266	Hs.163645	ESTs	3.2
	439274	AF086092	Hs.48372	ESTs	3.2
	440847	AA607511	Hs.130178	ESTs	3.2
75	441750	AA22234	Hs.143434	coronin 1	3.2
	455350	AW901809		gb:Q10-NN1020-170400-195-h22 NN1020 Homo	3.2
	430890	XS4232	Hs.2699	glypican 1	3.2
	420568	F05247	Hs.247735	protocadherin alpha 10	3.2
	410768	AF138185	Hs.65187	Homo sapiens clone 23700 mRNA sequence	3.2
80	427450	AW041526	Hs.178121	KIAA0626 gene product	3.2
	430456	AA314998	Hs.241503	hypothetical protein	3.2
	430181	AF065314	Hs.234785	cyclic nucleotide-gated channel alpha 3	3.2
	418512	AW489874	Hs.89981	diacylglycerol kinase, zeta (DGKZ)	3.2
	413912	AF243745	Hs.6266	Rho guanine nucleotide exchange factor (3.2
	450589	A1369275	Hs.243010	Homo sapiens cDNA FLJ14445 fs, clone HE	3.2
	424899	AL119387	Hs.119062	ESTs	3.2
	430277	R88520	Hs.120917	ESTs	3.2

	451455	A1937227	Hs.8821	hepatic antimicrobial peptide	3.2
	450878	AI89975	Hs.4775	juncophilin 3	3.2
	447745	AAW015920	Hs.161359	ESTs	3.2
	435458	F11872	Hs.4892	Human sapient, clone 2481 mRNA sequence	3.2
5	427279	AB033100	Hs.309546	KIA protein (similar to mouse pRab1)	3.2
	417417	F05745	Hs.89512	ATPase, Ca++ transporting, plasma membra	3.1
	438010	AW897846	Hs.5421	Human sapient, protein DKF2p761N09121	3.1
	439570	T99925	Hs.269151	ESTs, Weakly similar to ALU1, HUMAN ALU S	3.1
	432527	AW915202	Hs.102754	EST, Hs.102754	3.1
	416001	X86804	Hs.79371	salt (Drosophila)-like 2	3.1
	421988	AW404081	Hs.161333	ESTs	3.1
	426509	X031166	Hs.2050	protein-related gene, rapidly induced b	3.1
	408786	AA731187	Hs.294027	ESTs	3.1
	434894	AW028395	Hs.3153	beta-1,3-galactosyltransferase 1 (glucur	3.1
15	417273	AA684859	Hs.335951	human protein DKF2p66F10322	3.1
	418329	AAW047430	Hs.84152	cystathionine-beta synthase	3.1
	434546	AW52408	Hs.108314	ESTs, Hs.108314	3.1
	428632	AF578289	Hs.342329	ESTs, Weakly similar to ZNF1, HUMAN Z	3.1
	425790	BE171598	Hs.135222	ESTs, Weakly similar to 130022 hypothel	3.1
20	438192	AS890905	Hs.337620	Human sapient, AFGL3-1 mRNA, part, p	3.1
	424939	AK000059	Hs.153881	ESTs, Weakly similar to XEN-62 antigen mRNA, par	3.1
	403053	F95624	Hs.2186	erk-tyrosine translation elongation factor	3.1
	404299				3.1
25	407854	AF069291	Hs.40539	chromosome 8 open reading frame 1	3.1
	410181	AI488210	Hs.261285	proteinase regulator 1 (PR1, L), Arabidops	3.1
	418882	BE537037	Hs.273294	Human sapient, clone DKF2p66F109693	3.1
	449101	AA205847	Hs.23015	G protein-coupled receptor	3.1
	453240	AB169254	Hs.27935	hypothetical protein DKF2p56F133	3.1
30	440486	BE243513	Hs.7212	hypothetical protein PF1044	3.1
	408095	BE205612	Hs.83785	dihydrodipicolinate reductase	3.1
	438654	AI120078	Hs.291987	ESTs, Weakly similar to B2-25C8-B cell g	3.1
	414706	AW040125	Hs.76989	KIA0097 gene product	3.1
	438315	BE390513	Hs.27935	hypothetical protein MG04387	3.1
	428555	AL111472	Hs.172778	Human sapient, mRNA DKF2p56F0513 (p	3.1
	428658	BE159244	Hs.150200	ESTs, Weakly similar to F12-29C22	3.1
	4110126	BE169274	Hs.103378	KIA00636 gene product	3.1
	433512	A1243396	Hs.4855	voltage-gated sodium channel beta-3 subu	3.1
	425491	AA883316	Hs.255221	ESTs	3.1
40	452571	AF154046	Hs.1148	zinc finger protein	3.1
	412140	AA219691	Hs.73625	RAB8 interacting, kinesin-like (gabrin	3.1
	445255	NM_014841	Hs.12477	SARSin-associated, protein, 91 kDa	3.1
	432154	AI0701523	Hs.112575	ESTs	3.1
	435808	AW026515	Hs.31791	acylphosphatase 2, muscle type	3.1
	438458	AW971186	Hs.29808	ESTs, Hs.29808	3.1
45	448616	AF035621	Hs.21611	Human sapient, clone IMAGE2498025, mRNA	3.0
	428281	AA830856	Hs.29808	Human sapient, cDNA FLJ11212, is, clone C	3.0
	443906	AA346031	Hs.7913	ESTs	3.0
	417318	AW953307	Hs.128911	ESTs	3.0
	425919	AW298597	Hs.51984	Human sapient, clone IMAGE2498025, mRNA	3.0
	444153	AK001015	Hs.10414	hypothetical protein FLJ10478	3.0
	408790	AW580227	Hs.47850	neurotrophic tyrosine kinase, receptor	3.0
	403342	W03242	Hs.44893	Human sapient, clone TC22AT0011 mRNA seq	3.0
	414568	AW503398	Hs.255683	ESTs, Moderately similar to 130022 hypot	3.0
55	422758	AF152329	Hs.284180	proteohelmin gamma subfamily C, 3	3.0
	412633	AF121860	Hs.102590	3, sorting nexin 10	3.0
	428361	NM_015905	Hs.183588	transcription intermediary factor 1	3.0
	413469	L34059	Hs.8048	cathepsin A, type 1, R-phactin (reflind)	3.0
	416805	F13271	Hs.79981	Human clone 23595 mRNA sequence	3.0
	419518	U79289	Hs.90798	Human clone 23650 mRNA sequence	3.0
	422709	AK315331	Hs.153485	ESTs	3.0
	421335	H87655	Hs.26411	ESTs	3.0
	424901	Z11933	Hs.182505	POU domain, class 3, transcription fact	3.0
	426617	W58006	Hs.266258	endonuclease G-like 1	3.0
	427386	AW563561	Hs.337717	ESTs	3.0
65	429885-2	NA1_027050	Hs.225951	protein tyrosine phosphatase, receptor I	3.0
	435071	DE0683	Hs.35495	ESTs	3.0
	435092	AL137310	Hs.4749	Human sapient, mRNA DKF2p761E13121 (3.0
	436211	AK001158	Hs.334828	ESTs	3.0
	439936	AL134851	Hs.194778	Hypothetical protein FLJ10719; KIAA1794	3.0
	445895	BE247129	Hs.145558	ESTs	3.0
	432280	AB71925	Hs.117895	ESTs, Moderately similar to 1457A82-B cell	3.0
	445994	AA137152	Hs.286049	phosphoserine aminotransferase	3.0
	439528	AW905309	Hs.63802	ESTs, Highly similar to 100391 hypothel	3.0
70	430222	AK013218	Hs.157492	cell cycle	3.0
	432322	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.0
	439566	AF068387		gb-Human sapient, full length insert cDNA	3.0
	425782	U66468	Hs.159525	cell growth regulatory with Eph-rod domain	3.0
	415686	DA4643	Hs.1414	secreted molecular calcium-binding protein	3.0
	416874	H88752	Hs.42568	ESTs	3.0
80	410386	W678187	Hs.3327	Human sapient, cDNA FLJ22195 is, clone H	3.0
	414161	AA345421	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	404084	Z99348	Hs.124261	ESTs, Weakly similar to 130022 hypothel	3.0

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429163	AA884766		gbram20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.0
454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	3.0
418196	A745649	Hs.26549	KIAA1708 protein	3.0
434131	A058275	Hs.143659	ESTs	2.9
441255	R05350	Hs.171835	ESTs	2.9
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALUB_HUMAN ALU S	2.9
453905	NM_023114	Hs.36566	LIM domain kinase 1	2.9
416602	NM_006159	Hs.79359	net (chicken)-like 2	2.9
431173	AW971198	Hs.294068	ESTs	2.9
425599	AW382745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
436401	A1087958	Hs.29088	ESTs	2.9
422960	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	2.9
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1)	2.9
412490	AW003564	Hs.288850	Homo sapiens cDNA: FLJ22526 fs, clone H	2.9
433149	BE257672	Hs.42949	hypothetical protein HE55	2.9
434811	AW971205	Hs.114280	ESTs	2.9
425897	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21933 fs, clone C	2.9
462092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
453495	AA442105	Hs.33084	soluble carrier family 2 (facilitated glu	2.9
411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN !!!	2.9
419227	BE537383	Hs.89739	cholesterol receptor, nicotinic, beta po	2.9
427651	AW405731	Hs.18498	Homo sapiens cDNA: FLJ12277 fs, clone MA	2.9
441707	R0527	Hs.21963	hypothetical protein DKFZp618B0614	2.9
435741	A124068	Hs.113099	ESTs	2.9
437273	AL137451	Hs.120873	ESTs, Highly similar to 146266 hypothet	2.9
422939	AW3954055	Hs.98427	ESTs, Weakly similar to 138022 hypothet	2.9
433715	AA883521	Hs.222064	ESTs	2.9
439935	S75105	Hs.301676	glutamate receptor, ionotropic, kainate	2.9
437267	AW511443	Hs.258110	ESTs	2.9
453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 lent	2.9
402350				2.9
420592				2.9
408814	N62499	Hs.176227	hypothetical protein FLJ11155	2.9
411849	AW964970	Hs.18851	ESTs, Moderately similar to KIAA1276 pro	2.9
414653	U01116	Hs.77501	sarcoglycan, beta (43RD dystrophin-assoc	2.9
423751	AW235633	Hs.46525	ESTs	2.9
426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.9
450203	AF097994	Hs.301528	L-tyrosine/alpha-aminoacidipate aminotra	2.9
459311	R40192	Hs.21527	Human DNA sequence from clone GS1-115M0	2.9
425304	AA462844	Hs.31329	Ruvblast protein factor 11	2.9
428500	A1815395	Hs.184641	fatty acid desaturase 2	2.9
421641	A1638164	Hs.106334	Homo sapiens clone 23836 mRNA sequence	2.9
421141	AW117261	Hs.125914	ESTs	2.9
407870	A6032990	Hs.40719	hypothetical protein KIAA11654	2.9
456723	Z43902	Hs.4748	adenylate cyclase activating polypeptide	2.9
436456	AW292677	Hs.248122	G protein-coupled receptor 24	2.9
421483	NM_003388	Hs.104717	hypothetical protein MGC11333	2.9
412190	R16160	Hs.274461	ESTs	2.9
445131	NM_000929	Hs.290	phospholipase A2, group V	2.9
441658	A1611973	Hs.127525	ESTs	2.9
437367	A196874	Hs.28847	AD026 protein	2.9
423420	A1571364	Hs.126382	Homo sapiens mRNA: cDNA DKFZp7611224 (f	2.9
427958	AA418000	Hs.98280	potassium intermediate/small conductance	2.9
429084	AJ001443	Hs.196514	opticon factor 3b, subunit 3, 130kd	2.9
447067	R42096	Hs.21964	ESTs	2.9
430887	N66801	Hs.262087	KIAA1641 protein	2.9
441824	A16007871	Hs.7977	KIAA0411 gene product	2.9
424126	AA335535	Hs.98917	ESTs	2.9
408739	W01556	Hs.238797	ESTs, Moderately similar to 138022 hypot	2.9
447422	BE618703	Hs.98258	orthopedia (Drosophila) homolog	2.9
435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-4K	2.9
446997	AA363439	Hs.167858	Sp1-1 protein	2.9
43573	AF234887	Hs.57652	cachectin, EGF LAG seven-pass G-type rece	2.9
408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fs, clone PL	2.9
419586	A008485	Hs.144759	ESTs, Weakly similar to 138022 hypothet	2.9
417022	NM_014737	Hs.80905	Ras-associated (RAC2/RAF-3) domain form	2.8
408432	AW165262		gbram20a10.s1 NCL_CGAP_Cm1.1 Homo sapiens	2.8
420320	A1802051	Hs.96533	KIAA0363 protein	2.8
425241	AA324624	Hs.155247	aldolase C, fructose-bisphosphate	2.8
428570	AA431682	Hs.134832	ESTs	2.8
424415	NM_001075	Hs.146580	enkestat 2, (gamma, neuronal)	2.8
409185	AW961601	Hs.252406	hypothetical protein FLJ12296 similar to	2.8
411555	AF113537	Hs.70659	HMP19 protein	2.8
426847	S78723	Hs.298523	5-hydroxytryptamine (serotonin) receptor	2.8
456809	AW972512	Hs.20865	src-associated polypeptide, 30KD	2.8
420071	AD028958	Hs.94805	ATP-binding cassette, sub-family A (ABC1)	2.8
424572	N19650	Hs.150741	2,3'-cyclic nucleotide 3' phosphodiester	2.8
444670	H58373	Hs.332938	hypothetical protein MGC3370	2.8
411089	AA465454	Hs.163418	cell division cycle 2-like 1 (PTSLRE pr	2.8
416111	AA033813	Hs.79016	chromatin assembly factor 1, subunit A (2.8
440637	AW900115	Hs.7309	Homo sapiens clone 23741 mRNA sequence	2.8
408554	AA836381	Hs.315111	nuclear receptor co-repressor NR4C3 comp	2.8
403056	R58624	Hs.2186	eukaryotic translation elongation factor	2.8

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423449	AW97900	Hs.33067	ESTs	2.8
424188	AW954552	Hs.142634	zinc finger protein	2.8
429005	AA443143	Hs.50929	hypothetical protein FLJ13842	2.8
434981	AW182577	Hs.25077	ESTs	2.8
437435	AA249439	Hs.27027	hypothetical protein DKFZp762h1311	2.8
442748	AI018713	Hs.135787	ESTs	2.8
443312	N52025	Hs.46616	ESTs	2.8
450940	AI744843	Hs.143209	ESTs, Weakly similar to U30022 hypothesis	2.8
452738	AL133800	Hs.7098	hypothetical protein MGC12435	2.8
459182	AA584070	Hs.118145	ESTs	2.8
439793	AA018825	Hs.7934	Kruppel-like factor 4 (klf4)	2.8
425683	AW995441	Hs.10475	ESTs	2.8
434269	AK001981	Hs.3781	similar to murine leucine-rich repeat pr	2.8
429550	X78565	Hs.289114	hscartization (Tennacis C. cyclotactin)	2.8
433290	R20077	Hs.302185	Homo sapiens clone Z518 mRNA sequence	2.8
434275	AF123659	Hs.93605	leucine zipper, putative tumor suppressor	2.8
435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	2.8
435294	A1538226	Hs.32975	guanine nucleotide binding protein 4	2.8
425158	R93366	gb:U7904Ls1	Sources fetal liver spleen	2.8
428180	AI129767	Hs.182874	guanine nucleotide binding protein (G-pr	2.8
409348	AA015335	Hs.146000	ESTs	2.8
409887	AL137534	Hs.56876	Homo sapiens mRNA; cDNA DKFZp439h1419 (f	2.8
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vacuolar	2.8
430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
417642	BE302665	Hs.105451	hypothetical protein FLJ20357	2.8
419169	AW981390	Hs.262346	ESTs, Weakly similar to S72482 hypothesis	2.8
434508	AA140378	Hs.112982	ESTs	2.8
446775	AW293417	Hs.156455	ESTs	2.8
408838	AI665335	Hs.40369	ESTs	2.8
422555	BE290035	Hs.118400	singed (Drosophila)-like (sea urchin) fas	2.8
447397	BE247576	Hs.18442	E1 enzyme	2.8
412530	AA765268	Hs.266273	hypothetical protein FLJ13345	2.8
424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13396 fs, clone PL	2.8
446377	AW014022	Hs.170953	ESTs	2.8
445924	BE242158	Hs.24427	DKFZP56601646 protein	2.8
447710	AI420529	Hs.32841	ESTs	2.8
406409				2.8
416913	AW934714		gb:RC1-DT0001-031259-011-a11 DT0001 Homo	2.8
426400	M76361	Hs.169743	Homo sapiens clone Z5121 neuronal octact	2.8
413264	W25158	Hs.13471	hypothetical protein FLJ26033	2.8
458907	AW937420	Hs.95962	ESTs	2.7
422864	AA318323		gb:EST20390 Refina II Homo sapiens cDNA	2.7
430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	2.7
452023	AB032599	Hs.27355	KIAA1173 protein	2.7
423022	AL152042	Hs.272348	Homo sapiens mRNA; cDNA DKFZp761L1212 (f	2.7
452438	BE514230	Hs.29595	JMW protein	2.7
435408	H07897	Hs.4302	ESTs, Weakly similar to T29299 hypothesis	2.7
418791	AA305633	Hs.194628	ESTs	2.7
438921	AA382435	Hs.291829	ESTs	2.7
423454	NM_015040	Hs.128855	CSR1 protein	2.7
442091	AW770493	Hs.182874	guanine nucleotide binding protein (G-pr	2.7
442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fs, clone H	2.7
412436	AA655389		gb:u76001 s1 NCL_GCAP_Ab1 Homo sapiens	2.7
432821	BE170202	Hs.279005	retic acid ester family 21 (organic anion	2.7
416404	AA180138	Hs.107924	ESTs	2.7
441364	AW450466	Hs.126830	ESTs, Weakly similar to YD38_YEAST HYPOT	2.7
452022	AW989756	Hs.34145	ESTs, Weakly similar to B4647 GTP-bind	2.7
425304	AA374532	Hs.124673	Homo sapiens cDNA FLJ11417 fs, clone HE	2.7
428722	U76456	Hs.190787	issue inhibitor of metalloproteinase 4	2.7
419701	AW952323	Hs.125908	KIAA0591 protein	2.7
420372	AW980049	Hs.293660	Homo sapiens, clone IMAGE3535476, mRNA,	2.7
410318	AA084050	Hs.265929	ESTs, Weakly similar to S23550 retinovin	2.7
414603	RS8304	Hs.25119	ESTs, Weakly similar to YE40_YEAST HYPOT	2.7
416096	H18577	Hs.88974	cytochrome b-245, beta polypeptide (cho	2.7
420996	AW149342	Hs.24444	Homo sapiens cDNA FLJ22165 fs, clone H	2.7
424856	AA341746	Hs.95251	ESTs, Weakly similar to ZNA3_HUMAN ZINC	2.7
435304	AA339822	Hs.108887	ESTs	2.7
441027	AI911412	Hs.126444	ESTs	2.7
452545	N31940	Hs.14434	ESTs, Weakly similar to U30022 hypothesis	2.7
454201	AB023191	Hs.44131	KIAA0574 protein	2.7
448560	BE511883	Hs.23213	ESTs	2.7
426807	AA385315	Hs.156682	ESTs	2.7
425825	AI925508	Hs.159590	lymphocyte antigen 5 complex, locus H	2.7
440351	AF030533	Hs.7179	RAD1 (S. pombe) homolog	2.7
425390	AF026534	Hs.156114	protein tyrosine phosphatase, non-recept	2.7
427624	AA408245	Hs.24895	ESTs	2.7
426413	AA377823		gb:EST08085 Synovial sarcoma Homo sapien	2.7
422491	AA338848	Hs.117546	neurotatin	2.7
424580	AA158727	Hs.150555	protein predicted by clone Z3723	2.7
432415	T16971	Hs.289014	ESTs, Weakly similar to AA3932 mucin 2 p	2.7
414865	AI151755	Hs.274414	hypothetical protein FLJ14457	2.7
415027	HI7482	Hs.23079	ESTs	2.7
445568	H00918	Hs.268744	KIAA1795 protein	2.7

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5	433115	R66754	Hs.229706	GRB2-associated binding protein 1	2.7
	428862	NM_003346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.7
	447959	AI452784	Hs.270270	ESTs, Weakly similar to 2109260A B cell	2.7
	426420	BE383808	Hs.324340	NDRC family, member 4	2.7
	436899	AA764552	Hs.281567	ESTs	2.7
10	444100	AA383343	Hs.22119	CDCH14 (cell division cycle 14, S. cerevi	2.7
	426501	AW043782	Hs.263616	ESTs	2.7
	449092	U91641	Hs.22285	alpha2,8-sialyltransferase	2.7
	427311	AB030672	Hs.175411	KIA0855 protein	2.7
	435313	BE005774	Hs.153748	hypothetical protein FLJ22490	2.7
15	440429				2.7
	416289	W26333	Hs.337438	ESTs	2.7
	439308	AW163034	Hs.6467	synaptotagmin 3	2.6
	418146	A1955289	Hs.300759	ribosomal protein L36	2.6
	412046	Y07847	Hs.73088	RAS-related on chromosome 22	2.6
20	435640	A1932350	Hs.152825	ESTs	2.6
	435883	U87223	Hs.31622	conixin-associated protein 1	2.6
	428167	AA170021	Hs.16332	ESTs	2.6
	420026	AB014680	Hs.6786	carbohydrate (N-acetylglucosamine-6-O) s	2.6
	443715	A1583187	Hs.9700	cyclin E1	2.6
25	421247	BE391727	Hs.102910	general transcription factor IIII, polype	2.6
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.6
	411956	AB004682	Hs.77867	adenosine A1 receptor	2.6
	451697	AW449774	Hs.296380	POM (PDM121 rat homolog) and ZP3 fusion	2.6
	433701	AW445023	Hs.15155	ESTs	2.6
30	457358	AI479755	Hs.129010	ESTs	2.6
	430347	NM_000039	Hs.239706	GRB2-associated binding protein 1	2.6
	418027	AB037607	Hs.63293	hypothetical protein	2.6
	442491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.6
	425171	AW732240	Hs.16365	ESTs	2.6
35	455335	AW226845	Hs.250726	EST	2.6
	425402	A1215881	Hs.24970	ESTs, Weakly similar to B34323 GTP-bind	2.6
	453169	AB037815	Hs.32156	KIA1354 protein	2.6
	433647	AA603367	Hs.222294	ESTs	2.6
	450414	AJ070735	Hs.21446	KIA1716 protein	2.6
40	446233	A1252026	Hs.25205	ESTs	2.6
	415446	F06698	Hs.66075	ESTs	2.6
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	2.6
	413012	D63777	Hs.75137	KIA0193 gene product	2.6
	428671	BE297651	Hs.108462	line finger protein 179	2.6
45	427158	AA635603	Hs.166231	ESTs	2.6
	408968	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.6
	495616	A1048662	Hs.246858	EST	2.6
	402693				2.6
	495039	AA131424	Hs.50340	ESTs	2.6
50	422696	AW961469	Hs.154116	ESTs	2.6
	423130	AW897566	Hs.21213	ESTs	2.6
	430796	W67621	Hs.109590	geneHoxin 1	2.6
	438871	R05518	Hs.46736	hypothetical protein FLJ23476	2.6
	440192	AA672282	Hs.190596	ESTs	2.6
55	419708	AI000753	Hs.92374	hypothetical protein	2.6
	449436	AA860329	Hs.279307	hypothetical protein DKFZ4342117	2.6
	436870	AW204219	Hs.155580	calnexin	2.6
	448424	AW005892	Hs.31924	ESTs	2.6
	401324				2.6
60	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	433843	AA392805	Hs.44865	lymphoid enhancer-binding factor 1	2.6
	428001	H97426	Hs.219307	ESTs, Moderately similar to Transforming	2.6
	429139	F01082	Hs.66087	ESTs	2.6
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, D	2.6
65	440866	AW372514	Hs.86149	phosphoinositid 3-phosphate-binding prot	2.6
	444001	A095087	Hs.132299	ESTs, Moderately similar to S05657 alpha	2.6
	412049	NS3437	Hs.18768	adenylate kinase-5	2.6
	441763	BE313412	Hs.7961	Homo sapiens clone 25012 mRNA sequence	2.6
	425287	R88249	Hs.155524	peramut (Drosophila)-like 2	2.6
70	437149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probate	2.6
	452244	AW084176	Hs.223296	ESTs, Weakly similar to CB0222 hypoth	2.6
	453478	AF083989	Hs.33021	neuro-oncological ventral antigen 2	2.6
	418962	AA714835	Hs.271863	ESTs	2.6
	418886	AW961605	Hs.21145	hypothetical protein FG083M05.2	2.6
75	442357	A1340440	Hs.11614	HSPC055 protein	2.6
	428748	AW593206	Hs.98785	Hsp37 protein	2.6
	444984	H15474	Hs.132898	fatty acid desaturase 1	2.6
	434304	T32982	Hs.102720	ESTs	2.6
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.6
80	420682	BE047878	Hs.380383	Homo sapiens chromosome 19, centrom R2837	2.6
	452856	AF034799	Hs.30881	protein tyrosine phosphatase, receptor 1	2.6
	436440	AI471862	Hs.196008	Homo sapiens cDNA FLJ117123 lis, clone HE	2.6
	438827	AF069251	Hs.115325	RAB7, member RAS oncogene family-like 1	2.6
	433216	AF717412	Hs.47330	neuritin-3	2.6
	435380	AA679001	Hs.192221	ESTs	2.6
	426966	AF059214	Hs.154687	cholesterol 25-hydroxylase	2.6
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.6

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5	419304	A1271326	Hs.146101	ESTs, Weakly similar to T45070 protein k	2.6
	422991	H10940	Hs.48965	Homo sapiens cDNA: FLJ21693 fls, clone C	2.6
	446548	R13205	Hs.21413	solute carrier family 12, (potassium-chl	2.6
	435370	A994074	Hs.22958	ESTs	2.6
	408675	NM_015434	Hs.48964	DKFZP434B168 protein	2.5
10	450005	AJ007421	Hs.172957	sal (Drosophila)-like 3	2.5
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibit	2.5
	438549	BE386801	Hs.21858	trnucleotide repeat containing 3	2.5
	427851	AB26125	Hs.45546	ESTs	2.5
	411800	N35542	Hs.103042	microtubule-associated protein 19	2.5
15	457683	AB21877	Hs.140002	ESTs, Moderately similar to ALU1_HUMAN	2.5
	451422	AB002336	Hs.26395	erythrocyte membrane protein band 4.1-4	2.5
	430713	AA351847	Hs.2842	eukaryotic translation elongation factor	2.5
	428676	AL049842	Hs.194019	ESTs	2.5
	428963	AW302682	Hs.258208	Homo sapiens, clone MGC:15606, mRNA, com	2.5
20	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.5
	429550	AW293055	Hs.119357	ESTs	2.5
	438612	AA223599	Hs.6351	cleavage and polyadenylation specific to	2.5
	435760	AF231922	Hs.213004	chromosome 21 open reading frame 52	2.5
	427513	A476318	Hs.192480	ESTs	2.5
25	430061	AB037817	Hs.230188	KIAA1395 protein	2.5
	435922	BE301530	Hs.5010	Homo sapiens clone 24672 mRNA sequence	2.5
	417120	BE326521	Hs.159450	ESTs	2.5
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN	2.5
	412980	AB181590	Hs.20977	hypothetical protein MGC3129 similar to	2.5
30	427208	H06509	Hs.52423	KIAA1566 protein	2.5
	424327	AA431107	Hs.31205	ESTs	2.5
	438340	RA2246	Hs.21606	ESTs	2.5
	450550	T65617	Hs.101257	hypothetical protein MGC3295	2.5
	439444	A1277652	Hs.54578	ESTs, Weakly similar to 138022 hypotheti	2.5
35	400777			ESTs	2.5
	439478	AF043460	Hs.6574	deformed epidermal autoregulatory factor	2.5
	450407	NM_000810	Hs.24969	gamma-aminobutyric acid (GABA) A recepto	2.5
	450385	AB31024	Hs.24948	synuclein, alpha interacting protein (sy	2.5
	432558	R97268	Hs.172769	ESTs	2.5
40	402860			ESTs	2.5
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.5
	419063	BE047699	Hs.53454	ESTs	2.5
	414698	NM_002543	Hs.77729	oxidized low density lipoprotein (lectin	2.5
	452623	AB121124	Hs.20606	transcription factor-like 5 (basic helix	2.5
45	417791	AW965339	Hs.114717	ESTs	2.5
	418079	RA0058	Hs.6911	ESTs	2.5
	408495	W68796	Hs.237731	ESTs	2.5
	424704	L22971	Hs.188	phosphodiesterase 4B, cAMP-specific (du	2.5
	431370	AL198567	Hs.161962	Homo sapiens mRNA; cDNA DKFZ547D023 (tr	2.5
50	429803	W81489	Hs.223025	RAB31, member RAS oncogene family	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42hs kinase	2.5
	421413	BE547647	Hs.177781	hypothetical protein MGC5618	2.5
	408055	BE315170	Hs.8087	hMG-S protein	2.5
	415261	T40928	Hs.8346	ESTs	2.5
55	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.5
	417873	BE266559	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	2.5
	418388	R72332	Hs.25256	Homo sapiens cDNA FLJ11364 fls, clone HE	2.5
	421002	AF119030	Hs.100932	transcription factor 17	2.5
	422244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.5
60	423553	AA405635	Hs.96854	ESTs, Weakly similar to DYLC_HUMAN CYTO	2.5
	427961	AW293165	Hs.143134	ESTs	2.5
	426301	AW620666	Hs.98440	ESTs, Weakly similar to 138022 hypotheti	2.5
	428508	BE252383	Hs.184668	SRB131 protein	2.5
	428858	AA436760		gb-zv6211.1 Soares_totat_fetus_Nb2FB3_	2.5
65	428943	AW086160	Hs.37638	ESTs, Weakly similar to KIAA1392 protein	2.5
	424827	AL037330	Hs.86338	Homo sapiens cDNA FLJ11602 fls, clone HE	2.5
	435347	AW0148973	Hs.118963	ESTs	2.5
	437949	U78519	Hs.41654	ESTs, Weakly similar to A46010 X-linked	2.5
	438208	AL041224	Hs.65379	ESTs	2.5
70	442081	U29589	Hs.7139	cholinergic receptor, muscarinic 3	2.5
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	2.5
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
	442337	A1371029	Hs.129257	ESTs, Weakly similar to TC17_HUMAN TRANS	2.5
	427289	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.5
75	445556	A1910241	Hs.12897	activated protein 3-beta	2.5
	443086	A1628357	Hs.208937	ESTs	2.5
	459583	A1907673		gb-IL-BT152-080399-004 BT152 Homo sapien	2.5
80	TABLE 24B:				
	Play	Unique Ecos proberset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genebank accession numbers			
	Play	CAT Number	Accession		
80	408422	1058667_1	AW195262 R27868 AW811262		
	412225	1284108_1	AW902042 N77591		
	412636	129439_1	AA665089 AA135130 AA484059 AA102419 AW877765		

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5	416120	1571266_1	H46739 H51513 H19779
	416871	1626761_1	H68716 N90792 N04283
	416813	163001_1	AW534714 BE161007 BE162500 AW749802 AW749864 BE162498 BE161005 AA190449 AA513465 BE161006 BE162499
	422864	222336_1	AA318323 H111145 R15789 AA451945 AA476690 AA438364 Z43802 F11753 T65491 D81821
10	422949	222384_1	AA1941945 H65456 AA318323 AA318327 AA318332 AA169452 AA894424
	422977	223410_1	AA631498 A017191 AA481211 AA761823 AA714555 AA768099 AA808286 A934089 AA570222 AA574389 AA582438 A745346 AA964510 AA139642
	423756	231725_1	AA828125 AA834883 AA330555
	425168	247352_1	R96366 AL133829 AA351036 H78818 AA477084 Z28957 H80194
15	425517	252729_1	AF121178 BE162736 AA358827
	426413	266560_1	AA3177823 AW954494 A1022688
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	428679	294049_1	AA4431765 AA452015
20	428858	296451_1	AA436760 AW237453 BE327436 N43347 N56967
	429007	298301_1	D80642 AA443145 AL119015 AW904500
	429163	300543_1	AA884766 AW974271 AA582975 AA447312
	433532	368950_1	AW975367 AA598607 AA747735
25	436190	41555_1	AK61059 AA633055
	437034	437113_1	AA742543 AA608575 AW976668
	438458	457837_1	AW975186 AA807807 D29548
	438993	467651_1	AA828935 AA834879 A1826361
30	439568	473871_1	AF086387 Y77884 W27211
	440322	491866_1	AA870430 BE070282 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070199 BE070404 BE070270 BE070400
	444584	611495_1	A1168422 D80113 T59074
	447197	711622_1	R36075 A1366546 R36167
35	448451	75066_1	AW015994 R38988 AW000578 A156202 A1521706
	450425	84032_1	AW970107 AA513651 A4010406
	452453	918300_1	A19C2519 A19C2518 A19C2516
	454996	1248640_1	AW850180 AW850326
40	455350	1283853_1	AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798

TABLE 24C

Phy: Unique number corresponding to an Eos probe
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:485-495.
 Strand: indicates DNA strand from which exons were predicted.
 N1_position: indicates nucleotide positions of predicted exons.

40	Phy	Ref	Strand	N1_position
	400777	8131663	Plus	70745-71121
	400780	8131663	Minus	118372-118619
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
45	400860	9757499	Minus	151830-152104,152549-152744
	400992	9806828	Plus	140390-140822
	401324	9863791	Plus	234057-234174
	402408	9796239	Minus	110326-110491
50	402804	9508420	Plus	20393-20767
	402605	9509420	Plus	47880-47973
	402893	8559863	Minus	82366-82515
	402855	9662953	Minus	59763-59909
55	404029	7671252	Plus	108716-111112
	404048	3688074	Minus	54421-56806
	404049	3688074	Minus	57576-78155
	404283	2276311	Minus	88448-89564
60	404299	5738652	Minus	3826-4025
	404541	8318559	Plus	103456-103664
	404584	9857511	Plus	138651-139153
	404593	9944086	Minus	74522-75789
65	404721	9856648	Plus	173763-174294
	404819	4678240	Minus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17528,18261-18347,18443-18578
	405238	7249119	Minus	51779-51836
	405711	7018349	Plus	91191-91254,91510-91589
70	405819	4007557	Plus	2830-2967
	406311	9211559	Minus	137114-136033

TABLE 25A: ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)

Table 25A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Exon HuO3 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 35th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75	Phy	Unique Eos probe identifier number			
	Exon	Exemplar Accession number, Genbank accession number			
	UnigeneID	Unigene number			
	Unigene Title	Unigene gene title			
	R1:	Ratio of 75 th percentile tumor to 95 th percentile normal adult nervous system tissue			
80	Phy	UnigeneID	Unigene Title	R1	
	452441	N78723	Hs.108106	transcription factor	20.1
	436895	AF037335	Hs.5338	carbonic anhydrase XII	15.2
	453941	U39817	Hs.36820	Bloom syndrome	14.2
	443247	BE614387	Hs.333953	c-Myc target JPO1	12.4

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428330	L22524	Hs.22556	matrix metalloproteinase 7 (matrilysin)	12.0
447342	A119268	Hs.19322	Human sapiens, Similar to RIKEN cDNA 2010	11.7
422163	AF022208	Hs.112360	prolamin (mouse)-like 1	11.4
439451	AF086270	Hs.278554	heterochromatin-like protein 1	11.2
426800	AL033588	Hs.152203	MyoD family inhibitor	10.2
416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (10.0
444190	A1878918	Hs.10526	cysteine and glycine-rich protein 2	9.9
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklins)	9.9
449340	AN253788	Hs.195359	hypothetical protein MGIC10554	9.8
409731	AA125095	Hs.56145	thymosin, beta, identified in neuroblast	9.4
393978	BE139460	Hs.124673	Human sapiens cDNA FLJ11477 fs, clone HE	8.9
411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	8.9
456516	BE172704	Hs.222746	KIAA1610 protein	8.2
420022	AA814043	Hs.88045	ESTs	7.9
422631	BE218919	Hs.118793	hypothetical protein FLJ10688	7.9
453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.9
438527	A1965251	Hs.115325	RAB7, member RAS oncogene family-like 1	7.9
427581	NM_014788	Hs.179703	KIAA0129 gene product	7.9
418661	NM_001949	Hs.1189	E2F transcription factor 3	7.8
404584	A1253123	Hs.127356	ESTs, highly similar to S21424 nestin [H	7.8
429643	AA455680	Hs.167279	FYVE-finger-containing Rab5 effector pro	7.7
409538	AW453420	Hs.21335	ESTs	7.7
444655	BE513125	Hs.47783	B aggressive lymphoma gene	7.5
456759	BE259150	Hs.127792	delta (Drosophila)-like 3	7.5
412777	A1332773	Hs.270123	ESTs	7.4
436507	AW661793	Hs.211061	ESTs	7.3
432050	AW665996	Hs.130728	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.3
417061	A1675944	Hs.188591	Human sapiens cDNA FLJ12003 fs, clone HE	7.3
428976	AL037824	Hs.194695	ras homolog gene family, member 1	7.2
433244	AB040843	Hs.217285	KIAA1510 protein	7.1
439720	AA324975	Hs.128993	ESTs, Weakly similar to T00979 hypophel	7.0
420432	AW195262	Hs.3076	gb:nc76745.1 NCL_CGAP_CML1 Homo sapiens	7.0
434164	AW207019	Hs.148135	serine/threonine kinase 33	7.0
445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	7.0
439726	AW443893	Hs.235700	ESTs, Weakly similar to S8596 zinc fing	7.0
432655	NM_000206	Hs.3076	HMGB class II transcription factor	6.8
431117	AF003522	Hs.205500	delta (Drosophila)-like 1	5.8
453387	A1990741	Hs.252809	ESTs	5.8
418821	AA343602	Hs.183161	gb:ph1001.s1 NCL_CGAP_GC01 Homo sapiens	5.8
437034	AA742643	Hs.69328	MD-2 protein	5.5
411252	AB018549	Hs.69328	matrix metalloproteinase 9 (gelatinase B	6.4
424687	J05070	Hs.151738	ESTs, Weakly similar to A46010 X-linked	5.3
452553	A132084	Hs.271741	gb:EST387475 IMAGE sequences, MAGN Homo	6.3
433532	AW975367	Hs.38207	human DNA sequence from clone RP4-S3015	5.2
420311	AW445644	Hs.21868	ESTs	5.2
418997	R45137	Hs.21868	gb:nc132003.s1 NCL_CGAP_AA1 Homo sapiens	5.2
407304	AA565832	Hs.13872	cytokine-like protein C17	6.1
432626	AF193766	Hs.57471	ESTs	5.1
449448	D05730	Hs.57471	ESTs	5.0
403790				6.0
425517	AF121179	gb:AF121179 Homo sapiens liver (Chang L-	6.0	
420674	NM_000055	Hs.1327	bulky/cholesterase	6.0
435542	AA607376	Hs.263533	ESTs	5.9
418216	AA662240	AF159141	protein	5.8
439086	AF085947	gb:Human sapiens full length insert cDNA	5.8	
408037	AW271720	Hs.42233	hypothetical protein FLJ10300	5.7
412225	AW930242	gb:U00-NH1022-170400-193-022 NH1022 Homo	5.7	
435109	AA222153	Hs.132759	hypothetical protein MGC15729	5.7
435005	U80743	Hs.306094	kininucleotide repeat containing 12	5.7
429149	AW1913360	Hs.197952	ESTs, Weakly similar to I38022 hypophel	5.7
418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	5.6
405558				5.6
424232	BE093589	Hs.38178	hypothetical protein FLJ23468	5.6
442547	AA306997	Hs.217494	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
413063	AL033579	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	5.5
420560	AW200748	Hs.59115	ESTs	5.5
420896	BE250162	Hs.83765	dihydrodipicolate reductase	5.4
443539	A1076182	Hs.134074	ESTs, Moderately similar to ALU6_HUMAN A	5.4
425318	AA375125	Hs.147112	Human sapiens cDNA: FLJ22322 fs, clone H	5.4
429115	AA445728	Hs.289020	Human sapiens cDNA FLJ14698 fs, clone MA	5.3
453900	AW001582	Hs.226444	ESTs, Weakly similar to ALU6_HUMAN ALU S	5.3
444168	AW373979	gb:RF1-H10256-081199-011-401 H10256 Homo	5.3	
432789	D26361	Hs.3104	KIAA0042 gene product	5.3
437036	A571514	Hs.133022	ESTs	5.2
421267	BE391727	Hs.102910	general transcription factor IIIF, polyo	5.2
441523	AW514263	Hs.301771	ESTs, Weakly similar to ALU6_HUMAN III	5.2
451106	BE382701	Hs.25060	y-myc avian myelocytomatosis viral relat	5.1
457211	AW972565	Hs.32399	ESTs, Weakly similar to S157197 vasodilat	5.1
454157	AW162506	Hs.312481	ESTs, Weakly similar to S66669 hydropom	5.1
423343	AA324643	Hs.246106	ESTs	5.1
425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRP) protein	5.1
406679	AA070786	gb:nc69007.r1 Stratagene neurospethium	5.1	
442671	A1005668	Hs.134779	EST	5.1

[illegible]

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	404295				3.8
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.8
	428728	NM_016625	Hs.191381	hypothelial protein	3.8
5	409142	AL136877	Hs.50758	SMCA (structural maintenance of chromoso	3.8
	430172	AA685591	Hs.61889	ESTs	3.8
	447499	AA026280	Hs.147674	procadherin beta 16	3.8
	405884				3.8
	437236	AW137817	Hs.244353	ESTs	3.7
	418853	BE397036	Hs.12121	acid phosphatase 5, tartrate resistant	3.7
10	444143	AW747996	Hs.160999	ESTs, Moderately similar to A55194 throm	3.7
	426529	NM_014956	Hs.158282	KIAA0040 gene product	3.7
	425502	R98895	Hs.125823	ESTs	3.7
	419141	NM_007019	Hs.35002	ubiquitin carrier protein E2-C	3.7
	402424				3.7
15	429469	M54590	Hs.27	glycine dehydrogenase (decarboxylating;	3.7
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.7
	414872	U82010	Hs.177513	COX10 (yeast) homolog, cytochrome c oxid	3.7
	426071	AW130657	Hs.163635	ESTs	3.7
	419078	M53119	Hs.89584	insulinoma-associated 1	3.7
20	428037	N47474	Hs.89230	po/ssum intermediate/small conductance	3.7
	416547	H62914	Hs.265946	ESTs, Weakly similar to PC4259 fentin	3.7
	435899	AA764852	Hs.291567	ESTs	3.6
	436722	AW075977	Hs.138096	gb. EST388086 MAGE retrosequence, MAGN Homo	3.6
	440652	AQ16751	Hs.142977	ESTs	3.6
25	428450	NM_014791	Hs.184339	KIAA0175 gene product	3.6
	452103	RA2764	Hs.339654	ESTs, Weakly similar to 138022 hypothel	3.6
	429548	H58990	Hs.37699	ESTs	3.6
	439546	AF088056	Hs.16359	gb Homo sapiens full length insert cDNA	3.6
	443544	A076315	Hs.16359	ESTs	3.6
	418478	U38545	Hs.1174	cyclin-dependent kinase inhibitor 2A (ne	3.6
	435899	A1249107	Hs.269091	ESTs	3.6
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specifi	3.6
	438078	A016377	Hs.131693	ESTs	3.6
35	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	3.6
	416871	H98716	Hs.133226	gb.yr13d58.a1 Soares melanocyte 2HbH4H Ho	3.5
	424085	NM_002914	Hs.14623	replication factor C (activator 1) 214d	3.5
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.5
	452281	A0012339	Hs.274263	hypothelial protein FLJ10377	3.5
40	436123	AA057454	Hs.25406	ESTs, Highly similar to unnamed protein	3.5
	411256	AW534529	Hs.170010	gb. Q101010-01159-035-009 IT0010 Homo	3.5
	419239	AA468183	Hs.184589	Homo sapiens cDNA: FLJ23241 f1, clone C	3.5
	455065	BE064391		gb. R04-B10310-110300-015-008 BT0310 Homo	3.5
	435532	AW291488	Hs.117395	Homo sapiens, clone IMAGE:368299, mRNA	3.5
	447101	N72185	Hs.44189	ESTs	3.5
45	410530	UG5809	Hs.64173	ATPase, H+-transporting, lysosomal (vacu	3.5
	422156	N34524	Hs.355610.a1 Soares, multiple sclerosis, _	3.5	
	453618	NM_003462	Hs.33845	dyenin, axonemal, light intermediate pol	3.5
	439743	AL369955	Hs.263858	Homo sapiens mRNA full length insert cDN	3.5
	453384	AA355025	Hs.35222	KIAA0185 gene product	3.5
50	424554	NM_000546	Hs.1946	tumor protein p53 (Li-Fraumeni syndrome)	3.5
	420721	AA927802	Hs.159471	ZAP3 protein	3.5
	426764	AA732524	Hs.151484	ESTs, Weakly similar to ALUC2_HUMAN III	3.4
	420549	A1869584	Hs.124704	ESTs, Moderately similar to S65657 alpha	3.4
	448831	AL080123	Hs.22182	zinc finger protein 23 (K0X 16)	3.4
55	444371	BE540274	Hs.239	forkhead box M1	3.4
	402604				3.4
	442407	AW465684	Hs.32353	mitogen-activated protein kinase kinase	3.4
	414300	A304870	Hs.188680	ESTs	3.4
60	444670	H58373	Hs.323038	hypothelial protein MGC570	3.4
	414550	BE379808	Hs.60115856711	NH_MGC_533 Homo sapiens c	3.4
	452211	A1965513	Hs.233420	ESTs	3.4
	414418	AW429265	Hs.78084	hypothelial protein MGC2721	3.4
	449561	AW765634	Hs.133100	ESTs	3.4
	413257	BE075035	Hs.6M3-BT0584-263000-002-g05 BT0584 Homo	3.4	
65	453857	AL080235	Hs.33861	DKF ZP58561621 protein	3.4
	417104	NM_001350	Hs.52101	peckstein homology-like domain, family	3.4
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47ND, chr	3.4
	446189	H85224	Hs.214013	ESTs	3.4
	437385	AA757055	Hs.164090	ESTs	3.4
70	453552	AW005640	Hs.26384	ESTs, Moderately similar to S65657 alpha	3.4
	408286	A174325	Hs.271923	Homo sapiens cDNA: FLJ22785 f1, clone K	3.4
	455778	BE088746	Hs.6M2-BT0693-210300-123-009 BT10693 Homo	3.3	
	417546	H65569	Hs.18845	ESTs	3.3
	412871	M61393	Hs.73946	endothelial cell growth factor 1 (plate	3.3
75	456331	AW811324	Hs.510141-1310309-017-A02 ST0141 Homo	3.3	
	454294	AB000734	Hs.50640	JAK binding protein	3.3
	457131	AC002310	Hs.301463	Human Chromosome 16 BAC clone C19387SK-A	3.3
	410102	AW248508	Hs.279727	Homo sapiens cDNA: FLJ14035 f1, clone HE	3.3
	449676	AW380579	Hs.206657	ESTs	3.3
80	436211	AK001581	Hs.334828	hypothetical protein FLJ10719, KIAA1794	3.3
	453746	AL120611	Hs.334828	gb.DKF Zp761h113_1 761 (XMAA; hamy2)	3.3
	452799	A1548829	Hs.213786	ESTs	3.3
	435380	AA679001	Hs.192221	ESTs	3.3

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	426746	J03626	Hs.2057	uridine monophosphate synthetase [partial	3.3
	453262	H14948	Hs.107375	ESTs	3.3
	456473	A020788	Hs.25682	Homo sapiens mRNA for KIAA1863 protein,	3.3
	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fs, clone PL	3.3
5	445777	A550371	Hs.145364	ESTs	3.3
	423757	AL049337	Hs.132574	Homo sapiens mRNA, cDNA DKF Zp564P016 (fr	3.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	3.3
	404299				3.3
	404108				3.3
10	425189	H16622		gh:ym6007.r1 Sources infant brain 1MB H	3.3
	445316	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.3
	450193	A1916071	Hs.15607	Homo sapiens Fanconi anemia complement	3.2
	427725	U66839	Hs.180533	mitogen-activated protein kinase kinase	3.2
	424051	AL110203	Hs.138411	Homo sapiens mRNA, cDNA DKF Zp564P1922 (f	3.2
15	418958	NM.000078	Hs.59538	cholesterol ester transfer protein, plac	3.2
	449248	M33782	Hs.23391	Homo sapiens, Similar to transcription f	3.2
	439416	W58294	Hs.56254	ESTs	3.2
	401596	AA172106	Hs.110950	Rag C protein	3.2
	405380	AF123050	Hs.44532	dubiquitin	3.2
20	450325	A1935962	Hs.26299	ESTs	3.2
	428730	AA625047	Hs.25750	ESTs	3.2
	457536	AA305233	Hs.278712	eukaryotic translation initiation factor	3.2
	426836	N411720	Hs.172664	vesicle-associated membrane protein 8 (e	3.2
	442710	AD016531	Hs.23210	ESTs	3.2
25	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	3.2
	403970	AJ018210	Hs.144083	ESTs	3.2
	416192	NM_005036	Hs.599	paraneoplastic proliferative activated reexp	3.2
	446676	H09380	Hs.300965	ESTs	3.2
	451459	AT797515	Hs.270560	ESTs, Moderately similar to ALU1_HUMAN A	3.2
30	407603	AW955705	Hs.62804	Homo sapiens, clone XIMAGE-4299322, mRNA,	3.2
	413840	AJ301558	Hs.146381	RNA binding motif protein, X chromosome	3.2
	448751	BE551203	Hs.201792	ESTs	3.2
	432593	AW301003	Hs.51483	ESTs, Weakly similar to hypothetical pro	3.2
	458786	AK457098	Hs.280848	ESTs	3.2
35	455909	BE156417	Hs.278798	ESTs	3.2
	418311	AA685591		gm:mb6at 2s1 INCL CGAP: GCB1 Homo sapiens	3.2
	439710	AF086543		gm:Homo sapiens full length insert cDNA	3.2
	434559	AF147315		gm:Homo sapiens full length insert cDNA	3.1
	450800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fs, clone NT	3.1
40	439703	AW980614	Hs.146381	RNA binding motif protein, X chromosome	3.1
	414799	AT52416	Hs.77325	multi-helic growth factor binding prote	3.1
	437960	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fs, clone L	3.1
	434182	W20309	Hs.118520	G-protein gamma-12 subunit	3.1
	417900	BE250127	Hs.82506	CDCC20 (cell division cycle 20, S. cerev	3.1
45	434769	AA548884	Hs.134278	Homo sapiens cDNA FLJ12616 fs, clone NT	3.1
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.1
	426413	AA377823		gb:EST190805 Synovial sarcoma Homo sapien	3.1
	447959	A452784	Hs.270270	ESTs, Weakly similar to 2109260A B cell	3.1
	404389				3.1
50	421764	AB81535	Hs.148135	serine/threonine kinase 33	3.1
	419986	A1345455	Hs.78915	GA-binding protein transcription factor,	3.1
	416941	BE000150	Hs.48778	nban protein	3.1
	414761	AJ077228	Hs.77258	enhancer of zeste (Drosophila) homolog 2	3.1
	449611	AJ070354	Hs.197075	ESTs	3.1
55	437446	AA648368	Hs.295368	ESTs	3.1
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	427899	AA829286	Hs.332053	serum amyloid A1	3.1
	417642	BE330565	Hs.105461	hypothetical protein FLJ20367	3.1
	4528172	AW951200	Hs.294142	ESTs, Weakly similar to I380222 hypotheti	3.1
60	446131	NM.000929	Hs.290	phospholipase A2, group V	3.1
	440052	AB633744	Hs.195648	ESTs, Weakly similar to I380222 hypotheti	3.1
	426631	AA381071		gb:EST14100 Activated T-cells XI Homo s	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.1
	406767				3.1
65	447039	AV661798	Hs.282915	ESTs	3.1
	404802				3.1
	406927	M26480		gm:Homo sapiens (clone 104) retinoblasto	3.1
	419314	AW971924	Hs.87280	ESTs	3.0
70	435894	A078667	Hs.188011	ESTs	3.0
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	3.0
	443426	AF098168	Hs.9329	chromosome 20 open reading frame 1	3.0
	423202	AW961282	Hs.152049	ESTs, Weakly similar to I380222 hypotheti	3.0
	407047	X05965		gb:H.sapiens SOD-2 gene for manganese su	3.0
	418241	M26682	Hs.1149	LIM domain only 1 (rhomboid 1)	3.0
75	446599	Z97832	Hs.15476	differentially expressed in FDCP (mouse	3.0
	412950	BE018681	Hs.245342	hypothetical protein FLJ14642	3.0
	428670	AA431682	Hs.134832	ESTs	3.0
	446975	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	3.0
	437756	AA767537	Hs.197096	ESTs	3.0
	415984	L16991	Hs.79006	disacetylhydrolase kinase (hydmydylate kin	3.0
80	402374	AL135225	Hs.301865	dopachrome tautomerase (dopachrome deta	3.0
	443885	H91906	Hs.15284	ESTs	3.0
	434008	AA740878	Hs.112982	ESTs	3.0

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	452568	AA905634	Hs.300870	Homo sapiens mRNA, cDNA DKFZp547M072 (f	3.0
	414239	AI283330	Hs.182330	ESTs	3.0
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.0
5	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ13459 fts, clone PL	3.0
	410276	AA54545	Hs.68301	ESTs	3.0
	433855	N29662	Hs.44104	ESTs	3.0
	406028				3.0
	401626				3.0
	415949	H10562	Hs.21691	ESTs	3.0
10	418583	AA604379	Hs.86211	hypothetical protein	3.0
	417933	X02308	Hs.82562	thymidylate synthetase	3.0
	434577	R37316	Hs.179769	Homo sapiens cDNA: FLJ22487 fts, clone H	3.0
	430437	A176801	Hs.169943	Homo sapiens cDNA FLJ13459 fts, clone PL	3.0
15	427940	AA171812	Hs.38775	ESTs	2.9
	456930	C14904	Hs.105184	Homo sapiens cDNA FLJ12284 fts, clone MA	2.9
	421968	AW450481	Hs.161333	ESTs	2.9
	448775	AB025237	Hs.388	nucleic acid diphosphate linked moi	2.9
	438598	AB055943	Hs.126567	hypothetical protein MG51178	2.9
20	429512	AF062648	Hs.252587	putative tumor-transforming 1	2.9
	451189	AA016019	Hs.40905	ESTs	2.9
	401558				2.9
	426207	BE396557	Hs.30026	HSPC182 protein	2.9
	404721				2.9
	401354				2.9
25	417288	AJ984792	Hs.106812	hypothetical protein FLJ22004	2.9
	427648	AJ376772	Hs.180802	proteasome (prosome, macropain) subunit,	2.9
	435928	H64345	Hs.163861	ESTs	2.9
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	2.9
30	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	2.9
	439972	AJ348100	Hs.124662	ESTs	2.9
	431112	AA373601	Hs.144553	ESTs, Weakly similar to unnamed protein	2.9
	423751	AW235633	Hs.46525	ESTs	2.9
	406748	AW339106	Hs.217493	annexin A2	2.9
35	422154	T79045	Hs.128927	ESTs	2.9
	405588				2.9
	440511	AA309536	Hs.143562	ESTs	2.9
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	2.9
	445043	AW014413	Hs.196066	ESTs	2.9
40	410114	AW690540	Hs.271280	ESTs	2.9
	418217	AA504571		glaa00e12.1 NCL_CGAP_GCB1 Homo sapiens	2.9
	415849	R20529	Hs.6806	ESTs	2.9
	448140	AF146761	Hs.20450	BCAM-like membrane protein precursor	2.9
	453331	A1240665	Hs.8895	ESTs	2.9
45	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	2.9
	432380	T05430	Hs.6194	chondroin sulfate proteoglycan BEH4Bb	2.9
	454377	AA076811	Hs.6194	gb.7803C12 Chromosome 7 Fetal Brain cDNA	2.9
	421491	H99999	Hs.42736	ESTs	2.9
	452291	AF015592	Hs.28853	CDCT (cell division cycle 7, S. cerevisi	2.9
	415446	F05896	Hs.68075	ESTs	2.8
50	439518	W63326	Hs.130746	gb.tr060004.r1 Soares_fetal_hear1_NbH119W	2.8
	427221	L15409	Hs.174007	von Hippel-Lindau syndrome	2.8
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.8
	419451	AS071117	Hs.90535	synactin binding protein 2	2.8
55	447859	BC539108	Hs.22051	hypothetical protein MG515548	2.8
	424126	AA335635	Hs.96917	ESTs	2.8
	458695	AV60159	Hs.282284	ESTs, Weakly similar to 138022 hypothesis	2.8
	418973	AA233056	Hs.191518	ESTs	2.8
	440471	AA388146	Hs.307984	ESTs	2.8
60	421016	AA504593	Hs.101047	transcription factor 3 (E2A immunoglobul	2.8
	433647	AA603367	Hs.222294	ESTs	2.8
	415817	U68967	Hs.76867	protein tyrosine phosphatase, receptor-1	2.8
	421723	AA520409	Hs.320717	sodium channel, voltage-gated, type III,	2.8
	434964	AI638850	Hs.130746	ESTs	2.8
65	432022	AL162042	Hs.272348	Homo sapiens mRNA, cDNA DKFZp761L1212 (f	2.8
	400517	AF242388	Hs.149585	lengsin	2.8
	433023	AW694793	Hs.67409	thrombospondin 1	2.8
	448734	BE514070	Hs.328416	Homo sapiens mRNA, cDNA DKFZp564H1916 (f	2.8
	406736	AI254733	Hs.182426	ribosomal protein S2	2.8
	406207	AW373564	Hs.194637	BANP homolog, SMAR1 homolog	2.8
70	440196	N72847	Hs.125221	ESTs	2.8
	403961				2.8
	452193	AW965689	Hs.22509	ESTs	2.8
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fts, clone KA	2.8
75	440483	AI200836	Hs.150386	ESTs	2.8
	412391	AF1947710	Hs.150386	gb.RC0-MT0004-130300-01-1-e07 MT0004 Homo	2.8
	448769	N65037	Hs.38173	ESTs	2.8
	411632	AW854829		gb.QV2-C10261-201099-011-01 C10261 Homo	2.8
	438221	AI798853	Hs.122224	ESTs, Weakly similar to ALLUS_HUMAN ALLUS	2.8
	457578	AA578027		gb.n0001-1 NCL_CGAP_HSC1 Homo sapiens	2.8
	455510	AA420202	Hs.143640	ESTs, Weakly similar to hypoxanthine	2.8
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ15459 fts, clone NT	2.8
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (His	2.8
	433800	AI034361	Hs.135150	lung type-1 cell membrane-associated gly	2.8

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	425387	J04088	Hs.156346	topoisomerase (DNA II alpha (170K))	2.6
	418228	A4962181	Hs.111219	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	401324			ESTs	2.6
5	462234	AW152225	Hs.165909	ESTs, Weakly similar to U38022 hypothetical	2.6
	442310	A052649	Hs.9451	hypothetical protein MGC13768	2.6
	452204	A4581385	Hs.162473	ESTs, Weakly similar to U38022 hypothetical	2.6
	417144	AA382104	Hs.81337	lectin, galactoside binding, soluble, 9	2.6
	433933	A0754389	Hs.133494	Homo sapiens clone TCC0A/00164 mRNA sequ	2.6
10	437437	AA226869	Hs.16520	hypothetical protein DKFZp762L0311	2.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S65990 Hs	2.6
	407692			ESTs	2.6
	455530	AW964744		gl.RC1-HN0015-040400-011-403 HN0015 Homo	2.6
	436139	AA765786	Hs.120936	ESTs	2.6
	448330	AL036449	Hs.207163	ESTs	2.6
15	422542	AL120344	Hs.25074	mitogen-activated protein kinase-ectonin	2.6
	432753	NM_014075	Hs.336938	Homo sapiens PRO053 mRNA, complete cds	2.6
	434340	A063735	Hs.186755	ESTs	2.6
	436693	AW673223	Hs.301197	B-cell CLL/lymphoma 7C	2.6
	429482	AF076574	Hs.203552	3-phosphoadenosine 5'-phosphosulfate sy	2.6
20	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	2.6
	414217	A309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fs, clone L	2.6
	434165	AA871328	Hs.85361	myosin VIIA (Usher syndrome 1B) (autosoma	2.6
	414635	AA156720	Hs.185342	ESTs	2.6
	424489	T48051	Hs.140260	D-xylose precursor,	2.6
25	436496	AA261959	Hs.5210	glia maturation factor, gamma	2.6
	403797			ESTs	2.6
	434573	AW372340	Hs.159717	ESTs	2.6
	418941	NM_002332	Hs.89137	low density lipoprotein-related protein	2.6
30	415785	R82419	Hs.23603	ESTs, Moderately similar to ALU8_HUMAN A	2.6
	450608	AA010385	Hs.193229	ESTs	2.6
	425304	AA463844	Hs.21139	fibroblast growth factor 11	2.6
	432298	BE311859	Hs.274290	3-phosphoadenosine 5'-phosphosulfate sy	2.6
	410507	AA355288	Hs.40834	transitional epithelia response protein	2.6
35	427343	A080044	Hs.176877	protein kinase C binding protein 2	2.6
	420817	AW135716	Hs.117330	ESTs	2.6
	414399	L47345	Hs.155202	transcription elongation factor B (SII)	2.6
	446089	A086021	Hs.270651	ESTs, Moderately similar to A47582 B-cell	2.6
	440829	AF136407	Hs.7446	chromosome 6 open reading frame 5	2.6
40	408475	AA315514	Hs.47896	hypothetical protein MGC10940	2.6
	405846	AA274569	Hs.127658	ESTs, Moderately similar to Z105260A B c	2.6
	421482	AF016495	Hs.104624	aquaporin 9	2.6
	434846	AW295389	Hs.119768	ESTs	2.6
	428887	A0751848	Hs.49215	ESTs	2.6
45	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	2.6
	437369	AL359587	Hs.271568	hypothetical protein DKFZp762M115	2.5
	428981	AW920797	Hs.49427	Gem-interacting protein	2.5
	432180	Y18418	Hs.272822	RuvB1 (E coli homolog)-like 1	2.5
	418079	R40058	Hs.6911	ESTs	2.5
50	437820	AA769682	Hs.323836	ESTs, Weakly similar to alternatively sp	2.5
	439685	AW956781	Hs.292937	ESTs, Weakly similar to FXD2_HUMAN FORKH	2.5
	425681	AB018297	Hs.159183	KIAA0754 protein	2.5
	435177	A018174	Hs.42936	ESTs	2.5
	437323	AA371145	Hs.226627	leptin receptor	2.5
55	422114	AW194851	Hs.111801	arsenite resistance protein ARS2	2.5
	446478	AS23218	Hs.203456	ESTs	2.5
	426623	AA382826	Hs.132793	ESTs	2.5
	448764	A568807	Hs.182112	ESTs	2.5
	458385	A0651469	Hs.248214	ESTs	2.5
60	430726	N08939	Hs.13434	Homo sapiens clone 24418 mRNA sequence	2.5
	444888	A0851039	Hs.148569	ESTs	2.5
	456179	H75490	Hs.271930	ESTs	2.5
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.5
	406273	NM_000919	Hs.83520	peptidylglycine alpha-amidating monooxyg	2.5
65	418054	NM_002318	Hs.83354	lysozyme-like 2	2.5
	445936	BE543594	Hs.61478	hypothetical protein FLJ22329	2.5
	445967	AW848276		gl.II.3-CT0214-150200-074-E06 CT0214 Homo	2.5
	442303	A4869286	Hs.129168	ESTs	2.5
	455683	AF179897	Hs.104105	Mais (maize) homolog 2	2.5
70	434263	N34895	Hs.44648	ESTs	2.5
	416892	L24498	Hs.80409	growth arrest and DNA-damage-inducible,	2.5
	424528	AW0475971	Hs.238554	ESTs, Weakly similar to KIAA1204 protein	2.5
	405338	Y14443	Hs.88219	zinc finger protein 200	2.5
	412495	Y12395	Hs.315177	interferon-related developmental regulat	2.5
	423098	AA321980	Hs.204682	ESTs	2.5
75	410817	AJ262789	Hs.53059	protein disulfide isomerase related prot	2.5
	430641	AF038961	Hs.67110	mannose-6-phosphate utilization defect 1	2.5
	434928	AW970960	Hs.293821	ESTs	2.5
	440034	AW293376	Hs.143659	ESTs	2.5
80	444620	BE407797	Hs.23754	checkpoint with forkhead and ring finger	2.5
	406876	AJ382286	Hs.180842	ribosomal protein L13	2.5
	412370	AW944614		gl.RIC2-ET0021-280400-011-c25 ET0021 Homo	2.5
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.5
	430357	AW976789	Hs.165607	ESTs	2.5

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414653	U31116	Hs.77501	sarcoglycan, beta (3KB dystrophin-associ	2.5
415097	BE387371	Hs.118954	hypothetical protein FLJ12005	2.5
428619	AK002140	Hs.187378	hypothetical protein FLJ11278	2.5
413976	BE295452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	2.5
445223	AW291553	Hs.254983	ESTs	2.5
423626	X03533	Hs.1722	interleukin 1, alpha	2.5
410165	BE560228	Hs.71669	apoptosis-associated speck-like protein	2.5
406474				2.5
433508	AW298141	Hs.157975	ESTs	2.5
433915	AW148482	Hs.77873	871 homolog 3	2.5
437528	HS9646	Hs.169745	cnumts (Drosophila) homolog 1	2.5
420734	AW972872	Hs.250736	ESTs	2.5
415346	Z43106		glcHSC13E071 normalized infant brain cDN	2.5
419337	AW291112	Hs.269978	ESTs	2.5
444606	R03478	Hs.18941	ESTs	2.5
430061	AB037817	Hs.230188	KIAA1396 protein	2.5
413407	AI356293	Hs.75339	inositol polyphosphate phosphatase-like	2.5
411965	BE467339	Hs.280115	ESTs	2.5
405278	AA346683	Hs.52763	anaphase-promoting complex subunit 7	2.5
403142				2.5
401714				2.5
425681	X74794	Hs.154443	minichromosome maintenance deficient (S	2.5
416505	HS6470	Hs.16004	ESTs	2.5
431518	AA743462	Hs.165337	ESTs	2.5
448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypotelli	2.5
428301	AW628666	Hs.95440	ESTs, Weakly similar to I38022 hypotelli	2.5
404366				2.5
445733	R74546	Hs.29438	Homo sapiens cDNA FLJ12094 fs, clone HE	2.5
458583	AI907673		gbitL-BT152-080369-004 BT152 Homo sapien	2.5
402856	AW939559		gbr RCo-DT0076-110100-031-c09 DT0076 Homo	2.4
420751	J03219	Hs.99513	adrenergic, beta-1-, receptor	2.4
436805	AA721533	Hs.270751	ESTs	2.4
420285	AA259124	Hs.253878	ESTs, Moderately similar to ZN51_HUMAN Z	2.4
453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	2.4
453853	AL040500	Hs.188083	ESTs	2.4
407506	AW103586		gbr-xd63a06 x1 NCJ_CGAP_Ov23 Homo sapien	2.4
464530	BE142075		gbr CM3-010137-170999-012-02 HT01317 Homo	2.4
451026	AA013218	Hs.157492	cer-d4 (mouse) homolog	2.4
420779	L12358	Hs.95922	dopamine receptor D4	2.4
438322	AA804170	Hs.221349	ESTs	2.4
455908	BE198306		gbr QVD-HT0367-150200-114-04 HT0367 Homo	2.4
419625	U91616	Hs.91940	nuclear factor of kappa light polypeptid	2.4
440773	AA352702	Hs.332541	Homo sapiens, Similar to RIKEN cDNA 2700	2.4
450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	2.4
447247	AW505551	Hs.267815	Homo sapiens cDNA FLJ13290 fs, clone NT	2.4
429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40KD)	2.4
451802	AI817711	Hs.205074	ESTs	2.4
419417	R92491	Hs.39429	ESTs	2.4
407054	AF005074	Hs.22465	leukocyte immunoglobulin like receptor,	2.4
423597	BE752948	Hs.65531	hypothetical protein FLJ13833	2.4
427501	AI369280	Hs.131743	ESTs	2.4
451773	Z42044	Hs.26996	KIAA1278 protein	2.4
438945	AA732287	Hs.113528	ESTs	2.4
451594	AW296121	Hs.265253	Homo sapiens cDNA FLJ14115 fs, clone MA	2.4
440514	AA781530	Hs.127236	hypothetical protein FLJ12879	2.4
423721	AF176811	Hs.132004	cardiotrophin-like cytokine, neurotrophi	2.4
452125	BE312642	Hs.28077	GDP-mannose pyrophosphorylase B	2.4
415508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	2.4
453446	BE299996		gbr:500944574F1 NH_MGC_17 Homo sapiens c	2.4
419792	AA250890	Hs.150037	ESTs	2.4
452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotelli	2.4
410447	AW616134		gbr MR3-ST0220-290100-016-e04 ST0220 Homo	2.4
438662	AA223559	Hs.6351	cleavage and polyadenylation specific fa	2.4
402408				2.4
443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.4
414625	AA335738	Hs.76686	glutathione peroxidase 2	2.4
402048				2.4
432088	AA525454		gbr:m85c09 s1 NCJ_CGAP_P:20 Homo sapiens	2.4
431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	2.4
450203	AW859097		gbr L3-CT0220-310100-065-H11 CT0220 Homo	2.4
426249	F05422	Hs.168352	nucleosporin-like protein 1	2.4
446795	AF797713	Hs.155471	ESTs	2.4
414774	X02419	Hs.77274	plasminogen activator, urokinase	2.4
414252	AA346483	Hs.126191	ESTs	2.4
417918	AA295205	Hs.163754	hypothetical protein FLJ12606	2.4
427550	BA242818	Hs.179606	nuclear RNA helicase, DEAD variant of DE	2.4
404020				2.4
407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	2.4
417222	AI235424	Hs.42053	hypothetical protein MG02383	2.4
443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.4
452706	AW445390	Hs.257150	ESTs, Moderately similar to SURF_HUMAN S	2.4
401676				2.4
428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4

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5	436277	RB8520	Hs.120917	ESTs	2.4
	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	2.4
	405353				2.4
	408983	AA131483		gb:z008055.r1 Stratagene neuroepithelium	2.4
	431431	AL086711	Hs.252953	Human DNA sequence from clone RP3-403A15	2.4
10	407889	R34556	Hs.30800	ESTs, Weakly similar to S65557 alpha-1C-	2.4
	453335	AW857376	Hs.165238	fucosyltransferase 3 (galactoside 3(4)-L	2.4
	450621	AW527283	Hs.55918	hypothetical protein FLJ11354	2.4
	419652	AL157465	Hs.51973	ESTs	2.4
	427151	BE174431	Hs.63386	ESTs	2.4
15	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.4
	420681	AAB47602	Hs.106510	ESTs, Moderately similar to ALL2_HUMAN A	2.4
	405286				2.4
	455377	R49570	Hs.180236	ESTs	2.4
	428675	AI051815		gb:q658b05.s1 Soares_NHhPu_S1 Homo sapi	2.4
20	436360	AI562796	Hs.136754	ESTs	2.4
	418592	X95226	Hs.284153	Fanconi anemia, complementation group A	2.4
	415951	AJ000098	Hs.54210	eyes absent (Drosophila) homolog 1	2.4
	445530	W60363	Hs.58446	ESTs	2.4
	419870	AW403911	Hs.260175	phosphoprotein associated with GEMs	2.4
25	404594				2.4
	454276	AW264966	Hs.255374	ESTs	2.4
	423746	AW061817	Hs.132107	NADPH oxidase 1	2.4
	415558	AA885143	Hs.125719	ESTs	2.4
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	2.4
30	409553	L38847		gb:Human (clone p1790) rearranged duro	2.4
	444471	AB220554	Hs.11217	KIAA0877 protein	2.4
	451031	AI360187	Hs.4254	ESTs	2.4
	455302	AW997641		gb:RC6-BN0052-170200-011-006 BN0052 Homo	2.4
	434053	AI627352	Hs.235547	Homo sapiens, clone IMAGE:2905978, mRNA,	2.4
35	401048				2.4
	434420	AA688278	Hs.194864	hypothetical protein FLJ22578	2.4
	425848	BE242709	Hs.159537	vary-RNA synthetase 2	2.4
	449086	AI283357	Hs.208037	ESTs	2.4
	415238	R37780	Hs.21422	ESTs	2.4
40	448337	AW204453	Hs.3782	ESTs	2.4
	416991	N36389	Hs.141296	KIAA0226 gene product	2.3
	412600	L28824	Hs.74101	spleen tyrosine kinase	2.3
	418385	AW959613	Hs.301040	Homo sapiens, clone IMAGE:3357127, mRNA,	2.3
	440759	BE361793	Hs.21446	KIAA1715 protein	2.3
45	450437	X13956	Hs.24998	hypothetical protein MG410471	2.3
	412035	N78559	Hs.293629	hypothetical protein MG3121	2.3
	408739	AI566709	Hs.152426	ribosomal protein S2	2.3
	418506	AA084748	Hs.85359	G protein-coupled receptor 39	2.3
	410286	AI739159	Hs.61888	DNFZF568A/2124 protein	2.3
50	443740	RS6434	Hs.21062	ESTs	2.3
	405605				2.3
	416913	AW934714		gb:RC1-DT0001-031299-011-x11 DT0001 Homo	2.3
	425509	K01155	Hs.2050	pentoxifylline gene, rapidly induced b	2.3
	445828	F05802	Hs.81907	ESTs	2.3
55	457195	AB011099	Hs.196647	KIAA0527 protein	2.3
	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE:3535475, mRNA,	2.3
	423198	MB1933	Hs.1534	cell division cycle 25A	2.3
	457730	AW753613		gb:RC1-CT0268-060100-013-e01 CT0268 Homo	2.3
	412014	AI620650	Hs.43751	ESTs, Weakly similar to A46010 X-linked	2.3
60	447131	NM_004585	Hs.17466	melanocortin receptor responder (azaro	2.3
	446288	AW165020	Hs.149708	ESTs	2.3
	436954	AA740151	Hs.135425	ESTs	2.3
	411658	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo	2.3
	404240				2.3
65	456054	H85081		gb:pw7a09.r1 Soares_placenta_80weeks_	2.3
	416261	AA190926	Hs.190785	ESTs, Moderately similar to S65557 alpha	2.3
	406737	AI356586		gb:qy15h09.r1 NCI_CGAP_Bm23 Homo sapien	2.3
	458453	AI097452	Hs.135055	ESTs	2.3
	452330	AI879127	Hs.191979	KIAA1733 protein	2.3
70	405623	AW635269	Hs.314267	ESTs	2.3
	455470	AW947592		gb:PMG-MT0011-240300-001 c09MT0011 Homo	2.3
	436323	R17697	Hs.140963	ESTs, Weakly similar to I38022 hypotheti	2.3
	450000	AI552797	Hs.10866	hypothetical protein FLJ21709	2.3
	416171	H23896	Hs.125750	leucine-rich repeat-containing 2	2.3
75	419134	T88463	Hs.221771	ESTs	2.3
	445533	AW655733	Hs.258690	spinster-like protein	2.3
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFRA_HUMAN SPUC	2.3
	449911	AI262106	Hs.12653	ESTs	2.3
	417075	US5559	Hs.61134	interleukin 1 receptor, antagonist	2.3
80	411742	AW424753	Hs.17615	eukaryotic translation initiation factor	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-like	2.3
	423491	AA191766	Hs.126673	eukaryotic translation initiation factor	2.3
	407182	AA312551	Hs.230513	ESTs	2.3
	411446	AA178955	Hs.271439	ESTs, Weakly similar to I38022 hypotheti	2.3
	438644	AI126162	Hs.129037	ESTs	2.3
	432691	U29725	Hs.3080	mitogen-activated protein kinase 7	2.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	2.3

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5	411125	AA151847	Hs.58877	cytochrome b-245, alpha polypeptide	2.3
	404054				2.3
	430458	AA479300	Hs.225706	ESTs, Weakly similar to 380222 hypopheli	2.3
	440710	AW574562	Hs.125296	ESTs	2.3
	446727	AB011095	Hs.16032	KIAA0523 protein	2.3
10	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.3
	448919	A0574685	Hs.200141	ESTs	2.3
	415593	R45462	Hs.106541	ESTs	2.3
	411126	NM_000429	Hs.323715	methionine adenosyltransferase 1, alpha	2.3
15	408203	AA053137	Hs.42390	nasopharyngeal carcinoma susceptibility	2.3
	434841	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fs, clone NT	2.3
	450748	A1733053	Hs.130016	ESTs	2.3
	404185				2.3
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	2.3
20	451370	A1791929	Hs.300782	ESTs	2.3
	400034				2.3
	407723	AW071151	Hs.256783	ESTs	2.3
	431320	AW963474	Hs.183070	ESTs	2.3
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.3
25	453707	AW003879	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, con	2.3
	419225	U70073		gb:HSU70073 Human Homo sapiens cDNA clon	2.3
	444656	A277924	Hs.145199	ESTs	2.3
	405741				2.3
	400917				2.3
30	432667	AA736777	Hs.293370	ESTs	2.3
	437949	U78519	Hs.41634	ESTs, Weakly similar to A46010 X-linked	2.3
	450514	AC005785	Hs.25069	A kinase (PRK) anchor protein 8	2.3
	416400	BE243026	Hs.301969	KIAA0245 protein	2.3
	444019	BE173977	Hs.10096	putative nucleolar RNA helicase	2.3
35	405326				2.3
	412077	NS1107	Hs.47199	ESTs, Weakly similar to FLJ00004 protein	2.3
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fs, clone KA	2.3
	414528	AA148890	Hs.188836	ESTs	2.3
	414854	BE546797	Hs.51483	ESTs, Weakly similar to hypothetical pro	2.3
40	420352	BE558335		gb:6011173747.1 Ntr_MGC_16 Homo sapiens c	2.3
	439467	AW292275	Hs.158305	ESTs	2.3
	402627				2.3
	451711	AK000461	Hs.26390	cat eye syndrome chromosome region, cand	2.3
	424308	AW975531	Hs.154443	mitochondrion maintenance deficient (S,	2.3
45	438699	BE405301	Hs.134012	Ctq-related factor	2.3
	405915				2.3
	431503	NM_012129	Hs.258576	claudin 12	2.3
	423306	W85682	Hs.108198	ESTs	2.3
	442332	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	2.3
50	433964	D75991	Hs.30002	SH3-containing protein Sh3GLB2, KIAA1848	2.3
	434437	A5912666	Hs.187813	ESTs	2.3
	436191	BE407866	Hs.170253	hypothetical protein FLJ23262	2.3
	420096	H114028	Hs.54300	serologically distinct colon cancer antiq	2.3
	447942	F12628	Hs.334786	hypothetical protein MGC16040	2.3
55	403166				2.3
	422119	A1277829	Hs.111662	KIAA0590 gene product	2.3
	403751				2.3
	429451	A5006165	Hs.165946	GATA-binding protein 3	2.3
	427413	BE547647	Hs.177781	hypothetical protein MGC5618	2.3
60	409094	AW970396	Hs.265423	ESTs	2.3
	440491	R35252	Hs.24944	ESTs, Weakly similar to 2109260A B cell	2.3
	427722	AK000123	Hs.160479	hypothetical protein FLJ20116	2.3
	405747				2.3
	438210	AA780615	Hs.311601	EST	2.3
65	404652				2.3
	423574	AF055589	Hs.129738	potassium voltage-gated channel, Shaw-re	2.2
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation detec	2.2
	444424	A1654684	Hs.196377	ESTs	2.2
	434031	BE384155	Hs.23723	pseudouridylyl synthase 1	2.2
70	427650	AW601245	Hs.252759	ribosomal protein S3	2.2
	435220	D50030	Hs.104	HGF activator	2.2
	438279	AA805166	Hs.154752	HIV-1 rev binding protein 2	2.2
	424668	D83702	Hs.151573	cytochrome 1 (photolysis-like)	2.2
	4299961	BE246829	Hs.226770	DKF ZP566C0424 protein	2.2
75	424265	A1831229	Hs.128417	hypothetical protein FLJ14009	2.2
	415198	AW009480	Hs.943	natural killer cell transcript 4	2.2
	420536	AL117455	Hs.275438	histone deacetylase 7A	2.2
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associ	2.2
	443753	AW361578	Hs.134749	ESTs	2.2
80	424243	AA351938	Hs.23864	snr3-associated polypeptide, 18kD	2.2
	446572	AF559151	Hs.282561	ESTs	2.2
	412247	AF322375	Hs.73793	vascular endothelial growth factor	2.2
	421040	AA170528	Hs.135280	ESTs	2.2
	428212	ST1824	Hs.167588	neural cell adhesion molecule 1	2.2
	455584	BE207420		gp-PK3-BN0142, 200300-001-cM B04142 Homo	2.2
	406851	AA659784	Hs.180255	major histocompatibility complex, class	2.2
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.2

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	419675	U43431	Hs.91175	topoisomerase (DNA) III alpha	2,2
	418672	U44284	Hs.159743	ESTs	2,2
	456261	AA210718	Hs.104157	ESTs, Weakly similar to KIAA0694 protein	2,2
	415737	AA167626	Hs.118743	ESTs	2,2
5	447554	A1391598	Hs.36119	ESTs, Weakly similar to ALU1_HUMAN ALU S	2,2
	405159				2,2
	442177	AW661820	Hs.211413	ESTs	2,2
	446139	H77395	Hs.39749	ESTs	2,2
	458339	AW976853	Hs.172843	ESTs	2,2
10	401876				2,2
	438566	AF086387		gb.Homo sapiens full length insert cDNA	2,2
	425079	U09963	Hs.2257	vitronec (serum spreading factor, som	2,2
	441837	AA361743	Hs.179881	core-binding factor, beta subunit	2,2
	436644	AB015419	Hs.247710	protoproctolin-releasing peptide	2,2
15	431474	AL133990	Hs.190642	ESTs	2,2
	407739	NM_002285	Hs.38070	lymphoid nuclear protein related to AF4	2,2
	426244	AV647184	Hs.143601	hypothetical protein hCLA-iso	2,2
	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORN	2,2
	412715	NM_000647	Hs.74519	primase, polypeptide 2A (58kD)	2,2
20	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	2,2
	404170				2,2
	405902	M32074		gb.Human retinoic acid receptor gamma 2	2,2
	437302	AA770599	Hs.144055	ESTs	2,2
	401012				2,2
25	446502	A1302654	Hs.208024	ESTs	2,2
	442554	AW467378	Hs.129640	ESTs	2,2
	443021	AA368446	Hs.8904	16 superfamily protein	2,2
	421141	AW117261	Hs.125914	ESTs	2,2
	443070	BE388652	Hs.8994	Homo sapiens chromosome 14 BAC 98L12	2,2
30	446566	H57471	Hs.17914	membrane-spanning 4-domains, subfamily A	2,2
	427595	R88483	Hs.172852	ESTs	2,2
	428503	AA380153		gb.EST93093 Skin tumor 1 Homo sapiens cD	2,2
	431468	AW248431	Hs.256526	nuclear prelamin A recognition factor	2,2
	415185	AW975861	Hs.47367	KIAA1785 protein	2,2
35	437319	BE410958	Hs.56406	Homo sapiens cDNA FLJ13549 fs, clone PL	2,2
	402264				2,2
	413335	AB113318	Hs.48442	ESTs	2,2
	408212	AA297567	Hs.43728	hypothetical protein	2,2
40	405169				2,2
	451099	RS2795	Hs.29554	interleukin 13 receptor, alpha 2	2,2
	407335	AA631047	Hs.158761	Homo sapiens cDNA FLJ13054 fs, clone NT	2,2
	409715	W42591	Hs.23892	ESTs	2,2
	431921	N46465	Hs.58879	ESTs	2,2
45	443823	BE089782	Hs.9377	hypothetical protein	2,2
	422458	A564598	Hs.78768	malignant cell expression-enhanced gene/	2,2
	419726	U50330	Hs.1274	bone morphogenetic protein 1	2,2
	423178	AI033140	Hs.124993	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	2,2
	451089	AA803705	Hs.4190	Homo sapiens cDNA: FLJ22269 fs, clone C	2,2
	415215	AI822925	Hs.193211	Homo sapiens cDNA FLJ11421 fs, clone HE	2,2
50	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fs, clone H	2,2
	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	2,2
	406560	X55371	Hs.172550	polypyrimidine tract binding protein (the	2,2
	443376	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	2,2
	422558	R87268	Hs.177269	ESTs	2,2
55	408145	R45621	Hs.81057	hypothetical protein MG2718	2,2
	419865	NM_007020	Hs.93502	U1-eRNP binding protein homolog (70kD)	2,2
	439444	AT27552	Hs.54578	ESTs, Weakly similar to DB022/hypotheti	2,2
	438407	AW457122	Hs.125973	eukaryotic translation initiation factor	2,2
	405184	W31096	Hs.237617	Homo sapiens, clone IMAGE3447294, mRNA,	2,2
60	409130	BE076601	Hs.75658	phosphorylase, glycogen; brain	2,2
	428844	AW972635	Hs.301904	hypothetical protein FLJ12671	2,2
	429489	AF066203	Hs.204039	aristales-like homeobox 3	2,2
	433042	AW193534	Hs.281955	Homo sapiens cDNA FLJ11660 fs, clone HE	2,2
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2,2
65	438204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	2,2
	427498	NM_003926	Hs.178728	methyl CpG binding domain protein 3	2,2
	428006	H57654	Hs.303345	ESTs, Weakly similar to DB022/hypotheti	2,2
	445703	AV654845	Hs.27	glycine dehydrogenase (decarboxylating,	2,2
	431446	AW294299	Hs.255369	Homo sapiens cDNA FLJ10265 fs, clone HE	2,2
70	456660	AA905249	Hs.112252	solute carrier family 30 (zinc transport	2,2
	433099	NM_002504	Hs.3167	nuclear transcription factor, 2-kb bind	2,2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fs, clone HE	2,2
	415245	N59650	Hs.27252	ESTs	2,2
	443657	R14973		gb.Y4210.61 Soares fetal liver spleen	2,2
75	402521	AW651216	Hs.108945	KIAA035 protein	2,2
	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	2,2
	446630	AV658909	Hs.282642	ESTs	2,2
	415797	AI291896	Hs.72800	ESTs	2,2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2,2
80	453028	AB004532	Hs.31442	RiceO protein-like 4	2,2
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2,2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfat	2,2
	437033	AW248364	Hs.5409	RNA polymerase I subunit	2,2

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5	422732	AA57455	Hs.24937	transformer-2 alpha (Hsa-2 alpha)	2.2
	416388	AI417358	Hs.73677	ESTs	2.2
	452649	AF044924	Hs.30792	hook2 protein	2.2
	446615	BE513202	Hs.15589	PPAR binding protein	2.2
	426361	NM_015905	Hs.18358	transcriptional intermediate factor 1	2.2
	445279	AA490770	Hs.19282	ESTs	2.2
	422938	NM_001809	Hs.1594	centromere protein A (17K)	2.2
	403969				2.2
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	2.2
	429736	AF125324	Hs.21980	lumen vesicle factor receptor superfamily	2.2
10	447091	AW069548	Hs.157779	ESTs, Weakly similar to CA17_HUMAN COLLA	2.2
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.2
	426728	NM_007118	Hs.171957	1ple functional domain PTPRF interact	2.2
	438726	AB031103	Hs.6335	KIAA1277 protein	2.2
	433215	BE544203	Hs.24831	ESTs	2.2
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.2
	433610	AA806822	Hs.112547	ESTs	2.2
	429451	BE409861	Hs.207633	heme oxygenase (hemo) 1	2.2
	417980	R32235	Hs.207633	glycylglycyl-S-CoA	2.2
	405347				2.2
20	414406	BE297904	gb.60117814f.1 NH_MGC_17	Homo sapiens c	2.2
	401827				2.2
	446813	AA430650	Hs.16529	transmembrane 4 superfamily member (Hs)	2.2
	422294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cl	2.2
	404084				2.2
	456786	AK002084	Hs.132851	hypothetical protein FLJ11222	2.2
	435031	AI620291	Hs.116877	ESTs	2.2
	442609	AL020996	Hs.8516	telomerase protein N	2.1
	439732	AW629604	Hs.167641	hypothetical protein from EUROMAGE 1703	2.1
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.1
30	439233	AF066664	Hs.332252	ESTs	2.1
	409669	AW177551	Hs.230255	hypothetical protein MGC13098	2.1
	428574	BE268321	Hs.208912	hypothetical protein MGC861	2.1
	437470	AL139147	Hs.134742	hypothetical protein DKFZp5647D065	2.1
	408945	AW015089	Hs.4954	DKFZP564J1624 protein	2.1
	447587	AE729747	Hs.150186	hypothetical protein DKFZp566K1946	2.1
	429584	AS103864	Hs.207898	ESTs	2.1
	439130	AA306090	Hs.124707	ESTs	2.1
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.1
	442028	AI29437	Hs.48945	ESTs	2.1
40	430968	AW978330	gb.E37384925 IMAGE	rearrangements, MAGL Homo	2.1
	443609	AV650231	Hs.282941	ESTs, Highly similar to A Chain A, Human	2.1
	417164	AA338283	Hs.81361	heterogeneous nuclear ribonucleoprotein	2.1
	444534	AW271626	Hs.42294	ESTs	2.1
	438391	AE52248	Hs.25027	ESTs	2.1
	442003	AW297497	Hs.201891	ESTs	2.1
	456278	BE300369	Hs.289038	hypothetical protein MGC4126	2.1
	419376	BE243985	Hs.80680	major vault protein	2.1
	417810	U28419	Hs.82609	hydroxymethylglutathione synthase	2.1
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
50	452712	AW838616	gb.RC5.LT0554.140200-013-D01	LT0054 Homo	2.1
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	2.1
	421564	AB007864	Hs.105850	KAA/DNAI protein	2.1
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	2.1
	432742	AA564453	Hs.162339	ESTs	2.1
	435958	H98180	Hs.117975	ESTs	2.1
	421531	AA713505	Hs.291769	ESTs	2.1
	410431	BE261320	Hs.158196	transcriptional adaptor 3 (ADA3, yeast)	2.1
	420503	AI570943	Hs.337546	ESTs	2.1
	448127	AI478416	Hs.282883	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
60	452697	BE066058	Hs.299223	ESTs, Moderately similar to I78885 seim	2.1
	447112	HI7800	Hs.7154	ESTs	2.1
	405577				2.1
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.1
	451460	AI797550	Hs.209652	ESTs	2.1
	447402	H54520	Hs.18480	hypothetical protein FLJ20452	2.1
	435628	AA700785	Hs.13852	ESTs	2.1
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.1
	420582	BE047878	Hs.99093	Homo sapiens chromosome 19, contig R2837	2.1
	452020	AA722012	Hs.255757	ESTs, Weakly similar to AT2A_HUMAN POTEN	2.1
70	415586	Z45481	gb.HSC020E941	normalised infant brain cDNA	2.1
	452620	AA436504	Hs.119286	ESTs	2.1
	457066	BE244613	Hs.158272	ESTs, Weakly similar to CA13 MOUSE COLLA	2.1
	435472	AW972330	Hs.283022	triglyceride receptor expressed on myeloid	2.1
	431741	AA514783	Hs.191701	ESTs	2.1
	446840	AW294828	Hs.209203	ESTs	2.1
	446818	AI147060	Hs.146726	ESTs	2.1
	410174	AA306007	Hs.59451	DKFZP434C2M5 protein	2.1
	403822				2.1
	412760	AW379030	Hs.41324	ESTs	2.1
80	410553	BE383768	Hs.65236	95 kDa retinoblastoma protein binding pr	2.1
	426925	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fls, clone H	2.1
	424242	AA337476	Hs.293984	hypothetical protein MGC13102	2.1

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5	45260	BE070704	Hs.336432	ESTs	2.1
	45637	A192428	Hs.115185	ESTs, Moderately similar to PC4259 htm	2.1
	458922	BE501831	Hs.282053	ESTs	2.1
	439321	AW561535	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (tr	2.1
	415498	A3315241	Hs.90591	nucleophosmin 1	2.1
10	411829	AW865749	gb:QV3-SN0021-100500-1B5-c03 SN0021 Homo	2.1	
	457192	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.1
	422228	AW881145	gb:O10-T0033-010400-1B2-ad7 OT0033 Homo	2.1	
	425571	W31518	Hs.34665	ESTs	2.1
	422569	H41850	Hs.131846	PCAF associated factor 65 alpha	2.1
15	406610				2.1
	453638	AW814996	gb:MT1-ST0206-170400-024-M09 ST 0206 Homo	2.1	
	418595	A332658	gb:EST72906 Ovary II Homo sapiens cDNA 5	2.1	
	432323	DC380	Hs.5719	chromosome condensation-related SMC-asso	2.1
	410908	AA121686	Hs.10592	ESTs	2.1
20	420221	N25991	Hs.43725	ESTs	2.1
	424729	A3346108	Hs.221610	ESTs	2.1
	425598	ALP9689	Hs.150360	hypothetical protein similar to tenascin	2.1
	424901	Z11933	Hs.182505	POU domain, class 3, transcription facto	2.1
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	2.1
25	415635	F13168	gb:HSC3JF101 normalized infant brain cDN	2.1	
	418181	U37012	Hs.83727	cleavage and polyadenylation specific fa	2.1
	407103	AA424881	Hs.256301	hypothetical protein MG631310	2.1
	454389	AW752571	gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.1	
	400021				2.1
30	439228	NS1700	gb:yy72601.s1 Soares_multiple_sclerotic,	2.1	
	456505	AA504595	Hs.111418	ESTs	2.1
	405258				2.1
	444645	A1184564	Hs.101654	ESTs	2.1
	430246	A269069	Hs.109268	hypothetical protein FLJ12552	2.1
35	458697	AW024815	Hs.170088	GLUT4 enhancer factor	2.1
	403857				2.1
	402558				2.1
	422221	AA306649	Hs.165370	PYH oncogene related to SRC, FGR, YES	2.1
	441054	AA913591	Hs.126480	ESTs	2.1
40	437700	AI853390	Hs.288540	five-span transmembrane protein MB3	2.1
	454606	AW809752	gb:MR4-ST0124-1s1299-020-b06 ST0124 Homo	2.1	
	449554	AD014564	Hs.22816	KIAA0664 protein	2.1
	443148	AD034357	Hs.211194	ESTs, Weakly similar to ALUB_HUMAN ALU S	2.1
	453486	AU393021	Hs.173554	ubiquitin-cytochrome c reductase core pr	2.1
45	437695	AA769202	Hs.192142	ESTs	2.1
	425449	XS2056	Hs.157441	spleen focus forming virus (SFFV) provi	2.1
	447270	AC020251	Hs.331	general transcription factor IIC, polyb	2.1
	435577	AA694142	Hs.253726	ESTs, Weakly similar to TSCA RAT TESTIS	2.1
	436382	AW977063	Hs.250181	ESTs	2.1
50	435837	A168210	Hs.187726	Homo sapiens cDNA FLJ11431 fa, clone HE	2.1
	458287	AA897556	Hs.12867	ESTs	2.1
	423794	BE551781	Hs.231895	ESTs	2.1
	405349	AW078098	Hs.74316	desmoplakin (DPI, DPII)	2.1
	402721				2.1
55	451999	AW178401	Hs.27424	DEADH (Asp-Glu-Ala-Asp/His) box polypep	2.1
	417541	A1952191	Hs.180040	hypothetical protein FLJ22439	2.1
	414657	AW402389	Hs.920	modulator/recognition factor 1	2.1
	435760	AF231922	Hs.213004	chromosome 21 open reading frame 62	2.1
	428086	AL110193	Hs.224137	hypothetical protein	2.1
60	447853	A1434204	Hs.164285	ESTs, Weakly similar to AFG1_YEAST AFG1	2.1
	419234	NM_002110	Hs.89555	hemopoietic cell kinase	2.1
	431019	NM_005249	Hs.2714	forkhead box G1B	2.1
	421064	A1245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.1
	416435	A1431301	Hs.197503	KIAA0129 gene product	2.1
65	437014	AA808757	Hs.222531	ESTs, Weakly similar to S55901 interfero	2.1
	453689	T8309		gb:yd40603.1 Soares fetal liver spleen	2.1
	402239				2.1
	412280	AW205116	Hs.272814	hypothetical protein DKFZp344E1723	2.1
	426012	AA367507	Hs.75874	pregnancy-associated plasma protein A	2.1
70	430885	A1886568	Hs.194987	ESTs	2.1
	426076	AW902714	gb:EST374787 MAGL resequences, MAGG Homo	2.1	
	404561				2.1
	442532	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.1
	401775	W25086	Hs.19055	hypothetical protein DKFZp6702416	2.1
75	423857	AA333186	gb:EST35757 Embryo, 3 week 1 Homo sapien	2.1	
	458904	W37944	Hs.4007	Sarcomemal-associated protein	2.1
	409650	T08490	Hs.288959	HSCARG protein	2.1
	401729				2.1
	432615	AW977653	Hs.25319	nucleoside reductase M2 polypeptide	2.1
80	456741	W37608	Hs.184492	ESTs	2.1
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibod	2.1
	415079	RA3179	Hs.22895	hypothetical protein FLJ23548	2.1
	435982	AA832333	Hs.333045	ESTs	2.1
	403108				2.1
	436718	AW015227	Hs.289053	hypothetical protein FLJ14733	2.1
	440696	A162757	Hs.187660	putative Rab5 GDI/GTP exchange factor ho	2.1
	409745	AA077391	gb:7B14E12 Chromosome 7 Fetal Brain cDNA	2.1	

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	453485	BE620712	Hs.33026	hypothetical protein PP2447	2.1
	418177	NA4967	Hs.5653	ESTs	2.1
	457292	A1921270	Hs.334882	hypothetical protein FLJ14251	2.1
	454434	AA083568	Hs.261286	ESTs	2.1
5	400805				2.1
	424441	X14950	Hs.147097	H2A histone family, member X	2.1
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott) sy	2.1
	424576	BE154142	Hs.96833	ESTs	2.1
	423660	AL045428	Hs.130831	Homo sapiens mRNA, cDNA DKF Zp434L137 (fr	2.1
10	403509	AF21319	Hs.107659	HAAS539 gene product	2.1
	441940	AW268115	Hs.128152	ESTs	2.1
	439190	AW978693	Hs.253811	ESTs	2.1
	417791	AW665339	Hs.111471	ESTs	2.1
	432701	AA328656	Hs.143022	ESTs	2.1
15	427239	BE770447	Hs.174070	ubiquitin cancer protein	2.1
	459542	BE243103		gt:TCAAF2E0949 Pediatric acute myelogeno	2.1
	450385	A1631024	Hs.24948	synuclein, alpha interacting protein (sy	2.1
	425159	NM_004341	Hs.154968	carbamoyl phosphate synthetase 2, aspart	2.1
	425591	AJW29134	Hs.279727	Homo sapiens cDNA FLJ14025, clone HE	2.1
20	445101	T75202	Hs.12314	Homo sapiens mRNA, cDNA DKF Zp585C019 (f	2.1
	412811	H06382	Hs.21400	ESTs	2.1
	426369	AF134157	Hs.185487	Kreisler (house) mal-related leucine zip	2.1
	435974	AW029203	Hs.191552	ESTs	2.1
	418388	RT2332	Hs.29258	Homo sapiens cDNA FLJ11354 f1, clone HE	2.1
25	452235	AL039743	Hs.28514	testes development-related NYD-SP21	2.1
	452313	Y00486	Hs.28914	adenine phosphoribosyltransferase	2.1
	450704	H85157	Hs.40856	ESTs	2.1
	427530	AA405205	Hs.97960	ESTs, Weakly similar to T51146 ring-box	2.1
	402028				2.1
30	405362				2.1
	414718	H65348	Hs.107897	ESTs	2.1
	432924	R04522	Hs.163566	ESTs	2.1
	444875	A1200759	Hs.44737	ESTs	2.0
	445523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.0
35	456072	H54381		gt:yg89a03.41 Soares fetal liver spleen	2.0
	435331	A1239485	Hs.120189	ESTs	2.0
	443418	Z43704	Hs.21192	Homo sapiens clone 25155 mRNA sequence	2.0
	447250	RA878909	Hs.17883	protein phosphatase 1G (formerly 2C), ma	2.0
	448192	RA3915	Hs.4958	ESTs	2.0
40	448966	AW372914	Hs.85149	phosphoinositide 3-phosphate-binding prot	2.0
	406055	AF224266	Hs.272073	interleukin 20	2.0
	410790	AW803357	Hs.45465	gt:BL2-UM0079-090300-050-A08 UM0079 Homo	2.0
	436872	X15624		gt:Human H1 RNA	2.0
45	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKF Zp434K1815 (f	2.0
	446307	T50063	Hs.5094	ESTs	2.0
	436588	AA759233	Hs.126506	ESTs	2.0
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ11329 f5, clone OV	2.0
	430420	AW140027	Hs.26373	Homo sapiens cDNA: FLJ23249 f5, clone H	2.0
50	432026	AF224266	Hs.272073	interleukin 20	2.0
	414460	L00727	Hs.898	dystrophin myotonic-protein kinase	2.0
	433507	A1817336	Hs.191791	ESTs	2.0
	427964	AA418082	Hs.98286	ESTs, Weakly similar to T20655 hypothesi	2.0
	443108	W86975	Hs.203707	ESTs	2.0
55	434504	A187341	Hs.121590	hypothetical protein FLJ112827	2.0
	454310	AW918390	Hs.175613	homolog of Xenopus Claspin	2.0
	443566	A/290284	Hs.153872	ESTs	2.0
	449722	BE280074	Hs.23960	cyclin B1	2.0
	452632	AA156193	Hs.3071	proteoglycans membrane binding protein	2.0
60	412352	AW945484	Hs.194252	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.0
	429341	X/3874	Hs.2393	phosphorylase kinase, alpha 1 (muscle)	2.0
	435883	AF255346	Hs.62919	Jun dimerization protein p21SNF1	2.0
	400774	F58624	Hs.2186	eukaryotic translation elongation factor	2.0
	453944	AW972369	Hs.255270	Homo sapiens, clone IMAC:3502107, mRNA,	2.0
65	419277	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.0
	448529	T26460	Hs.22550	ESTs	2.0
	443206	AB011470	Hs.9075	serine/threonine kinase 17a (apoptosis-i	2.0
	435960	AA444988	Hs.338629	ribosomal protein L44	2.0
	456660	A1658870	Hs.184513	ESTs	2.0
	449030	A1365582	Hs.57100	Homo sapiens mRNA for FLJ00016 protein,	2.0
70	411048	AK001742	Hs.67991	hypothetical protein DKF Zp434G0522	2.0
	406624	AF052672	Hs.2186	gt: Homo sapiens clone ccsn68-1 immunoge	2.0
	450666	T89868	Hs.18799	ESTs, Weakly similar to C80022 hypothet	2.0
	446143	BE245342	Hs.306079	ucsf1 homolog	2.0
	437698	R61837	Hs.7990	ESTs, Moderately similar to B54005 colic	2.0
75	428607	AA362330	Hs.124223	ESTs	2.0
	448246	AW411209	Hs.233563	hypothetical protein FLJ10983	2.0
	422554	A1148006	Hs.222120	ESTs	2.0
	432682	AC376400	Hs.159588	ESTs	2.0
80	422140	BE295918	Hs.112193	muB (E. coli) homolog 5	2.0
	406215	BE514290	Hs.43812	synuclein 10	2.0
	417129	AJ381800	Hs.300654	calcitonin gene-related peptide receptor	2.0
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.0
	434928	AW015595	Hs.4267	Homo sapiens clones 24714 and 24715 mRNA	2.0

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5	411380	AW841619		gb:PC1-CN0017-120200-012-b09 CN0017 Homo	2.0
	430603	AA148164	Hs.247280	HBV associated factor	2.0
	425905	AB032959	Hs.318584	novel C/EBP type Zinc finger (ring finger)	2.0
	401125				2.0
	412539	AW411491	Hs.2186	eukaryotic translation elongation factor	2.0
10	448740	BE260532	Hs.9028	seitin 2	2.0
	454390	AB020713	Hs.56966	KIAA0905 protein	2.0
	415012	NM_004383	Hs.77793	c-src tyrosine kinase	2.0
	410407	X56839	Hs.63287	carbonic anhydrase IX	2.0
	434748				2.0
15	456485	AI363037	Hs.97871	Homo sapiens, clone IMAGE:3645253, mRNA,	2.0
	430294	AB38226	Hs.32976	guanine nucleotide binding protein 4	2.0
	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	2.0
	451944	AW445218	Hs.210876	ESTs	2.0
	436295	AJ227900		gb:Homo sapiens partial mRNA; ID E02-16B	2.0
20	456457	AA252905	Hs.194477	E3 ubiquitin ligase SMURF2	2.0
	491123	D59020	Hs.23106	KIAA0130 gene product	2.0
	409214	AW405967	Hs.333388	Homo sapiens, clone IMAGE:3957135, mRNA,	2.0
	437819	AW51491	Hs.334053	hypothetical protein FLJ23544	2.0
	453348	BE272318	Hs.8595	hypothetical protein FLJ12438	2.0
25	424382	AA351898	Hs.23839	ESTs	2.0
	447079	AA280057	Hs.106280	ESTs, Weakly similar to dJ963K2.2 (Hsa	2.0
	449501	AB52924	Hs.219147	ESTs	2.0
	422893	X59111	Hs.121555	myosin II	2.0
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	2.0
30	434845	BE267057	Hs.325321	hypothetical protein R32184_1	2.0
	410422	ALJ40204	Hs.334858	Homo sapiens, clone MGC:15203, mRNA, com	2.0
	430255	AF007003	Hs.32822	Homo sapiens mRNA for KIAA1551 protein,	2.0
	451656	BE327098	Hs.212752	ESTs	2.0
	442068	BE312873	Hs.314932	ESTs	2.0
35	446846	AW197626	Hs.271501	ESTs, Moderately similar to S08886 fringe	2.0
	442690	AI014727	Hs.160047	ESTs, Weakly similar to S08095 kno-1 pr	2.0
	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.0
	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.0
	402798				2.0
40	404554				2.0

TABLE 25B:

Phy. Unique Eos probest identifier number
CAT number Gene cluster number
Accession: Genbank accession numbers

45	Phy	CAT	Accession
	407509	1026254_1	AW103986 BE156395 BE150391 BE156190 BE156184 BE156388 BE156394
	408432	1026667_1	AW155262 R27368 AW811262
	402193	110747_1	AA134543 AA065156 AA076448
	409745	115297_1	AA077391 A347416 Hs148353 A0088754 AW207451 AW960912 AA521874 AA266833 AA150722 BE152353 AW188822 BE152450
50	410447	1203929_1	AW816134 BE063456 AW748795 BE150839
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	411259	123790_1	AW834039 AW834040 AW834047 AW834010 BE003128 AW852479
	411380	1242343_1	AW841619 AW851958 AW851801 AW851985
	411632	1252631_1	AW854829 AW854806 AW854841 AW854825 AW854822 AW854830 AW854835 AW854826
55	411658	1262987_1	AW855598 AW856068 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855605
	411829	1263029_1	AW855746 BE179419 BE179492
	412225	1284108_1	AW902042 N77591
	412370	1281952_1	AW946614 AW946622 AW946663 AW946667 AW946615 AW946619
	412391	1262625_1	AW947710 AW947698 AW947697 AW947713
60	412527	1356943_1	BE076335 BE074899 BE075005 BE075005 BE075032 BE075008 BE075037
	413604	137195_1	BE1767 BE152515 Z4534 H23971
	414406	1443333_1	BE297904 BE294312
	414550	1460900_1	BE379808
	415346	1345481_1	Z43108 F06265 R13085
65	415406	1536026_1	T26510 F07328 R53367
	415586	1540116_1	Z45481 F12393 T74437
	415635	1540853_1	F13166 R21289 T77628
	416871	1626761_1	H58716 N90752 N24283
	416913	163001_1	BE258335 AW196816 BE161807 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW13465 BE161006 BE162499
70	417980	1712564_1	R32235 R32247 R32219
	418333	1712_1	WB2113 AA702794 BE044516 W51984 AA679375 T94184 AA679335 BE0303126 AW502118 BE467367 AA584550 AW139964 R33353 AW088477
			AB878495 AW502624 W81697 WB1696 AA447817 AA447667 F13631 AW026071 AA055366 AW026902 AA677404 AA831618 AA126782 AA889402
			AA765894 AA765530 AA656808 AA590419 A0267368 AA456946 RB3354 AF246624 AW163616 AW16014493
			AA302648 AW837061 AA225428
75			AA504571 AA262343 AA411737 AW990608 AA406543
			U70073
			AA685951 AW974261 AA236240 A077451 AA531399 AW974262
			BE258335 AW196816 AA258118 AW843305 R14744 ASAC388 BE071923 R36280
			AW881145 AA490718 M85637 AA304575 T06067 AA331991
80			N34524 AA305071 AW554803 AA052335 AA33430 A0203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW35512
			AI334966 V12951 H62656 H53902 RB8994 AW835732
			HB0277 BE141658 AA305496 AW066286 AA436754
			AA408125 AA834883 AA330555
			AA331886 AW962659 AW962655 T89841
	425189	247825_1	H16622 R17322 AA351959

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5	425517	257728_1	AF121179 BE162736 AA358827
	426076	260504_1	AW962714 AA362277 AA360278
	426413	266650_1	AA377823 AW954494 A102668
	426503	268283_1	AA380153 AA380233 AA963529
	426531	268760_1	AA381071 AA381084 AA380662
	426879	310034_1	A091815 AA460162 AA460761
	430968	326269_1	AW972830 AA527647 AA498920 AA570362
	432088	341195_1	AA526454 W74039 RB9502 T77379
10	433532	368550_1	AW975367 AA559607 AA742735
	434559	38889_1	AF147315 AW173079 T53029
	435065	393229_1	BE064391 BE064395 AA663613 N69644
	436190	41555_1	AK001059 AA633055
	436395	41905_1	AJ227900 A0949333 AW051119 F00947
	436532	421602_1	AA721522 AW975443 T93070
15	438722	425756_1	AW975977 AA729469 AA747132
	436672	42851_1	X15624
	437034	431713_1	AA742643 AA808575 AW976668
	439086	46552_1	AF085477 M70981 H78589
20	439228	47001_1	NS1700 AF085511 NS1702
	439518	47334_1	W76326 AF086341 W77300
	439546	47360_1	AF088056 W76297 W72448
	439566	47387_1	AF086387 W77884 W72711
	439710	47559_1	AF085433 W62291 W62225
	443657	579685_1	R14973 R14967 A081006
25	444168	593826_1	AW379879 A1126285 H12014
	444386	604004_1	BE065183 A1143358 BE065367
	451129	858076_1	BE072881 BE072945 A0752181
	452712	928309_1	AW838616 AW838669 BE144403 A1914520 AW888910 BE184854 BE184784
	454446	967533_1	BE299996 BE297115 BE270415 BE295214 BE296526
30	453638	975640_1	AW814596 AL047199 AW850379
	453746	979731_1	AL170611 BE006170 BE006189
	454377	114761_1	AA078811 AW14764
	454389	115082_1	AW752571 AW847602 AA077979
35	456065	1226145_2	AW808752 AW810271 AW808944 AW810319 AW810215 AW810356 AW810167
	456430	127352_1	BE142075 BE142148 BE142189 AW816249 BE142147 BE142002 BE142406 BE142094 BE142020 BE142074 BE142000 BE142375
	456431	127352_1	AW81168 BE142133
	456431	127443_1	AW811324 AW811325 AW811326 AW811327 AW811328 AW811332 AW811336 AW811335
	456479	1278529_1	AW813110 AW813113
	456507	1247021_1	AW848276 AW848416 AW848160 AW847945 AW847947 AW848063 AW848113
40	455023	1246186_1	AW850507 AW850501 AW850507
	455302	127642_1	AW879541 AW871177
	455470	1252846_1	AW947952 AW947961 AW947950 AW947957 AW947953 AW947957 AW947961 AW947957 AW947950 AW947955 AW947975 AW947957
	455514	1321649_1	AW947955
45	455530	1322256_1	AW983871 BE0960302 AW983867 AW983865 AW983860 AW983853 AW983852
	455530	1324741_1	AW984744 AW984759
	455584	1364506_1	BE007420 BE007419 BE007421 BE007422
	455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088852
	455908	1382301_1	BE156306 BE156188 BE156298 BE156377 BE156374
	456072	1470255_1	HS4381 HS4463 BE393262
50	455954	1594780_1	HS0501 C01228
	457374	329758_1	AA453662 AW97396 BE154814
	457578	359518_1	AA578027
	457730	359505_1	AW753613 AW753857 BE150074 BE150693 BE150034 AA800851 AA650155 AA654653 BE150419

55	TABLE 29C:		
	Pkey:	Unique number corresponding to an Eos probelet	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
60	NL position:	Indicates nucleotide positions of predicted exons.	

	Pkey	Ref	Strand	NL position
	400832	7465000	Plus	186273-186402,186878-187275
65	400859	9757499	Minus	51868-62018,98131-98294,99474-99570
	400917	7283186	Minus	132558-173631
	400982	8096828	Plus	140350-140622
	401012	7230638	Minus	736-1137
	401048	7232177	Plus	132430-132761
70	401125	8570296	Minus	126853-126884
	401324	9863791	Plus	234057-234174
	401384	6505038	Minus	58360-58545
	401508	7139678	Plus	103510-104090
	401626	8575943	Minus	238100-238432
	401676	9965536	Plus	3891-4691
75	401714	6715702	Plus	96484-96481
	401729	8134566	Minus	90951-90978
	401827	2262095	Plus	94725-94860,98452-98660
	401876	8059107	Plus	59513-59641
	402028	7139781	Plus	88749-89237
80	402064	6117294	Plus	100165-100360,100445-100912
	402230	7590131	Plus	38175-38304,42133-42366
	402408	9796239	Minus	110326-110491
	402424	9796344	Minus	64928-65073

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	402516	9798099	Minus	195342-195511
	402604	9909420	Plus	20353-20375
	402627	9931216	Plus	12136-12272, 16487-16628, 17654-17798, 18494-18621, 18933-19089, 20669-20710, 21134-21293, 22865-22973, 23686-23820, 26626-26895, 29279-29469
5	402721	9969253	Minus	144428-144715
	402798	3355547	Plus	23396-23697
	402856	9901268	Minus	90119-90411
	403048	4210991	Plus	44275-44592, 49656-49555
	403108	9980955	Plus	93253-93567
10	403142	9444521	Plus	89296-90131
	403166	9838127	Minus	67793-67940, 69655-68956, 70394-70507
	403478	9958258	Plus	116458-115564
	403680	7331517	Minus	157184-157415
	403751	7225815	Minus	158794-160929
15	403790	8084957	Minus	87265-87947, 89835-90002
	403797	8098986	Minus	123055-125008
	403857	7709910	Minus	2524-3408
	403881	7710245	Minus	107250-107585, 108924-109213
	403961	7596976	Minus	110393-110603
20	403989	8656909	Plus	31237-31375, 32405-32506
	404020	8655966	Minus	174449-174653
	404054	3548795	Plus	66713-69175
	404094	9944055	Plus	2795-2969
	404108	8247074	Minus	63803-64942
25	404170	9930793	Plus	166836-169248
	404185	4572584	Minus	129171-129327
	404240	5002624	Minus	116132-116407, 116653-116922
	404295	9856563	Minus	75747-75947
30	404299	5738532	Minus	3826-4025
	404366	9964977	Plus	96589-96801
	404554	7243881	Plus	42637-42839
	404561	9795980	Minus	69035-70100
	404584	9837511	Plus	139651-139153
	404589	9931665	Minus	32824-32965
35	404642	9796810	Plus	102999-103145
	404652	9796989	Minus	108172-108256
	404721	9856648	Minus	173763-174294
	404750	7706327	Plus	82849-83627
40	404802	4581357	Minus	30953-30600
	404894	6939892	Plus	87221-87505
	405159	9966262	Plus	79659-78904
	405269	7129210	Plus	129930-130076
	405288	6139075	Minus	126268-126436
	405353	2811095	Plus	118525-118992
45	405362	2337862	Minus	105000-105142, 105980-106091, 140445-140556, 142519-142541
	405558	1521110	Plus	45022-46444, 53853-5083
	405588	5002511	Plus	46190-46386
	405605	5836195	Minus	117070-117270
	405701	4263151	Plus	93243-93394
50	405741	9969947	Minus	156747-158075, 156936-157209
	405747	8469069	Minus	153933-154090
	405771	7018349	Plus	91191-91254, 91510-91589
	405808	9529207	Plus	109758-111166
55	405884	8750747	Plus	62883-62883
	405915	7712162	Minus	43717-43859
	406028	8312303	Minus	177469-177829
	406085	9123888	Plus	18665-18843
	406169	6684220	Minus	12620-14251
	406267	7528342	Minus	2570-2731
60	406326	9212385	Plus	84508-84655
	406347	9255981	Plus	90900-91091
	406474	9795567	Plus	52758-53211
	406577	7711730	Plus	113771-11509
65	406610	8312226	Plus	13006-13334

TABLE 26A. ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 26A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix Eos Hu13 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

	Play	Unique Eos probe/est identifier number
75	ExAccn:	Example Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of 75 th percentile normal central nervous system tissue to 85 th percentile tumor

80	Play	ExAccn	UnigeneID	Unigene Title	R1
	433655	AW960427	Hs.79059	transforming growth factor, beta receptor	136.7
	417275	BC33379	Hs.265449	pancreatin	29.0
	430829	AW461999	Hs.194024	ESTs	25.7
	410657	AF053228	Hs.65248	dyncin, cytoplasmic, intermediate polype	22.6

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	419554	D14720	Hs.93883	myelin protein zero (Charcot-Marie-Tooth	21.2
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	18.5
	416133	NM_001683	Hs.89512	ATPase, Ca++-transporting, plasma membra	15.5
5	416108	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	15.2
	417167	AW026437	Hs.4290	ESTs	14.8
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1
	439830	AA946666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	12.6
	430608	AW148552	Hs.167798	ESTs	12.6
10	412636	NM_004415	Hs.74316	desmoplakin (DPL, DPK)	12.5
	429096	AB011106	Hs.195012	KIA0034 protein	12.2
	412638	AA810199	Hs.203308	ESTs	12.2
	432690	AA329646	Hs.23904	ESTs, Weakly similar to FN0099 con3 prot	12.1
	458844	A0264155	Hs.152981	CDP-diacylglycerol synthase (phospholipid	11.9
15	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.9
	442593	R33904	Hs.31961	ESTs	10.6
	446333	A1200919	Hs.153651	ESTs	10.4
	420290	AW077318	Hs.154480	ESTs	10.3
	414220	BE296094	gb:601118321F1 NIH_MGC_17 Homo sapiens c	10.3	
20	414290	A1568801	Hs.71721	ESTs	10.2
	426345	AA376667	Hs.10283	RNA binding motif protein 8B	10.0
	414637	R38690	Hs.12392	ESTs	10.0
	419643	F06056	Hs.81791	chromosome 11 open reading frame 25	9.5
	407173	T64349	gb:yc10508.1 Stratagene lung (837210) H	9.5	
	412454	R50745	Hs.167330	ESTs	9.5
	433366	AF102143	Hs.8540	Ribosomal growth factor 13	9.5
	415315	F12240	Hs.250655	prothymosin, alpha (gene sequence 2B)	9.3
	441790	AW294909	Hs.132208	ESTs	9.2
	448117	H48129	Hs.172582	ESTs	9.1
30	430661				9.0
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypotheti	9.0
	412453	R20205	Hs.167330	ESTs	9.0
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	8.9
35	450931	AA376836	Hs.76728	ESTs	8.7
	420108	BE520016	Hs.162470	PTCD10 protein	8.3
	446544	A0531592	Hs.7047	ESTs, Weakly similar to Unknown (H.sapie	8.2
	423479	NM_014326	Hs.129208	death-associated protein kinase 2	8.2
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33950 finger pr	8.2
40	418035	Z37976	Hs.83337	latent transforming growth factor beta b	8.0
	458490	U83171	Hs.57293	small inducible cytokine subfamily A (cy	8.0
	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKF Zp56-B1264 (J	8.0
	408428	NM_014787	Hs.44896	DnaJ (hsp40) homolog, subfamily B, membe	7.9
	437073	A0854608	Hs.94122	ESTs	7.9
45	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	7.9
	438150	AA037534	Hs.79059	transforming growth factor, beta recepto	7.9
	440209	H05049	Hs.22269	neurexin 3	7.8
	408119	W26213	Hs.101672	ESTs, Weakly similar to T060311 hypotheti	7.8
	417421	AL130201	Hs.82120	nuclear receptor subfamily 4, group A, m	7.8
50	410587	AA370706	Hs.86412	chromosome 9 open reading frame 5	7.8
	420611	A1889077	Hs.211388	Homo sapiens BAC clone CTB-60N22 from Tq	7.7
	405900				7.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ26761	7.7
55	426356	BE536836	Hs.98682	hypothetical protein FKSG32	7.7
	423440	R25234	Hs.143434	contactin 1	7.7
	445148	A1214510	Hs.146304	ESTs	7.6
	416294	D86580	Hs.79170	KIA00227 protein	7.6
	424087	N69333	Hs.143434	contactin 1	7.6
	434749	R61866	Hs.101277	ESTs	7.5
60	405071				7.5
	421224	AW402154	Hs.125812	ESTs	7.4
	442225	AW987434	Hs.11810	CD411 protein	7.4
	459476	BE185844		gb:IL547031-110500-067-c06 H10731 Homo	7.1
	430573	AA744550	Hs.136345	ESTs	7.1
	401836				7.1
65	448936	AB020651	Hs.23653	KIA00844 protein	7.1
	430152	AB001325	Hs.234642	aquaporin 3	7.1
	419474	AW958619	Hs.155949	ESTs	7.1
	401780				7.1
70	446052	AA358760		gb:EST67699 Fetal lung II Homo sapiens c	7.0
	423605	AF047826	Hs.129887	cadherin 19, type 2	7.0
	433098	AW190593	Hs.151143	ESTs	7.0
	449511	A1436187	Hs.296261	guanine nucleotide binding protein (Gpr	6.9
	451285	AW137912	Hs.227553	Homo sapiens chromosome X map Xp11.23 L-	6.8
75	428414	AL049860	Hs.184216	DNF ZP564C152 protein	6.8
	419273	BE271180	Hs.234940	ESTs, Weakly similar to R8022 hypotheti	6.8
	443155	R54485	Hs.23772	ESTs	6.8
	450561	A149674	Hs.23509	ESTs	6.8
	433068	NM_005456	Hs.286215	cytidyltransferase	6.8
80	440729	AA904739	Hs.128204	ESTs	6.8
	448426	BE018315	Hs.260776	tankyrase, TRF1-interacting ankyrin-beta	6.7
	425889	AA328082	Hs.209569	ESTs	6.6
	415681	A1375882	Hs.72630	ESTs	6.5

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	413510	F13044	Hs.181363	gb.HSCB#H101 normalized infant brain cDN	6.4
	427892	Y15014	Hs.44571	UDP-Gal4betaGlcNAc beta 1,3-galactosyltr	6.4
	453344	BE346075	Hs.7130	ESTs	6.4
	450642	R39773	Hs.17130	copine IV	6.4
5	432251	AW972883	Hs.232165	poly(phenyl rubra vera 1; cell surface	6.4
	429322	D86984	Hs.109243	KIAA4231 protein	6.4
	444927	AW016637	Hs.199425	ESTs	6.4
	447482	AB033059	Hs.18705	KIAA1233 protein	6.4
	400337	S56407	Hs.248632	FL14	6.3
10	440703	AL137663	Hs.7372	Homo sapiens mRNA; cDNA DKFZp404G227 (fr	6.3
	446129	AW244073	Hs.145946	ESTs	6.3
	454076	AW204712	Hs.61957	ESTs	6.3
	425276	AA359933	Hs.109439	gb.EST9040 Fetal lung II Homo sapiens c	6.3
15	421813	A1934365	Hs.26303	ectodysplasin (osteodysplasin factor, mime	6.3
	434773	AA811143	Hs.164568	Fibroblast growth factor 7 (keratinocyte	6.2
	408480	A1350337	Hs.209890	EST	6.2
	451301	A1769514	Hs.157068	ESTs	6.2
	430754	AW962610	Hs.40827	ESTs	6.2
20	438256	AA805530	Hs.119598	ribosomal protein L3	6.2
	422743	BE304578	Hs.31412	Homo sapiens cDNA FLJ11422 ff, clone HE	6.2
	453355	AW295374	Hs.67103	ESTs	6.2
	426388	AW081394	Hs.67103	gb.FM-BT045-220199-286_1 BT046 Homo sapi	6.1
	452502	A1994296			6.1
	402546				6.1
25	457534	A1761307	Hs.232226	ESTs	6.1
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	6.1
	404958				6.1
	432951	BE546532	Hs.25882	Homo sapiens mRNA for KIAA1853 protein,	6.1
	442979	AW440782	Hs.174743	ESTs	6.1
30	422262	AL022315	Hs.113987	lectin, galactoside-binding, soluble, 2	6.0
	408713	NM_007248	Hs.47042	ectonucleoside diphosphate diphosphatidyl	6.0
	454065	BE394598		gb.S0131180F1 1H1_MGC_44 Homo sapiens c	6.0
	430004	U27768	Hs.227571	regulator of G-protein signalling 4	5.9
	401521				5.9
35	425087	R62424	Hs.126959	ESTs	5.9
	442508	AF181813	Hs.14637	kidney- and liver-specific gene	5.9
	417761	T13727	Hs.21435	ESTs	5.9
	424806	AA382523	Hs.105689	MSTP031 protein	5.9
40	441625	T12411	Hs.183745	hypothetical protein FLJ13456	5.9
	457483	AB034594	Hs.272558	endomucin-1	5.9
	417175	R44588	Hs.94002	ESTs	5.8
	437483	AL390174		gb.Homo sapiens mRNA; cDNA DKFZp547J184	5.8
	436427	A1344378	Hs.143395	ESTs	5.8
	411939	A1365885	Hs.146246	ESTs	5.8
45	459053	A1807052	Hs.210061	ESTs	5.7
	411052	AW614950		gb.MR1-ST0205-130400-023-006 ST0206 Homo	5.7
	431063	Z89499	Hs.326843	hypothetical protein bA129H2.1	5.7
	450382	AA367658	Hs.60257	Homo sapiens cDNA FLJ13398 fs, clone PL	5.7
50	408478	NM_003806	Hs.45740	gamma-aminobutyric acid (GABA) A recepto	5.7
	442676	A1733595	Hs.130897	ESTs	5.7
	448443	AV659082	Hs.134228	ESTs	5.7
	400865				5.7
	459080	AW192083	Hs.290565	ESTs	5.6
55	407552	A1215902	Hs.88845	ESTs, Highly similar to T50835 hypotheti	5.6
	431984	AL080239	Hs.272284	Human DNA sequence from clone GS1-256022	5.6
	425705	AF007833	Hs.159265	knuppel-related zinc finger protein hckr	5.6
	442238	AW135374	Hs.270948	ESTs, Mode-styly similar to F41525 hypot	5.6
	422994	AW891802	Hs.296276	ESTs	5.6
60	457148	AF091035	Hs.184627	KUAA0118 protein	5.6
	428356	AL046991	Hs.10338	ESTs	5.6
	415927	AL120168	Hs.78919	Kel blood group precursor (McLeod pheno	5.5
	402092				5.5
	440526	A1832243	Hs.211471	ESTs	5.5
65	444409	A1792140	Hs.49265	ESTs	5.5
	417877	A1025829	Hs.86320	ESTs	5.4
	458238	AW071521	Hs.335541	beta-amyloid binding protein precursor	5.4
	430707	U56979	Hs.250851	H factor 1 (complement)	5.4
	456189	H91010	Hs.44940	ESTs	5.4
	427424	AA402453	Hs.113011	ESTs	5.4
70	437354	AA749215	Hs.291886	ESTs	5.4
	455611	BE073870		gb.CM1-8T0614-160300-148-02 BT0614 Homo	5.4
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	5.3
	427861	AA813185	Hs.98183	ESTs	5.3
75	408556	U49516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	5.3
	444709	A1753134	Hs.148494	ESTs	5.3
	427831	R02504	Hs.332943	ESTs	5.3
	403180				5.3
	418026	BE379727	Hs.83213	tutty acid binding protein 4, adipocyte	5.3
80	430339	W26508	Hs.238625	integral membrane protein 2B	5.2
	431596	T34708	Hs.272927	Gac33 (5, covalent) homolog A	5.2
	430531	AB035301	Hs.272721	cathepsin B, type 2	5.2
	437403	A1208149	Hs.121196	ESTs	5.2
	438285	AA782845	Hs.22790	ESTs	5.2

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	439801	N73885	Hs.124169	ESTs	5.2
	438507	AA899052	Hs.211275	ESTs	5.2
	449222	AW263984	Hs.197621	ESTs	5.2
5	402834	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1521 mRNA,	5.2
	419442	T61429	Hs.221565	ESTs	5.2
	436777	AA731199	Hs.291330	ESTs	5.2
	445071	AI230246	Hs.149504	ESTs	5.1
	408016	AW136827	Hs.256096	ESTs	5.1
10	412647	AA534589	Hs.49686	ESTs	5.1
	438553	AW595874	Hs.23648	Homo sapiens cDNA FLJ13097 fs, clone NT	5.1
	436773	AW078629	Hs.32110	PC4 and SFRS1 interacting protein 1	5.1
	409263	AA069573	Hs.50319	ESTs	5.1
	453830	AA534296	Hs.20953	ESTs	5.1
	459580	AA022888	Hs.176055	ESTs	5.1
15	417816	P07728	Hs.268668	ESTs	5.1
	423457	F08208	Hs.283844	similar to rat tricarboxylate carrier-li	5.1
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	5.0
	416490	AF060116	Hs.79348	regulator of G-protein signalling 7	5.0
20	417284	N62819	Hs.107242	Homo sapiens cDNA FLJ12955 fs, clone NT	5.0
	447135	T58148	Hs.98906	g1-yb9806 s1 Saratoga lung (S37210) H	5.0
	448605	AL109678	Hs.21597	Homo sapiens mRNA full length insert cDN	5.0
	442240	A0791893	Hs.292719	ESTs	4.9
	459599	BE407712	Hs.133958	oxalate kinase, mitochondrial 1 (ubiqui	4.9
25	427972	AA864670	Hs.181304	positive gene product	4.9
	432944	AA570687	Hs.38512	ESTs	4.9
	440198	BE560093	Hs.01345159F1 NIH_MGC_8	Homo sapiens cD	4.9
	444047	A087452	Hs.133595	ESTs	4.9
	419040	AW619158	Hs.289044	Homo sapiens cDNA FLJ12048 fs, clone HE	4.9
30	444922	A0921750	Hs.144871	Homo sapiens cDNA FLJ13752 fs, clone PL	4.8
	436670	A0890021	Hs.201536	ESTs	4.8
	448072	A1459336	Hs.24908	ESTs	4.8
	409306	AL139043	Hs.293549	ESTs	4.8
	412622	AW664708	Hs.171959	ESTs	4.8
35	414943	D06547	Hs.124193	ESTs	4.8
	429254	H10133	Hs.51846	hypothetical protein DKFZp781C121	4.8
	453567	A1742835	Hs.33368	hypothetical protein FLJ11175	4.8
	407906	AA389665	Hs.41185	Homo sapiens mRNA cDNA DKFZp664O1262 f	4.8
	441028	A0333660	Hs.17558	Homo sapiens cDNA FLJ14446 fs, clone HE	4.7
40	405130				4.7
	455225	AW996689		gb OV3-BN0845-150400-151-g09 BN0046 Homo	4.7
	442118	AF051159		gb-AV657159 GUC Homo sapiens cDNA clone	4.7
	443347	A052543	Hs.133244	melanoma-derived leucine zipper, extra-r	4.7
45	402176				4.7
	416577	BE063207	Hs.79381	granulatin	4.7
	432221	AK001781	Hs.296543	Homo sapiens cDNA FLJ10919 fs, clone OV	4.7
	420480	AL137381	Hs.98173	hypothetical protein	4.7
	400800	Y10262	Hs.45925	eyes absent (Drosophila) homolog 3	4.6
	435161	AF124155	Hs.272091	ESTs	4.6
50	404793				4.6
	430855	US6581	Hs.248121	G-protein-coupled receptor 22	4.6
	438571	AW020775	Hs.56022	ESTs	4.6
	445924	AI264671	Hs.164165	ESTs	4.6
	444585	AW170015	Hs.6594	ESTs	4.6
	421044	AF061871	Hs.311738	Human DNA sequence from clone RP1-238D15	4.6
	418274	AI458387	Hs.128677	Human DNA sequence from clone RP1-50Q24	4.6
	426475	W56339	Hs.107057	ESTs	4.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fs, clone MA	4.5
	414272	AB511603	Hs.46588	ESTs	4.5
60	444235	AS64022	Hs.138207	ESTs	4.5
	414327	BE408145	Hs.185254	ESTs, Weakly similar to T24435 hypotheti	4.5
	414630	BE410857		gb:601301177F1 NIH_MGC_21 Homo sapiens c	4.5
	414456	H74314		gb-yu56e10.r1 Soares fetal liver spleen	4.5
	401924				4.5
65	414699	AI815523	Hs.79330	synuclein, alpha (non A4 component of am	4.5
	423449	AI497900	Hs.33067	ESTs	4.5
	405138				4.5
	413544	BE147225		gb-IP42-HT0225-031299-003411 HT0225 Homo	4.5
	453880	AI803166	Hs.28462	ESTs, Weakly similar to B08022 hypotheti	4.5
70	433521	T66087	Hs.112492	Homo sapiens unknown mRNA sequence	4.4
	441184	AA522009	Hs.150269	ESTs	4.4
	425876	A0028977	Hs.225974	KIAA1054 protein	4.4
	445401	AW601346	Hs.148836	ESTs	4.4
	452340	NW_002202	Hs.505	SL1 transcription factor, LIM/homeodoma	4.4
	404789				4.4
75	444331	AW193342	Hs.24144	ESTs	4.4
	429726	AW603326	Hs.27151	ESTs	4.4
	445093	A0033356	Hs.22998	neurexin 1	4.4
	451959	AA066203	Hs.27337	hypothetical protein FLJ20523	4.4
	415716	N59294	Hs.179652	nucleosome assembly protein 1-like 1	4.4
80	417888	R22063	Hs.92025	g1-yb3105 s1 Soares placenta N62AP Homo	4.4
	419856	AA002314	Hs.92025	KCNAB3 gene product	4.4
	425864	US6420	Hs.159903	olfactory receptor, family 5, subfamily	4.4
	435078	AW518838	Hs.40937	ESTs	4.4

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	413493	BE144444		gb.VR0-HT0168-141199-002-409 HT0168 Homo	4.3
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	4.3
	459650	R25754	Hs.301185	ESTs	4.3
5	404828				4.3
	423782	A1472209	Hs.323117	ESTs	4.3
	425267	AA460567	Hs.22668	ESTs	4.3
	426802	AA385182	Hs.46699	ESTs	4.3
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticot	4.3
10	412112	BE160342		gb.RC3-HT0622-130400-012-a09 HT0622 Homo	4.3
	401322	N47812	Hs.306198	C23-3s protein	4.2
	419055	AJ365384	Hs.11571	Homo sapiens cDNA FLJ11570 fs, clone H-E	4.2
	410171	H07892	Hs.12431	ESTs	4.2
	419564	U08989	Hs.91139	solis carrier family 1 (neurotrophin	4.3
	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20845 fs, clone AD	4.2
15	455040	AWB52286		gb.QV0-CT0225-100400-187-a09 CT0225 Homo	4.3
	438533	AA40266	Hs.170673	ESTs. Weakly similar to T24832 hypophel	4.3
	459305	AA447679	Hs.144558	ESTs. Weakly similar to ALU1_HUMAN ALU S	4.2
	418489	U75421	Hs.85302	adenosine deaminase, RNA-specific, B1 (n	4.2
20	433388	AF038171		gb.Homo sapiens clone 23671 mRNA sequenc	4.2
	454356	AW390363	Hs.11522	hypothetical protein from Xq28	4.2
	442339	BE259666	Hs.227501	ESTs. Weakly similar to 1901303A Leu zip	4.2
	412149	AA283362		gb.H147277 HTCDL1 Homo sapiens cDNA 5'3'	4.2
	443098	AB02461	Hs.296276	ESTs	4.2
	452197	AWC23595	Hs.232048	ESTs	4.2
25	451117	AA015752	Hs.205173	ESTs	4.2
	404601	AW474752	Hs.75514	nucleoside phosphorylase	4.2
	410378	R2324	Hs.41603	DnaI (Hsp40) homolog, subfamily B, membe	4.2
	422528	AB011182	Hs.118087	KIAA0610 protein	4.2
	440323	AA070614	Hs.127992	ESTs	4.1
30	425767	AF054176	Hs.159483	chromosome 1 open reading frame 7	4.1
	434640	AA478496	Hs.3852	KIAA0568 protein	4.1
	410362	H04811	Hs.93164	proprotein convertase subtilisin/kexin 1	4.1
	413121	T96090	Hs.142678	ESTs	4.1
	405403	AA668224	Hs.66534	Homo sapiens cDNA: FLJ22547 fs, clone H	4.1
35	450235	AA007512	Hs.17538	ESTs	4.1
	446754	H03020	Hs.30597	ESTs. Weakly similar to B34067 hypophel	4.1
	41613	BE048255		gb.tz4905.y1 NCL_CGAP_Bm52 Homo sapien	4.1
	408496	A0683002	Hs.136182	ESTs	4.1
	430261	AA305127	Hs.237225	hypothetical protein HT023	4.1
40	434101	AA023805	Hs.258299	KIAA1522 protein	4.1
	451637	T92157	Hs.16970	ESTs	4.1
	41772	BE170301		gb.QV4-HT0536-040500-193-405 HT0536 Homo	4.1
	437630	AJ252762	Hs.153026	SWAP-70 protein	4.0
45	430212	AA469153		gb.nc67804.s1 NCL_CGAP_P1 Homo sapiens	4.0
	400216				4.0
	429830	AJ537276	Hs.225841	DKFZP434D183 protein	4.0
	453165	S74727	Hs.32042	aspartacylase (aminocyclase 2, Canavan	4.0
	418347	R37633	Hs.4847	ESTs	4.0
	405354				4.0
50	427931	AW206612	Hs.186996	ESTs	4.0
	428775	AA434579	Hs.143691	ESTs	4.0
	449422	AA001373	Hs.59821	ESTs	4.0
	453864	AWC21407	Hs.21968	hypothetical protein	4.0
55	456407	AW968614		gb.EST330050 MAGE: resequencs, MAG1 Homo	4.0
	441869	NM_003947	Hs.8004	huntinglin-associated protein interact	4.0
	402784	T65158	Hs.102399	ESTs. Moderately similar to S65657 alpha	4.0
	425195	AA330205	Hs.94379	VP10 domain receptor protein	4.0
	429628	H05641	Hs.12068	ESTs	4.0
	410087	F12079	Hs.332579	ESTs	4.0
60	409840	AW502122		gb.UA-HF-BR0p-ay-c-08-U-1 NIH_MGC_5	4.0
	452854	AA437061	Hs.14060	prokineticin 1 precursor	4.0
	419510	AA462213	Hs.190173	ESTs. Weakly similar to A46010 X-linked	4.0
	427443	AA402713	Hs.97872	ESTs	4.0
	414990	C17758	Hs.221652	Homo sapiens cDNA FLJ14323 fs, clone PL	3.9
65	412678	AA115575	Hs.114914	ESTs	3.9
	405629				3.9
	420299	AJ056871	Hs.15276	ESTs	3.9
	453098	Z25935	Hs.86379	ESTs	3.9
	435752	AF230801		gb.Homo sapiens growth hormone receptor	3.9
70	441005	Z41305	Hs.303172	Homo sapiens mRNA, cDNA DKFZp264/G133 (l	3.9
	414516	AJ37802	Hs.135560	ESTs. Weakly similar to T43658 hypophel	3.9
	442257	AW503831	Hs.323370	Human EST clone 25267 major transposon	3.9
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.9
	406697	K21388	Hs.123017	Human unproductively rearranged Ig mu-ch	3.9
75	442650	AW014723	Hs.334612	ESTs	3.9
	412677	AW029608	Hs.17384	ESTs	3.9
	422788	AL117352	Hs.120828	Human DNA sequence from clone RP5-876810	3.9
	405377				3.9
	414376	BE393856	Hs.66915	ESTs. Weakly similar to 16.7kd protein [3.9
80	453341	AJ758912	Hs.296341	adenylate cyclase-associated protein 2	3.9
	431960	AW241821	Hs.301927	c6.1A	3.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	3.9
	427264	AA400117	Hs.125747	ESTs	3.9

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	422746	NM_004484	Hs 119651	glypican 3	3.9
	452346	BE243534		gb:TCBAP1D0885 Pediatric pre-B cell acute	3.9
	414666	NM_004466	Hs 76828	glypican 5	3.8
	418217	A910547	Hs 13442	ESTs	3.8
	419118	AA234223	Hs 190004	ESTs	3.8
	445017	A0205493	Hs 176860	ESTs	3.8
	405867				3.8
	427760	BE405561		gb:601299855F1 NH_MGC_21 Homo sapiens c	3.8
	453963	X02544	Hs 572	oncosmucoid 1	3.8
	457821	H41768	Hs 124322	ESTs, Weakly similar to A47582 B-cell gr	3.8
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	3.8
	435600	AL047034	Hs.119747	ESTs	3.8
	456083	U46922	Hs.17252	fragile histidine triad gene	3.8
	413341	H78472	Hs.151225	ESTs, Weakly similar to T18967 hypophel	3.8
	449057	AB037784	Hs.72541	KIAA1353 protein	3.8
	421855	F06504	Hs.27384	ESTs, Moderately similar to ALU1_HUMAN A	3.8
	414764	AW013887	Hs 72047	ESTs	3.8
	404391				3.7
	433629	R13140	Hs.13359	ESTs	3.7
	424738	A963740	Hs.46826	ESTs	3.7
	401315				3.7
	407706	AA191085	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7
	440530	AA828646	Hs.174187	ESTs	3.7
	435930	AA820338	Hs.273781	ESTs	3.7
	409662	AW452320	Hs.279726	ESTs	3.7
	437268	A754947	Hs.227571	regulator of G-protein signalling 4	3.7
	445698	A246205	Hs.153244	ESTs	3.7
	408553	R19546	Hs.187617	ESTs	3.7
	417091	AA193283	Hs.291990	ESTs	3.7
	446556	AW655006	Hs.5004	ESTs	3.7
	421326	N67655	Hs.26411	ESTs	3.7
	430138				3.7
	459150	BE155356		gb:FMI-HT0350-160300-009-406 HT0350 Homo	3.7
	457221	AW383197	Hs.218260	ESTs	3.7
	451660	A1807927	Hs.249801	ESTs	3.7
	401600	BE247275	Hs.151787	US snRNP-specific protein, 116 kD	3.7
	444818	AG342568	Hs.279765	ESTs	3.7
	447795	AW295151	Hs.163612	ESTs	3.7
	427562	R56424	Hs.26534	ESTs	3.6
	412258	AA27678	Hs.324841	hypophelical protein FLJ2622	3.6
	454339	AF1361080		gb:DNA+HT0316-051199-426-405 HT0316 Homo	3.6
	438274	AF066092	Hs.48372	ESTs	3.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	422897	AA679784	Hs.4290	ESTs	3.6
	429656	XG5602	Hs.211584	neurofilament, light polypeptide (8kD)	3.6
	421908	AW938200	Hs.285814	sorcery (Drosophila) homolog 4	3.6
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	3.6
	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 B simil	3.6
	406085				3.6
	417154	A1874701	Hs.21388	ESTs	3.6
	447176	242549	Hs.160893	ESTs	3.6
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	3.6
	445231	BE410360	Hs.298573	KIAA1720 protein	3.6
	411607	AWB53498		gb:RC1-CT0252-170300-025-H02 CT0252 Homo	3.6
	405897				3.6
	441470	BE503874	Hs.301966	ESTs	3.6
	423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6
	441236	A1854546	Hs.136570	Homo sapiens cDNA: FLJ21268 fs, clone C	3.6
	450236	AW162980	Hs.24584	KIAA1376 protein	3.6
	425364	AF052150	Hs.155569	Homo sapiens clone 24533 mRNA sequence	3.6
	426775	AA384564	Hs.108829	ESTs	3.6
	414631	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	3.6
	418876	AW501916	Hs.117897	ESTs	3.6
	400878				3.6
	425153	AW023193	Hs.27046	ESTs	3.6
	432222	A104395		gb:an03c03.x1 Stratagene schizo brain S1	3.5
	415047	F13142		gb:HSC3UD31 normalized infant brain cDN	3.5
	401532				3.5
	446495	D60923	Hs.153460	ESTs	3.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2105260A B cell	3.5
	445898	AF070623	Hs.13423	Homo sapiens clone 24462 mRNA sequence	3.5
	455901	BE155527	Hs.79306	gb:FMI-HT0350-150400-013-406 HT0350 Homo	3.5
	416421	AA134006		eukaryotic translation initiation factor	3.5
	455697	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	3.5
	405678				3.5
	418207	C14685	Hs.34772	ESTs	3.5
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.5
	417027	AA192306	Hs.23926	triadin	3.5
	402637	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5
	417702	R09235	Hs.191146	ESTs	3.5
	445687	W60382	Hs.149297	ESTs	3.5
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypophel	3.5
	413164	BE068494		gb:AR1-BT0371-050500-009-at2 BT0371 Homo	3.5

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414593	BE386754	Hs	gb.601273349F1 NIH_MGC_20 Homo sapiens c	3.5
453220	AB033089	Hs	32452 Homo sapiens mRNA for KIAA1263 protein,	3.5
45621	A646602	Hs	55468 ESTs	3.5
454437	A248173	Hs	191450 hypothetical protein MGC12936	3.5
446066	A343931	Hs	149383 ESTs	3.5
423374	AB037770	Hs	127856 KIAA1349 protein	3.5
419347	C15944	Hs	90005 superiorcervical ganglia, neural speci	3.5
418516	NM_006218	Hs	85701 phosphoinositide-3-kinase, catalytic, al	3.5
451776	W45679	Hs	169854 hypothetical protein SP192	3.5
432305	M2402	Hs	274313 insulin-like growth factor binding prote	3.5
456995	T89832	Hs	170278 ESTs	3.5
403323				3.5
425022	M85724	Hs	154207 centromere protein C 1	3.5
435394	AA149250	Hs	56105 ESTs	3.4
438003	AB22593	Hs	72688 ESTs	3.4
450715	A126484	Hs	31570 ESTs, Weakly similar to KIAA1324 protein	3.4
411474	AW848427		gb.IL3-CT0214-150200-075-H10: CT0214 Homo	3.4
415076	NM_000857	Hs	77890 guanylate cyclase 1, soluble, beta 3	3.4
423826	U03025	Hs	1707 cocaine- and amphetamine-regulated trans	3.4
458495	BE544158		gb.601076707F1 NIH_MGC_12 Homo sapiens c	3.4
427173	BE255017	Hs	97540 ESTs	3.4
408112	AW461982	Hs	249613 ESTs	3.4
440920	K33522	Hs	145894 ESTs	3.4
418868	AK656856	Hs	292597 ESTs	3.4
458234	BE551408	Hs	127196 ESTs	3.4
419555	AA244416		gcm067011x1 NCJ_OGAP_Pv1 Homo sapiens	3.4
414314	BE312591		gb.601150275F1 NIH_MGC_19 Homo sapiens c	3.4
400425	AY004252	Hs	287385 PR domain containing 12	3.4
414366	BE549143		gb.60107456F1 NIH_MGC_12 Homo sapiens c	3.4
434053	AW445136	Hs	134846 ESTs	3.4
445997	A953052	Hs	201577 KIAA1829 protein	3.4
433461	AK636047	Hs	197623 ESTs	3.4
428006	AA118743	Hs	58306 KIAA1862 protein	3.4
424955	U58331	Hs	151899 sarcoglycan, delta (35kD dystrophin-asso	3.4
443294	A1733625	Hs	133053 ESTs	3.4
428212	AW444451	Hs	134812 ESTs	3.4
457673	AA551569	Hs	272034 hypothetical protein PRO2822	3.4
446390	AA233393	Hs	14992 hypothetical protein FLJ11151	3.3
428536	A1143139	Hs	2286 vitamin-like 1	3.3
428597	AA382258	Hs	145901 ESTs	3.3
410366	A267598	Hs	302689 hypothetical protein	3.3
458258	AW406646	Hs	127971 ESTs	3.3
401738				3.3
409538	T97480	Hs	50002 small inducible cytokine subfamily A (cy	3.3
423785	T27017	Hs	155528 Homo sapiens clone 24400 mRNA sequence	3.3
433328	AW298159	Hs	23644 ESTs, Weakly similar to S65824 reverse t	3.3
414541	BE293116	Hs	76392 aldehyde dehydrogenase 1 family, member	3.3
434998	AW975157	Hs	26037 ESTs	3.3
456393	A587391	Hs	53574 homeo box D3	3.3
426527	NM_001037	Hs	170238 sodium channel, voltage-gated, type I, b	3.3
454267	AA437199	Hs	656 cell division cycle 25C	3.3
400302	N48056	Hs	1915 folate hydrolase (prostate-specific memb	3.3
434077	AF118659	Hs	321151 Homo sapiens PRO1412 mRNA, complete cds	3.3
436602	A1793222	Hs	16487 ESTs	3.3
445904	A8300099	Hs	23251 Down syndrome critical region gene 4	3.3
417936	RS3657	Hs	170044 ESTs	3.3
423310	AA325225	Hs	124023 Homo sapiens cDNA FLJ14828 f1, clone NT	3.3
438624	T84297	Hs	52411 ciliary acid binding protein 1, liver	3.3
453406	A1523987	Hs	61784 hypothetical protein FLJ14451	3.3
420164	AW339037	Hs	24908 ESTs	3.3
447826	AW775317	Hs	258556 ESTs	3.3
415975	AA653410	Hs	533557 proteinophan	3.3
444612	AW138111	Hs	22902 ESTs	3.3
418504	BE159718	Hs	85335 Homo sapiens mRNA; cDNA DKFZp664D1462 (f	3.2
415242	RA5986	Hs	295014 ESTs	3.2
418188	AW138413	Hs	151880 ESTs	3.2
430355	NM_006219	Hs	239818 ESTs	3.2
421640	AW966552		gb.EST378726 MAGE: resequences, MAGI Homo	3.2
432359	AA076049	Hs	274415 Homo sapiens cDNA FLJ10229 f1, clone HE	3.2
408806	AW847814	Hs	288005 Homo sapiens cDNA: FLJ21532 f1, clone C	3.2
400409	AF153341	Hs	226254 Homo sapiens winged helix/orkhead trans	3.2
446015	T33068	Hs	133531 hypotheical protein FLJ10571	3.2
425495	AA368454	Hs	78026 ESTs, Weakly similar to similar to ankyr	3.2
403092				3.2
452971	AB973878	Hs	51789 ESTs	3.2
454186	BE141030		gb.MRD.HT0067-201099-002411 HT0067 Homo	3.2
401485				3.2
401949				3.2
457452	AW972675		gb.EST384766 MAGE: resequences, MAGL Homo	3.2
454100	AB83231	Hs	126043 chromosome 21 open reading frame 51	3.2
446440	AA172467	Hs	62402 p21/Cdc42/Rac1-activated kinase 1 (yeast	3.2
421200	AA264811	Hs	264433 ESTs	3.2
403142	NM_000437	Hs	234392 platelet-activating factor acetylhydrola	3.2

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5	433197	AB040889	Hs.281022	KIAA1456 protein	3.2
	443009	AV645470		gb:AV645470 GLC Homo sapiens cDNA clone	3.2
	440827	A733110	Hs.128128	ESTs	3.2
	432799	NM_016161	Hs.278960	alpha-1,4-N-acetylglucosaminyltransferase	3.2
	409267	AW370362		gb:RC1-B10255-181099-012.407 B10255 Homo	3.2
10	459225	BC296010	Hs.271468	Homo sapiens mRNA for FLJ10038 protein,	3.2
	416789	AA223439	Hs.75933	cyclin t	3.2
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFp761D09121 (3.2
	420156	AW492528	Hs.6187	ESTs	3.2
	455577	BD095341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.2
15	400617	AF151064	Hs.36069	hypothetical protein	3.2
	437129	AL049327	Hs.302057	Homo sapiens mRNA; cDNA DKFp554E16 (fr	3.2
	451820	AW058357	Hs.337353	ESTs	3.2
	467535	AA89685	Hs.278672	membrane component, chromosome 11, surf	3.2
	419956	AL137539	Hs.40096	ESTs	3.1
20	456235	AA203637		gb:z58h12r1 Soares_fetal_liver_spleen_	3.1
	423930	AA332697	Hs.42721	ESTs	3.1
	403796				3.1
	414805	AA114015	Hs.75746	aldehyde dehydrogenase 1 family, member	3.1
	445886	A793176	Hs.145596	ESTs	3.1
25	414401	A760159	Hs.124833	ESTs	3.1
	441573	BE563656	Hs.6529	ESTs, Weakly similar to I78885 serineth	3.1
	450725	RT1389	Hs.175551	ESTs	3.1
	458905	AJ062933	Hs.23294	hypothetical protein FLJ14393	3.1
	417968	A078534	Hs.125602	ESTs	3.1
30	458361	A795268	Hs.133273	ESTs	3.1
	423346	AJ267677	Hs.127416	synapjanin 1	3.1
	454486	AW857077		gb:RC1-C70302-140300-016-404 CT0302 Homo	3.1
	408341	AW182952	Hs.249557	ESTs	3.1
	410669	AW905749	Hs.318885	superoxide dismutase 2, mitochondrial	3.1
35	420407				3.1
	434610	AJ333863	Hs.215474	ESTs, Moderately similar to alternative1	3.1
	436590	A1149729	Hs.120557	ESTs	3.1
	441921	A773376	Hs.164478	hypothetical protein FLJ21939 similar to	3.1
	454573	AW812807		gb:RC3-ST0186-070100-016-c04 ST0186 Homo	3.1
40	426470	AJ878681	Hs.203862	guanine nucleotide binding protein (G pr	3.1
	424345	AA730407	Hs.159156	protocadherin 11	3.1
	408217	A433201	Hs.275860	tumor protein, transcriptionally-controlle	3.1
	417313	AA155602		gb:z3202r1 Soares_NHRMPu_S1 Homo sapi	3.1
	427322	AK002017	Hs.176227	hypothetical protein FLJ11155	3.1
45	411003	AA181018	Hs.13005	hypothetical protein FLJ13520	3.1
	425335	AA536330	Hs.198113	ESTs	3.1
	426716	NM_005379	Hs.171921	sema domain, immunoglobulin domain (lg)	3.1
	468078	AK001256	Hs.22975	KIAA1576 protein	3.1
	429608	UA6250	Hs.210852	T-box, brain, 1	3.1
50	424308	AA569402	Hs.111	fibroblast growth factor 9 (gla)-activat	3.1
	428465	AW970976	Hs.293653	ESTs	3.1
	411656	AF105564	Hs.71345	neurofilament 3 (150kD medium)	3.1
	447965	AW292577	Hs.54445	ESTs	3.1
	413918	AW015898	Hs.77245	ESTs	3.1
55	419582	H13139	Hs.52282	paired-like homeodomain transcription fa	3.1
	425810	AS23627	Hs.31903	ESTs	3.1
	427365	AA416931	Hs.126065	ESTs	3.1
	429560	AW139155	Hs.154095	hypothetical protein DKFp434A00320	3.1
	430708	U73308	Hs.278485	olfactory receptor, family 1, subfamily	3.1
60	468084	AA67800	Hs.271000	ESTs, Weakly similar to I80022 hypothe	3.1
	454506	AW847346		gb:RC0-CT0205-240999-021-e01 CT0205 Homo	3.0
	414629	AA345824	Hs.75688	carboxylesterase 1 (monocytic/macrophage	3.0
	427963	MT9141	Hs.13204	ESTs	3.0
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activat	3.0
65	448175	BE295174	Hs.225160	hypothetical protein FLJ13102	3.0
	414486	BE409757	Hs.23189	ESTs, Moderately similar to TBG2_HUMAN T	3.0
	458360	AJ027207	Hs.132523	ESTs	3.0
	451829	AW964081	Hs.247377	ESTs	3.0
	445179	A949743	Hs.224768	ESTs	3.0
70	433090	AJ720050	Hs.145362	immortalization-activated protein	3.0
	432018	AA524447	Hs.152377	ESTs	3.0
	407988	NA7760	Hs.295107	hypothetical protein FLJ13357	3.0
	405911				3.0
	418808	AJ821836	Hs.10359	ESTs	3.0
75	431900	AW972048	Hs.192534	ESTs	3.0
	452893	H18017	Hs.22869	ESTs, Moderately similar to KIAA1395 pro	3.0
	423952	AW877787	Hs.136102	KIAA0853 protein	3.0
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	3.0
	405753				3.0
80	410711	AB002316	Hs.65746	KIAA0318 protein	3.0
	411279	AW848776		gb:QV4-OT0067-010300-121-d01 OT0067 Homo	3.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fs, clone PL	3.0
	427071	AA397958	Hs.192719	ESTs	3.0
	434961	AW974956		gb:EST387061 MAGE resequences, MAGN Homo	3.0

TABLE 26B:

Phylo Unique Ecol probe identifier number

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1

CAT number	Gene cluster number	
	Accession	Genbank accession numbers
5	Prey	CAT number
	Accession	Accession
10	42840	1112594_1
	42840	1150071_1
	411052	1230374_1
	411229	1237516_1
	411474	1247047_2
	411607	1261261_1
	411772	1273382_1
	412112	1277883_1
	413164	1351422_1
	413493	1373555_1
25	413510	1374377_1
	413544	1375670_1
	414220	1420940_1
	414314	1435026_1
	414395	1438636_1
	414495	1447055_1
	414593	1464099_1
	414630	1468063_1
	415047	1517450_1
	417313	160844_1
35	417886	1706992_1
	419555	18584_1
	421249	200649_1
	421640	204833_1
	421813	207854_1
	422760	221034_1
	425225	22775_1
	430212	314743_1
	432222	343347_1
	433389	36497_1
45	434981	395357_1
	435752	41050_1
	437483	43755_1
	440198	48824_2
	442609	57198_1
	446052	65980_1
	446218	65685_1
	447135	70953_1
	452345	912205_1
	452502	919732_1
55	454005	966401_1
	454186	1046791_1
	454339	1212972_1
	454486	1215703_1
	454506	1219557_1
	454673	1226599_1
	455040	1250026_1
	455225	1262318_1
	455677	133389_1
	455917	1346117_1
70	455987	1351148_1
	455991	1381589_1
	456235	166865_1
	456407	166896_1
	457452	320361_1
	459150	919196_1
	460661	8118474
	460685	8118768
	460685	8118768
	460685	8118768
75	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
80	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
	460685	8118768
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	460685	8118768
	460685	8118768
	460685	8118768

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5	400865	1945037	Minus	44482-45526
	400878	9864757	Plus	31493-32842
	401024	8117489	Plus	60551-60602
	401315	9212516	Minus	198566-199619
	401465	7341723	Plus	58059-68239,68941-69077
10	401521	7705251	Plus	9127-9234
	401532	7798785	Plus	124414-124590,125050-125418
	401738	2982169	Minus	41547-41757
	401780	7249190	Minus	26397-26617,26929-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401836	7334063	Plus	71981-72064
15	401949	3492899	Plus	160728-161660
	402092	7249154	Minus	107533-106094
	402176	7543687	Minus	10-750
	402546	7637348	Plus	24573-25170
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
20	403180	7523296	Minus	63603-63759
	403323	8349082	Minus	120365-120945
	403796	6099898	Minus	75173-77654
	404391	3135305	Minus	26030-26173,27853-27997
	404769	8099713	Minus	175801-176823
25	404793	7232206	Minus	61087-61590
	404828	6384915	Minus	26291-27253
	404907	7331453	Minus	102880-103828
	404958	7407941	Minus	2731-4531
	405071	7706797	Minus	11115-11552
30	405130	8216045	Plus	150235-150449
	405138	8578241	Plus	90033-90516
	405354	2642452	Plus	52213-53089
	405377	5649375	Plus	216556-216848
	405629	4508116	Minus	101676-101866
35	405678	4078670	Plus	151821-152027
	405793	1405887	Minus	89197-89453
	405800	2791346	Plus	19271-19813
	405867	6758731	Minus	74553-75173
	405911	6758736	Plus	101006-101643
40	405977	8247789	Minus	135548-136177

TABLE 27A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 27A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 5980 probesets on the Affymetrix Ecos Hs03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

Phy: Unique Ecos probe set identifier number

ExAccn: Exemplar accession number, Genbank accession number

UnigenID: Unigenet number

Unigene Title: Unigene gene title

R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor

R2: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue

55	Phy	ExAccn	UnigenID	Unigene Title	R1	R2
	417275	X63578	Hs.295449	parvalbumin	29.0	30.0
	430829	AF4651999	Hs.184024	ESTs	25.7	6.2
	410657	AF0636228	Hs.65248	dynin, cytoplasmic, intermediate polypeptide	22.6	25.8
	419554	D14720	Hs.33853	myelin protein zero (Charcot-Marie-Tooth)	21.2	30.3
60	416133	NM_001683	Hs.89512	ATPase, Ca ²⁺ -transporting, plasma membrane	15.5	16.8
	416018	AW138239	Hs.78877	proprotein convertase subtilisin/kexin 1	15.2	18.0
	417167	AW206437	Hs.4290	ESTs	14.8	17.7
	433940	H05129	Hs.7459	cyclic AMP-regulated phosphoprotein, 21	13.4	18.1
	413324	V00571	Hs.75294	corticotropin releasing hormone	13.1	18.0
65	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEIN	12.6	16.5
	408068	AW148652	Hs.167398	ESTs	12.6	16.9
	429598	AB011106	Hs.196012	NOA4/OS34 protein	12.2	21.1
	416380	AA070199	Hs.203638	ESTs	12.2	16.0
	442593	R33904	Hs.31961	ESTs	10.8	15.0
70	446353	A1290919	Hs.153661	ESTs	10.4	13.2
	426365	AA376667	Hs.10263	RNA binding motif protein 88	10.0	5.9
	414937	R33966	Hs.12342	ESTs	9.7	10.8
	419643	F06066	Hs.51791	chromosome 11 open reading frame 25	9.5	10.9
	412454	RS5745	Hs.167330	ESTs	9.5	14.1
75	439366	AF100143	Hs.6540	fibroblast growth factor 13	9.4	12.3
	441790	AW294909	Hs.132308	ESTs	9.2	3.2
	446117	H09129	Hs.172962	ESTs	9.1	12.8
	433558	AA833757	Hs.201769	ESTs, Weakly similar to T24435 hypothesis	9.0	14.7
	412453	R20205	Hs.167330	ESTs	9.0	13.7
80	408020	AL120071	Hs.48598	flavinocinn leucine rich transmembrane p	8.9	8.9
	409031	AA376836	Hs.76176	ESTs	8.7	8.6
	446544	A0531932	Hs.7047	ESTs, Weakly similar to Unknown [Hsapie	8.2	8.0
	403480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	8.0	8.3
	410200	AA082557	Hs.101915	Stargardt disease 3 (autosomal dominant)	8.0	8.9

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5	408478	NM_014787	Hs 44896	DnaJ (Hsp40) homolog, subfamily B, member	7.9	9.6
	437073	AB88608	Hs.94122	ESTs	7.9	11.3
	408434	AW195317	Hs. 107716	hypothetical protein FLJ22344	7.9	16.4
	440209	H05049	Hs. 22269	neuramin 3	7.8	34.3
	408119	VS5213	Hs. 101672	ESTs. Weakly similar to T00331 hypothetical	7.6	9.0
10	429611	A889077	Hs. 211398	Human sapiens BAC clone CTB-60K2 from Tq	7.7	5.0
	423440	R25234	Hs. 143434	contactin 1	7.7	9.9
	445148	AZ14510	Hs. 146304	ESTs	7.6	9.1
	416294	D88860	Hs. 79170	KIAA0227 protein	7.6	7.6
	424087	H63333	Hs. 143434	contactin 1	7.6	10.3
15	437479	H61866	Hs. 101777	ESTs	7.5	9.3
	430573	AA744650	Hs. 136345	ESTs	7.1	2.8
	448958	AB020651	Hs. 22653	KIAA0844 protein	7.1	10.4
	419474	AW968918	Hs. 155849	ESTs	7.1	3.0
	432605	AF047108	Hs. 129887	cathepsin 19, type 2	7.0	6.9
20	430398	AW190593	Hs. 151143	ESTs	7.0	9.2
	449511	A1436187	Hs. 295761	guanine nucleotide binding protein (G pr	6.9	3.1
	428414	AL049980	Hs. 184216	DKFZP564C152 protein	6.8	5.0
	443155	RS4485	Hs. 23772	ESTs	6.8	3.5
	450561	RI49674	Hs. 25909	ESTs	6.8	8.1
25	433068	NM_006456	Hs. 288215	sialyltransferase	6.8	2.0
	423589	AA328082	Hs. 209569	ESTs	6.6	10.5
	415681	A079862	Hs. 72630	ESTs	6.5	9.0
	413510	F13044		gp.HSC3HH101 normalized infant brain cDN	6.4	7.1
	427992	Y15014	Hs. 181353	UDP-Gal-beta-GlcNAc beta 1,3-galactosyltr	6.4	9.5
30	450642	R39773	Hs. 7130	copia IV	6.4	5.7
	428322	D88864	Hs. 199243	KIAA0231 protein	6.4	6.2
	441482	AB033059	Hs. 18705	KIAA1233 protein	6.4	2.3
	448129	AW244073	Hs. 145846	ESTs	6.3	8.3
	421913	A1534365	Hs. 109439	ortologycin (osteoinductive factor, mime	6.3	2.1
35	434273	AA913143	Hs. 26303	ESTs	6.2	10.3
	409400	AC350337	Hs. 164568	Reelin/ost growth factor 7 (lateralocyte	6.2	3.5
	451301	A795914	Hs. 206980	EST	6.2	12.4
	438356	AA805530	Hs. 48527	ESTs	6.2	8.1
	428358	AW061394	Hs. 97103	ESTs	6.2	8.6
40	455202	A154266		gp.PH-BT046: 220199-205, 1 BT046 Homo sapi	6.1	2.8
	409165	AL137573	Hs. 43143	Human sapiens mRNA: cDNA DKFZp564A2463 (f	6.1	6.3
	442979	AW440782	Hs. 174743	ESTs	6.1	6.3
	408713	NM_001248	Hs. 47042	otomucleoside triphosphate diphosphohyd	6.0	3.8
	430004	U27758	Hs. 227571	regulator of G-protein Signaling 4	5.9	21.4
45	425987	BE2424	Hs. 129328	ESTs	5.9	8.1
	441695	T12411	Hs. 183745	hypothetical protein FLJ13456	5.9	3.1
	417175	RA4558	Hs. 94002	ESTs	5.8	12.5
	437463	AL390174		gp.Homo sapiens mRNA: cDNA DKFZp564j184	5.8	2.2
	438427	A1344378	Hs. 143339	ESTs	5.8	13.8
50	450382	AA397558	Hs. 60257	Human sapiens cDNA FLJ13588 fs, clone PL	5.7	4.4
	408478	NM_008086	Hs. 45740	gamma-aminobutyric acid (GABA) A recepto	5.7	12.5
	442676	A173585	Hs. 130897	ESTs	5.7	6.8
	446143	AW559082	Hs. 134228	ESTs	5.7	6.4
	450900	AW192083	Hs. 206655	ESTs	5.6	15.6
55	431984	AL080236	Hs. 272284	Human DNA sequence from clone GS1-256022	5.6	8.2
	428356	AL046991	Hs. 103336	ESTs	5.6	6.2
	417677	A025829	Hs. 86320	ESTs	5.4	4.9
	425290	AF203032	Hs. 159169	neurofilament, heavy polypeptide (200kD)	5.3	13.1
	406556	A049516	Hs. 46352	5-hydroxytryptamine (serotonin) receptor	5.3	6.6
60	431930	AB035301	Hs. 272211	cachexin 7, type 2	5.2	6.0
	438285	AA762845	Hs. 22790	ESTs	5.2	7.3
	433091	N73885	Hs. 124169	ESTs	5.2	2.7
	449222	AW226984	Hs. 197821	ESTs	5.2	8.1
	408016	AW136827	Hs. 256096	ESTs	5.1	2.5
65	436953	AW959074	Hs. 23648	Human sapiens cDNA FLJ13097 fs, clone NT	5.1	3.0
	408673	AW076629	Hs. 82110	PC4 and SFRS1 interacting protein 1	5.1	7.3
	420763	AA068753	Hs. 50319	ESTs	5.1	12.9
	463830	AA534296	Hs. 20953	ESTs	5.1	3.4
	441535	AL135735	Hs. 7885	phosphatidylinositol binding clathrin as	5.0	4.8
70	416490	AF090116	Hs. 79348	regulator of G-protein signalling 7	5.0	20.1
	417284	H62889	Hs. 107742	ESTs	5.0	3.9
	446805	AL105678	Hs. 21597	Human sapiens mRNA: full length insert cDN	5.0	6.1
	442240	A1791883	Hs. 292719	ESTs	4.9	6.7
	427972	AA648870	Hs. 161304	putative gene product	4.9	5.2
75	416340	AW019158	Hs. 208040	Human sapiens cDNA FLJ12048 fs, clone HE	4.8	2.8
	444932	A1921750	Hs. 144671	Human sapiens cDNA FLJ13752 fs, clone PL	4.8	3.7
	408936	AL138043	Hs. 293549	ESTs	4.8	6.6
	414943	D06047	Hs. 124193	ESTs	4.8	3.1
	427924	H10133	Hs. 91846	hypothetical protein DKFZp761C121	4.8	2.3
80	427905	AA358665	Hs. 41185	Human sapiens mRNA: cDNA DKFZp564O1262 (f	4.8	9.1
	416577	BE063207	Hs. 79381	grancalcin	4.7	2.2
	420490	AL137361	Hs. 58173	hypothetical protein	4.7	2.8
	404793				4.6	7.2
	430935	U65681	Hs. 248121	G-protein-coupled receptor 22	4.6	2.4
	438571	AW020775	Hs. 56022	ESTs	4.6	5.4
	444585	AW170015	Hs. 6594	ESTs	4.6	6.0
	414272	A1651603	Hs. 46888	ESTs	4.5	2.2

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414699	AB15523	Hs.17930	synuclein, alpha (non A4 component of am	4.5	30.9
423449	AH91900	Hs.13067	ESTs	4.5	20.8
433521	T96087	Hs.112482	Homo sapiens unknown mRNA sequence	4.4	2.0
429876	AB026977	Hs.225974	KIAA1054 protein	4.4	19.2
429126	AW626326	Hs.27151	ESTs	4.4	10.2
449093	AB035355	Hs.22958	neurexin 1	4.4	9.4
415716	N92894	Hs.179662	nucleosome assembly protein 1-like 1	4.4	15.1
419656	AB002314	Hs.92025	KIAA0315 gene product	4.4	8.2
425864	U56420	Hs.159903	efficiency receptor, family 5, subfamily	4.4	2.4
435078	AW518888	Hs.40937	ESTs	4.4	5.7
432712	AB016247	Hs.288021	sterol-C5-desaturase (fungal ERG3), delta	4.3	5.9
426867	AA460967	Hs.22668	ESTs	4.3	6.0
412112	BE180342		gb:RC3 HT0622:130400.012-a07 HT0622 Homo	4.3	3.2
410171	H07892	Hs.12431	ESTs	4.3	5.3
442339	BC259682	Hs.227591	ESTs, Weakly similar to 1901303A Leu zip	4.2	5.0
427249	AA285362		gb:HT1277 HTC0L1 Homo sapiens cDNA 5'UT	4.2	3.5
422520	AB011182	Hs.110687	KIAA0610 protein	4.2	3.9
434460	AA478486	Hs.3852	KIAA0368 protein	4.1	8.3
410362	H04611	Hs.53164	proprotein convertase subtilisin/kexin 1	4.1	7.0
449754	H00620	Hs.30977	ESTs, Weakly similar to E334087 hypophos	4.1	3.9
408496	A1683002	Hs.136182	ESTs	4.1	4.7
434101	AA625205	Hs.295959	KIAA1622 protein	4.1	6.3
432022	AA469133		gb:nc6704.s1 NC1_CGAP_P1 Homo sapiens	4.0	2.5
431165	ST4127	Hs.32042	aspartacycline (aminocyclase 2, Cntrav	4.0	7.4
456407	AW966514		gb:EST1300590 MAGE: resequences, MAGJ Homo	4.0	5.1
411659	NM_003947	Hs.8004	hmglin-1-associated protein interacto	4.0	32.3
429628	H06964	Hs.13268	ESTs	4.0	4.5
410387	F12675	Hs.332579	ESTs	4.0	6.9
419510	AA652913	Hs.190173	ESTs, Weakly similar to A45010 X-linked	4.0	2.6
441905	Z41305	Hs.303172	Homo sapiens mRNA: cDNA DKFZ547G133 (f	3.9	21.7
412677	AW029608	Hs.17384	ESTs	3.9	2.2
453341	A1758912	Hs.216341	adenylyl cyclase-associated protein 2	3.9	1.2
410854	H40164	Hs.80296	Purkinje cell protein 4	3.9	2.2
414655	NM_004466	Hs.76828	glycophorin 5	3.8	6.2
418217	A1910647	Hs.13442	ESTs	3.8	3.2
421855	H06504	Hs.27384	ESTs, Moderately similar to ALU4_HUMAN A	3.8	2.2
414764	AW013887	Hs.72047	ESTs	3.8	10.7
433620	R13140	Hs.13359	ESTs	3.7	2.7
424738	A1953740	Hs.46826	ESTs	3.7	2.1
407706	AA191005	Hs.26612	ESTs, Moderately similar to S23650 retro	3.7	5.3
407268	A1754847	Hs.227571	regulator of G-protein signalling 4	3.7	53.7
423135	H07555	Hs.26411	ESTs	3.7	21.7
446918	A1342668	Hs.279785	ESTs	3.7	2.6
427562	RS6424	Hs.26534	ESTs	3.6	3.6
439274	AF060992	Hs.46372	ESTs	3.6	34.5
425281	H23329	Hs.290580	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6	6.0
422897	AA675784	Hs.4290	ESTs	3.6	5.1
429656	X02606	Hs.215184	neurofilament, light polypeptide (68kD)	3.6	24.6
417154	A1674701	Hs.21388	ESTs	3.6	5.8
447176	Z42549	Hs.160893	ESTs	3.6	6.4
405977				3.6	3.9
423568	NM_005256	Hs.129818	growth arrest-specific 2	3.6	2.5
441235	A1884586	Hs.135570	Homo sapiens cDNA FLJ21268 lit. clone C	3.6	5.4
426775	AA384564	Hs.108829	ESTs	3.6	3.4
414831	M31155	Hs.77439	protein kinase, cAMP-dependent, regula	3.6	2.8
425153	A19023193	Hs.27046	ESTs	3.6	4.9
446485	D06923	Hs.153400	ESTs	3.5	9.8
445988	AF070623	Hs.13423	Homo sapiens clone 24465 mRNA sequence	3.5	16.6
416421	AA134008	Hs.79306	eukaryotic translation initiation factor	3.5	5.0
418207	C14685	Hs.34772	ESTs	3.5	6.2
425383	D83407	Hs.156007	Down syndrome critical region gene 1-lk	3.5	2.3
417027	AA192306	Hs.23926	triacin	3.5	6.2
400367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	3.5	5.3
408776	AA057365	Hs.63356	ESTs, Weakly similar to (38022) hypothe	3.5	5.5
453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	3.5	23.6
419347	C15944	Hs.90005	superior cervical ganglia, neural spall	3.5	42.3
433803	A1823593	Hs.27868	ESTs	3.4	3.6
450715	A1269484	Hs.315570	ESTs, Weakly similar to KIAA1324 protein	3.4	4.1
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.4	9.8
423826	U20325	Hs.1707	cocaine- and amphetamine-regulated trans	3.4	4.7
427173	BE25017	Hs.97540	ESTs	3.4	2.4
446992	N33522	Hs.145894	ESTs	3.4	3.5
418866	AB526656	Hs.292657	ESTs	3.4	4.5
458234	BE551408	Hs.127196	ESTs	3.4	4.5
434053	AAW45136	Hs.134946	ESTs	3.4	3.9
426536	A143139	Hs.2288	visinin-like 1	3.3	42.3
410386	A167589	Hs.302689	hypothetical protein	3.3	14.4
425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	3.3	4.6
434998	AW975157	Hs.26037	ESTs	3.3	4.7
456369	AW961991	Hs.93574	homeo box D3	3.3	4.4
426527	NM_001037	Hs.170328	sodium channel, voltage-gated, type I, b	3.3	5.2
403002	N40056	Hs.1915	folate hydrolase (prostate-specific memb	3.3	9.0
419875	AA853410	Hs.93557	proenkephalin	3.3	3.6

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[illegible][illegible]

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	446318	AI949389	Ha.18067	ESTs	27	4.1
	445183	AB007877	Ha.12385	KIAA0417 gene product	27	5.3
	457012	RA1480	Ha.127630	ESTs	27	19.0
5	431988	AC002302	Ha.77202	protein kinase C, beta 1	27	7.2
	430223	NM_002514	Ha.235935	nephroblastoma overexpressed gene	27	2.8
	447932	AA337474	Ha.20021	vesicle-associated membrane protein 1 (s	27	3.8
	450214	BE439753	Ha.227571	regulator of G-protein signalling 4	27	6.9
	434731	AA648049	Ha.121518	ESTs	27	5.0
10	428639	AI767756	Ha.82302	Homo sapiens cDNA FLJ14814 f1, clone NT	27	5.2
	407109	AA458135	Ha.23223	ESTs	27	2.5
	422420	UC3398	Ha.1534	tumor necrosis factor (ligand) superfamily	27	3.3
	443305	AI060693	Ha.133318	ESTs	27	5.9
	435648	H24347	Ha.27524	ESTs	27	15.0
	418407	AL044818	Ha.84928	nuclear transcription factor Y, beta	27	2.7
15	436771	AW979887	Ha.262979	ESTs	27	6.0
	428689	NM_014351	Ha.189810	sulfotransferase family 4A, member 1	27	4.8
	440503	NM_006539	Ha.7235	calcium channel, voltage-dependent, gamma	27	4.4
	441006	AW605267	Ha.7627	CGI-80 protein	27	3.1
	410330	AW023630	Ha.46786	ESTs	26	29.5
20	434398	AA121098	Ha.3838	serum-inducible kinase	26	2.5
	438831	BE263273	Ha.6438	synapsin II	26	7.8
	415066	Z98492	Ha.5975	PRO1073 protein	26	3.4
	412643	AW971239	Ha.255892	ESTs	26	2.2
	430458	AA314998	Ha.241503	hypothetical protein	26	17.9
25	416498	U33632	Ha.79351	potassium channel, subfamily K, member 1	26	2.9
	401421				26	2.0
	415830	X98330	Ha.90821	ryanodine receptor 2 (cardiac)	26	4.2
	441817	AW996706	Ha.293332	ESTs	26	3.8
	439203	AA448930	Ha.8453	KIAA1587 protein	26	4.2
30	426054	U12431	Ha.156109	ELAV (embryonic lethal, abnormal vision,	26	5.1
	444583	AW994403	Ha.100861	hypothetical protein FLJ14600	26	3.7
	417919	AI528703	Ha.85379	ESTs	26	3.0
	434293	NM_004445	Ha.3795	EphA6	26	3.2
	431716	D89053	Ha.268012	lathy-acid-Coenzyme A ligase, long-chain	26	6.4
35	443037	AW507035	Ha.299165	synaptin 7	26	2.2
	440735	D65919	Ha.255846	ryomegalin	26	7.1
	404648				26	3.0
	429955	AA463571		gb:z7209r1 Scores_total_fetus_Nb2HF8_	26	3.5
40	435508	AW604381	Ha.121121	ESTs, Weakly similar to S00755 peckstn	26	3.9
	441190	H26073	Ha.25046	ESTs	26	3.1
	432778	AI137026	Ha.274528	hypothetical protein FLJ23563	26	2.8
	442731	AI658157	Ha.131044	ESTs	26	4.1
	416836	D54745	Ha.80247	cholecystokinin	26	14.9
45	440071	NM_005672	Ha.22960	breast carcinoma amplified sequence 2	26	2.4
	438321	AA709133	Ha.180144	ESTs	26	2.8
	439693	AI741816	Ha.125897	ESTs	26	3.6
	443212	AW269515	Ha.102500	hypothetical protein FLJ20481	26	2.8
50	429581	AL122104	Ha.136654	Homo sapiens mRNA; cDNA DKFZP434A1527 (f	26	3.8
	407868	NM_009050	Ha.40537	proline-rich Glu (S-carboxyglutamic acid	26	3.1
	443952	AW022228	Ha.322922	ESTs	26	27.9
	444124	RA3097	Ha.5818	ESTs	26	5.3
	411379	AI816344	Ha.12554	ESTs, Weakly similar to NPL4_HUMAN NUCLE	26	38.0
	440474	AI207936	Ha.7195	gamma-aminobutyric acid (GABA) A recepto	26	3.8
55	445277	AI284218	Ha.159204	ESTs	26	2.2
	410111	AI520205	Ha.189647	ESTs	26	3.5
	445162	AB011131	Ha.12376	piccolo (presynaptic cytomatrix protein)	26	4.8
	410718	AI520783	Ha.191435	ESTs	26	4.5
	417201	T50432	Ha.262904	ESTs, Moderately similar to AF097994.1 L	26	2.9
60	420274	AW968000	Ha.143389	ESTs, Weakly similar to T1c318 ubiquitin	26	2.8
	433496	AF064254	Ha.49765	VLCs-H1 protein	26	4.7
	437331	AL353633	Ha.21710	hypothetical protein DKFZP761G0313	26	3.3
	437368	AI471369	Ha.182605	ESTs	26	3.0
	411985	BE441626	Ha.168915	ESTs	26	3.6
65	410025	BE220489	Ha.113592	ESTs, Moderately similar to IS4374 gene	26	9.2
	414680	AA743331	Ha.272572	hemoglobin, alpha 2	26	3.6
	429556	AI374651	Ha.22542	ESTs	26	23.9
	429608	AA443428	Ha.48797	ESTs	26	2.8
	438109	AI076621	Ha.71387	ESTs, Moderately similar to ALU7_HUMAN A	26	3.1
	439780	AL109688		gblHomo sapiens mRNA full length insert	26	2.3
70	440888	N45600	Ha.326880	ESTs	26	3.9
	445246	AI217713	Ha.147558	ESTs	26	2.6
	440152	AB002316	Ha.7006	KIAA0378 protein	24	23.6
	432740	AF061034	Ha.278898	tumor necrosis factor alpha-inducible ce	24	2.1
	415122	D60708	Ha.22245	ESTs	24	3.9
75	432298	AL118812	Ha.274293	Homo sapiens mRNA; cDNA DKFZP616G1111 (f	24	9.8
	437948	AA772920	Ha.302527	ESTs	24	9.8
	421360	AA297012	Ha.103839	erythrocyte membrane protein band 4.14	24	2.8
	427115	AW972853	Ha.112237	ESTs	24	2.2
80	452074	BE299035	Ha.27747	G protein-coupled receptor 37 (endothel	24	10.0
	436339	AI14838	Ha.111	Rheoblast growth factor 9 (gila activat	24	3.5
	434520	AA205273	Ha.177011	hypothetical protein	24	3.1
	411529	AA432348	Ha.317596	Homo sapiens cDNA FLJ12927 f1c, clone NT	24	3.0
	442272	AA588302	Ha.129172	ESTs	24	2.1

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5	422927	AW047388	Hs.301423	calcium binding protein 1 (calbain)	2.4	2.7
	446467	H14718	Hs.11506	Human clone 23583 mRNA sequence	2.4	2.8
	415827	H17462	Hs.23009	ESTs	2.4	15.0
	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.4	3.9
	445201	AA084662	Hs.12403	soniastatin	2.4	3.7
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp566C1416 (l	2.4	2.4
	420328	Y19062	Hs.96870	starfin (Drosophila, RNA-binding protein	2.4	4.3
10	432122	AA526514	gb:06002.s1 NC1_CGAP_Ox2 Homo sapiens	2.4	4.3	
	444125	A112482	Hs.118121	ESTs	2.4	3.5
	430538	AB023435	Hs.242921	differentiation-associated Na-dependent	2.4	10.8
	457519	X69438	Hs.3052	early growth response 4	2.4	2.4
	409371	RS1736	Hs.12381	ESTs	2.4	2.1
	456303	AA224872	Hs.115068	ESTs	2.4	3.2
15	440105	AA634010	Hs.6332	Homo sapiens clone 23809 mRNA sequence	2.4	23.4
	400879				2.4	4.1
	435296	R49685	Hs.24980	ESTs	2.4	6.5
	400950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	2.4	18.5
	450332	BE244005	Hs.27610	retinoic acid- and interferon-inducible	2.4	2.2
20	433298	AF252297	Hs.91546	cytochrome P450 retinol metabolizing pr	2.4	2.7
	400974	AW015458	Hs.297017	ESTs	2.4	2.5
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	2.4	2.8
	415153	N94205	gb:2527408.r1 Soares fetal liver spleen	2.4	2.5	
	417503	AA568782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4	2.6
25	452034	F12234	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	3.0
	424940	AA955308	Hs.194327	ESTs	2.3	6.3
	431706	A016096	Hs.295341	acylphyl cyclase-associated protein 2	2.3	4.1
	419125	A542452	Hs.130881	B-cell CLL/lymphoma 11A (bcl-6) longer pro	2.3	2.9
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporters	2.3	6.7
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.3	3.2
30	449681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	2.3	5.2
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibitor	2.3	54.7
	410785	A054772	Hs.56180	nucleosome assembly protein 1-like 2	2.3	3.1
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.3	5.0
35	414828	AA156651	gb:205050.s1 Soares_pregnant_uterus_JNH	2.3	2.4	
	445556	A1910241	Hs.12887	actin-related protein 3-beta	2.3	8.5
	420869	U07616	Hs.173304	amygdalin (Sirt) Mann syndrome with br	2.3	26.3
	454521	AA186715	Hs.335429	Riken cDNA 9130422.N19 gene	2.3	2.5
	423420	AI571364	Hs.128382	Homo sapiens mRNA; cDNA DKFZp761122M (l	2.3	7.6
	439450	RS1613	Hs.125304	ESTs	2.3	26.3
40	427127	AW802282	Hs.22285	pyruvate dehydrogenase phosphatase	2.3	2.2
	447179	AW015633	Hs.151292	ESTs	2.3	3.8
	414711	AI310440	Hs.288735	Homo sapiens cDNA FLJ13522 fs, clone PL	2.3	2.3
	433449	AW772282	gb:bn17005.x1 NC1_CGAP_Kid11 Homo sapien	2.3	2.8	
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.3	2.9
	416778	H15585	Hs.79976	steroid sulfatase (microsomal), arylsulf	2.3	7.8
	425130	AA448208	Hs.99163	ESTs	2.3	4.1
	456664	AW963354	Hs.334409	metallothionein 1G	2.3	2.5
	438283	AI458321	Hs.37282	ESTs	2.3	4.2
	417465	AW007086	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.3	3.0
	412180	AW857231	gb:CMG:NN0005-100300-279-c02 NN0005 Homo	2.3	3.7	
	449891	A1968719	Hs.195387	ESTs	2.3	3.2
	416101	R24854	Hs.268906	ESTs	2.3	6.5
	439731	A1953135	Hs.45140	hypothetical protein FLJ14084	2.3	17.8
55	415734	NM_0104747	Hs.787148	KIAA0237 gene product	2.3	40.1
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	2.3	2.9
	420230	AL034344	Hs.284136	forhead box C1	2.3	2.4
	451559	AL115980	Hs.20935	hypothetical protein DKFZp7610221	2.3	5.7
	404635				2.3	2.1
	456765	AI497900	Hs.33057	ESTs	2.3	4.1
	455517	AW984068	gb:RCO:HN0006-160300-011-e06 HN0006 Homo	2.3	2.4	
	408206	AF041853	Hs.43670	kinesin family member 3A	2.2	18.5
	411770	NM_014278	Hs.71992	heat shock protein (hsp 10 family)	2.2	3.9
	430105	XT0207	Hs.25640	cholinergic receptor, nicotinic, alpha p	2.2	2.6
	458694	F12832	Hs.13298	ESTs	2.2	4.9
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.2	4.4
	439642	W01441	Hs.153967	ESTs	2.2	2.4
	450138	AW151204	Hs.200879	ESTs	2.2	4.9
	454222	BE144344	Hs.7589	ESTs, Weakly similar to A6010 X-linked	2.2	3.7
70	405326				2.2	2.7
	431342	AW971018	Hs.21659	ESTs	2.2	5.2
	453101	AW952776	Hs.36493	ESTs	2.2	3.3
	408897	N52004	Hs.203709	lipopolysaccharide specific response-7 p	2.2	2.8
	451398	AI793124	Hs.144479	ESTs	2.2	4.6
75	438208	AL041224	Hs.65379	ESTs	2.2	10.4
	408449	NM_004408	Hs.166161	dynamitin 1	2.2	6.1
	414130	AS70631	Hs.71992	Homo sapiens cDNA: FLJ21893 fs, clone H	2.2	3.1
	445016	U79716	Hs.12246	nefilin	2.2	3.9
	424375	AF070547	Hs.146312	Homo sapiens clone 24620 mRNA sequence	2.2	2.3
	424645	NM_014682	Hs.151449	KIAA0535 gene product	2.2	11.7
80	409729	IS1515	Hs.106280	ESTs	2.2	4.9
	432809	AA565809	Hs.131703	ESTs	2.2	19.9
	427890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	2.2	10.4
	428532	AF157326	Hs.184786	TBP-interacting protein	2.2	6.5

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	413074	A871368	Hs.8417	hypothetical protein DKFZp761M0423	2.2	3.4
	414442	AA156238	Hs.32501	ESTs	2.2	3.2
	452768	AW069459	Hs.61539	ESTs	2.2	2.0
	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/typtophan 5-mo	2.2	3.2
5	426281	AK000987	Hs.169111	oxidation resistance 1	2.2	2.3
	478411	AW291464	Hs.10336	ESTs	2.2	2.3
	413787	A132558	Hs.75544	tyrosine 3-monooxygenase/typtophan 5-mo	2.2	3.1
	451734	NM_006176	Hs.26944	neurogranin (protein kinase C substrate,	2.2	8.5
	439108	AW163034	Hs.6467	synaptoglycin 3	2.2	7.9
10	405385				2.2	2.4
	447295	AL371549	Hs.200696	ATPase, Class VI, type 11C	2.2	2.2
	452667	T87219	Hs.13219	ESTs	2.2	3.1
	422234	AF119818	Hs.113287	discs, large (Drosophila) homolog associ	2.1	8.3
	410339	A916499	Hs.298258	ESTs	2.1	3.2
15	412321	D87461	Hs.75244	DC2A-like 2	2.1	4.5
	447104	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fs, clone NT	2.1	2.2
	451952	AL120173	Hs.301663	ESTs	2.1	36.5
	415841	Z46637	Hs.7093	ESTs	2.1	2.4
	441086	A929489	Hs.213490	ESTs, Weakly similar to N33_HUMAN N33 PR	2.1	2.2
20	450407	NM_000810	Hs.24569	gamma-aminobutyric acid (GABA) A recepto	2.1	6.6
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	2.1	5.3
	449712	R56545	Hs.6100	ESTs	2.1	4.5
	409660	AW452065	Hs.258905	ESTs	2.1	2.1
25	430434	AL019548	Hs.241420	Homo sapiens mRNA for KIAA1756 protein,	2.1	5.4
	434138	AA625804		gb268601.1 s1 Soares_tss1c_NHT Homo sap	2.1	3.0
	448610	NM_006157	Hs.21602	net (chicken)-like 1	2.1	4.8
	418948	A217087		gb268601.1 s1 Soares_tss1c_NHT_BAH159V	2.1	2.9
	414478	AW050226	Hs.824	crystallin, mu	2.1	3.4
	440425	A1159600	Hs.7191	Homo sapiens cDNA FLJ13663 fs, clone PL	2.1	3.7
30	451249	AA016227	Hs.27280	ESTs	2.1	4.1
	451475	T19093	Hs.26450	KIAA0725 protein	2.1	2.1
	446743	AB032962	Hs.21896	KIAA1138 protein	2.1	20.7
	430814	U89336	Hs.247993	NGS protein	2.1	2.7
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	2.1	2.3
35	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	2.1	4.5
	427335	AA448542	Hs.251577	G antigen 7B	2.1	2.2
	450909	F13336	Hs.27373	Homo sapiens mRNA: cDNA DKFZp564D1763 (f	2.1	2.3
	435832	AA425688	Hs.41641	Bruno (Drosophila)-like 4, RNA binding	2.1	5.9
	446383	T05816	Hs.92511	ESTs	2.1	2.9
40	412768	AW990444	Hs.26239	Human DNA sequence from clone RP11-43882	2.1	2.1
	453976	BE463830	Hs.153714	ESTs	2.1	4.2
	451111	R39039	Hs.328455	EST	2.1	3.3
	452238	F01811	Hs.187931	ESTs	2.1	4.9
45	445279	R41900	Hs.22245	ESTs	2.1	3.8
	448739	A1937084	Hs.179080	ESTs	2.1	3.1
	418338	NM_005252	Hs.84154	neuronal pentraxin I	2.1	8.3
	446725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.1	5.4
	443537	D13305	Hs.203	cholecystokinin B receptor	2.1	4.1
50	454066	X20356	Hs.37058	calcitonin/calcitonin-related polypeptide	2.1	6.4
	422954	A918130	Hs.21374	ESTs	2.1	7.2
	451292	H23016	Hs.200576	ESTs	2.1	3.9
	423563	R34734	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.1	3.1
	424806	A566086	Hs.153716	Homo sapiens mRNA for Hmo333 protein, 3	2.1	4.7
55	463309	AA040620	Hs.5672	hypothetical protein AF140225	2.1	2.2
	433340	AB032438	Hs.6536	brain-specific Na-dependent inorganic ph	2.1	4.7
	402698	BE314624	Hs.3128	polymerase (RNA) II (DNA directed) polyp	2.1	5.4
	435406	F26698	Hs.4884	calcium/calmodulin dependent protein kin	2.1	6.6
	444972	R42550	Hs.12626	ESTs	2.1	4.1
	446500	AW958345	Hs.12958	ESTs	2.1	2.4
60	441134	W29092	Hs.7678	cellular retinoic acid-binding protein 1	2.1	5.8
	433361	AW469373	Hs.300141	ribosomal protein L39	2.1	2.7
	452546	X95475	Hs.31092	EthAS	2.1	5.0
	426167	AF039023	Hs.157496	SRAN binding protein 6	2.0	2.2
65	453666	AB0115681	Hs.135229	ESTs, Weakly similar to A2BP_HUMAN ATAX	2.0	3.1
	424632	AB014523	Hs.151406	KIAA0623 gene product	2.0	3.5
	448589	AF017090	Hs.21564	KAA1107 protein	2.0	4.1
	430416	AC005531	Hs.57806	Homo sapiens PAC clone RP4-701016 from 7	2.0	2.3
	445627	AW815475	Hs.7363	ESTs	2.0	2.1
70	417092	H87508	Hs.181165	eukaryotic translation elongation factor	2.0	2.5
	453653	AW505554	Hs.144559	ESTs	2.0	4.7
	453550	AF258487	Hs.23514	mitochondrial ceramidase	2.0	3.7
	453586	AW915243	Hs.122598	EST1	2.0	2.1
	423191	D61506	Hs.8417	hypothetical protein DKFZp761M0423	2.0	2.1
75	411562	AL050201	Hs.70769	hypothetical protein DKFZp595E1923	2.0	2.8
	431645	AF078849	Hs.265483	dynein light chain-A	2.0	2.5
	429834	AB029645	Hs.226386	synapsin I	2.0	3.6
	439607	BE544565	Hs.159460	ESTs	2.0	17.5
	408033	AW133045	Hs.242256	ESTs	2.0	4.0
	430317	AB020645	Hs.239189	glutaminase	2.0	2.7
80	419631	AW188117	Hs.303154	pooreye protein 3	2.0	2.6
	432660	A2784430	Hs.64004	ESTs	2.0	2.3
	454048	H05626	Hs.6921	ESTs	2.0	15.9
	426917	AA913614	Hs.172854	DKFZP586B0923 protein	2.0	3.1

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	423246	AL119114	Hs.77196	spectrin, alpha, non-erythrocytic 1 (alp)	2.0	2.9
	415989	AI267700	Hs.317584	ESTs	2.0	4.8
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL1_HUMAN SORL1	2.0	5.1
	424983	A174234	Hs.169911	ESTs	2.0	15.9
	446862	AA485662	Hs.53131	Human sapiens cDNA FLJ113155 fls, clone NT	2.0	2.7
	450008	AI241555	Hs.60171	ESTs	2.0	3.5

	TABLE 27b:	
Play:	Unique Eos probe/est identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	

	Play	CAT Number	Accession
	408274	104999_1	R17315 Z43964 AA053547
	412100	1277224_1	AW892731 H05052 Z45006
	412112	1277883_1	BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345

	413153	1350049_1	NW4205 BE067565 BE067556
	413510	1374377_1	F13044 T77009 BE145525 BE145493
	414828	149563_1	AA156651 AA156622 R14472
	418944	189808_1	AJ217057 AW866030 W36035 W36792 AA232635 AY9536943
	419558	185594_1	AW953679 AW953860 AA244438 H82527 AA361046 AA364483 H82526

	421249	200649_1	AA255362 AW752395 AW847156 AA285373 AW879575 AW879558
	421640	204833_1	AW966552 AW966553 AA294989 AA385977
	429995	311738_1	AA463571 A277645 AL118763
	430272	314437_1	AA491153 A718603 AA480225
	432122	341756_1	AA285154 AW973343 AA554293

	433449	366532_1	AW772282 AA592974
	434138	390572_1	AA625804 AW418787 AW074833 AB75642 AI393384
	437483	43755_1	AL390174 AW658917
	439780	47873_1	AL108568 R23665 R26578
	452502	919733_1	AI904296 BE007223 R30687
	455517	1321782_1	AW984068 AW984072 AW984077
	455407	184986_1	AW989614 AA243205 AA281411

	TABLE 27c:	
Play:	Unique number corresponding to an Eos probe/est	
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosomes 22" Dunham, et al. (1999) <i>Nature</i> 402: 489-495.	
Strand:	Indicates DNA strand from which exons were predicted.	
NL position:	Indicates nucleotide positions of predicted exons.	

	Play	Ref	Strand	NL position
	400979	8072554	Plus	160042-161028
	401213	9858408	Plus	98243-98380,98489-98619
	401421	7452889	Minus	142291-142461
	403092	8954241	Plus	174720-175016,175104-175405,175508-175813
	404848	9796894	Minus	115334-116020
	404793	7232206	Minus	61087-61590
	404835	6970743	Plus	85462-85664,88139-88287,90338-91018,94827-94990
	405326	4375975	Plus	10633-10709,30905-30893,38078-38253,55112-55327,57718-57818,66696-66841
	405385	6552772	Plus	48332-48454
	405793	1405387	Minus	89197-89453
	405911	6758795	Plus	101008-101643
	405977	8247789	Minus	135548-136177

TABLE 28a: About 139 genes up-regulated in glioma compared to normal adult tissues
 Table 28a lists about 139 genes up-regulated in glioma compared to normal adult tissues. In order to identify new genes that are associated with glioma, a non-redundant set of 6614 genes that have been previously identified were removed from the starting collection of 53690 probesets on the Affymetrix Eos-Hu3 GeneChip array. Genes associated with glioma were selected from the remaining 53025 probesets such that the ratio of "average" glioma to "average" normal adult tissues was greater than or equal to 2.5, and the "average" glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes). The "average" glioma level was set to the 94th percentile value amongst various glioblastoma, astrocytoma, and oligodendroglioma specimens; the "average" normal adult tissue level was set to the 85th percentile value amongst various non-malignant organs and tissues and other non-malignant brain tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. Predicted protein domains are noted.

	Play	Unique Eos probe/est identifier number	Exemplar Accession number, Genbank accession number		
	UnigeneID	Unigene number			
	Unigene Title:	Unigene gene title			
	Prot. Domains:	Predicted Protein Domains			
	R1:	glioma vs normal adult tissues			
	Play	ExAccn	Unigene ID	Unigene Title	Protein Domains
	443902	W28470	Hs.17601	Hs.17601	Wt-1/lymphoma-sensitive factor 4
	441476	R44566	Hs.173134	ESTs	
	446048	A272364	Hs.182081	KOA1811 protein	
	407061	X97148	Hs.334658	KIA0273 gene product	
	443423	NM_014759	Hs.334658	KIA0273 gene product	
	439769	AA448818	Hs.53596	Human sapiens mRNA full length insert	
	429319	AL023754	Hs.199008	similar to calcium/calmodulin depend	
	443412	W64893	Hs.93005	angiotensin receptor-like 1	
	425533	T47802	Hs.93005	angiotensin receptor-like 1	

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408610	AW026692	Hs.285090	ESTs	ion_trans_K_intra/KvZchan	3.4
450678	AL109703	Hs.25314	Homo sapiens mRNA full length insert	Y_phosphatase:ART:TM:SS	3.4
419171	NM_002846	Hs.89655	protein tyrosine phosphatase, recep		3.4
445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA seque		3.3
412581	AA224244	Hs.182704	ESTs, Moderately similar to alterna		3.3
424911	AA984364	Hs.7913	ESTs		3.3
452753	AA028049	Hs.277728	SEC14 (S. cerevisiae)-like 2	CRAL_TIR0	3.2
436648	R18656	Hs.352285	ESTs	phnase,phnase_C,PMF22_C	3.2
452130	AK234543	Hs.26988	SGC32445 protein	TB2_DPI_WA22:TM:SS	3.2
448948	AF131851	Hs.22241	hypothetical protein		3.2
428470	AA528794	Hs.128644	ESTs		3.2
419344	U94906	Hs.277445	diacylglycerol kinase, zeta (104kD)	ank,DAGKc,DAGKc,DAG_Pe-ti	3.2
439783	AI125750	Hs.24835	hypothetical protein FLJ14594	igL,LRRLNRT,LRRCCT,TM:SS	3.2
411358	RC4749	Hs.94751	KIAA1691 protein		3.1
409433	AA074382	Hs.135295	ADAMTS14		3.2
456940	H46986	Hs.31861	ESTs		3.1
423744	D26158	Hs.1701	ELAV (embryonic lethal, abnormal vi	nm,Gen666	3.1
432227	U28389	Hs.274122	erythrocyte membrane protein band 4	WIP:TM	3.1
440181	X96783	Hs.23179	synaptobrevin V	C2:TM:SS	3.1
422274	NM_015564	Hs.114169	KIAA0415 protein	LRRLNRTN,LRRCCT,TM:SS	3.1
424607	NM_016848	Hs.151123	neuronal Shc	P10,SH2	3.1
146889	BE219510	Hs.234074	Homo sapiens mRNA: cDNA DWF-Zp751G02	EGF_Rhubd_glycop:TM:SS=	3.1
438152	NM_014518	Hs.6290	deleted in bladder cancer chromosome	TM:SS	3.1
438992	AI043453	Hs.5755	Raf2 interacting protein 8	RUN:SS	3.1
445330	R52656	Hs.21891	ESTs	7tm_1	3.0
451766	NM_001406	Hs.20689	ephrin-B3	Ephrin:TM:SS	3.0
444457	AJ291445	Hs.52565	ESTs	Fork_head	3.0
458247	R14439	Hs.205194	ESTs		3.0
424616	U72671	Hs.151250	intercellular adhesion molecule 5,	igJCAM_n:TM:SS	3.0
408871	R38990	Hs.13485	ESTs		3.0
428940	NM_010429	Hs.274728	SEC14 (S. cerevisiae)-like 2	CRAL_TIR0:TM	3.0
458124	AAW00548	Hs.126590	ESTs		3.0
410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA seque		3.0
444608	H20019	Hs.285084	ESTs	ank,ras,PH,ArfGap,HCO03_co	3.0
437695	Z83844	Hs.5730	hypothetical protein d37E16.5	HydroLase:TM	2.9
424016	AW163929	Hs.61480	hypothetical protein MGCI5730	ig:SS	2.9
421580	AL031185	Hs.289106	Human DNA sequence from clone CTA-9	Collagen:TM:SS	2.9
418055	R18516	Hs.351299	ESTs, Weakly similar to I38022 hypo	ZZ.ZZ	2.9
444819	AB978336	Hs.148433	ESTs		2.9
420524	AB011675	Hs.188647	amiloid-sensitive cation channel	ASCT:TM	2.9
416237	H00634	Hs.155863	ESTs		2.9
432270	AK001008	Hs.274223	Homo sapiens cDNA FLJ10145 fs, clo		2.9
405569	BE311675	Hs.194673	phosphoprotein enriched in astrocy	mle_carr:TM:SS	2.9
426128	NM_001471	Hs.167017	gamma-aminobutyric acid (GABA) B re	DEC:TM	2.9
447758	H17302	Hs.93967	ESTs, Weakly similar to NBHUC3 deco	LRRLNRTN,LRRCCT,TM:SS	2.9
445331	H04489	Hs.12620	Homo sapiens clone 23568, 23621, 23	PC_rep	2.9
431010	BE251246	Hs.246214	complexin 1	TM	2.9
433065	N52602	Hs.343650	Homo sapiens PAC clone RP4-651K2 k	EB1,CH:TM	2.9
455845	AB025185	Hs.172740	microtubule-associated protein, RPI	ABC_tran,ABC_membrane,PRK	2.9
454360	L78207	Hs.54470	ATP-binding cassette, sub-family C	SDP_X-box,7tm_2,EGF_cadh	2.9
438859	AI559626	Hs.93522	Homo sapiens mRNA for KIAA1647 prot	P10,SH2,SH2,SH2	2.8
410515	F12085	Hs.4257	ESTs	hormone_rec,zf:CA	2.8
434022	R18374	Hs.117955	ESTs	Carla_CARPH34_effector,T	2.8
428960	AF052224	Hs.194684	bassoon (presynaptic cytomatrix pro	W40:TM	2.8
426290	AB007918	Hs.169182	KIAA0449 protein	C2:TM	2.8
417287	AB831678	Hs.285714	KIAA1559 protein	PTP2:TM:SS	2.8
427575	AK000546	Hs.116652	hypothetical protein FLJ20539	Band_41,FERM	2.8
417041	AI056549	Hs.96297	ESTs		2.8
452707	AI093823	Hs.45070	ESTs	C2_P02:TM	2.8
424873	AB018294	Hs.153610	KIAA0751 gene product	Ets:TM	2.8
403028	NM_004454	Hs.43607	ets variant gene 5 (ets-related mol	P10	2.8
415935	H09663	Hs.106490	ESTs	ion_trans	2.8
437899	AW905038	Hs.90242	ESTs		2.8
428248	AI126772	Hs.40479	ESTs	Catolysin,VHP,p450	2.8
414001	AE163347	Hs.103812	ESTs, Moderately similar to ALU1_HU	G0:TM	2.8
406634	AA386235	Hs.76376	GDP dissociation inhibitor 1	G-gamma:TM	2.8
453439	AB57438	Hs.32976	guanine nucleotide binding protein	nm	2.8
426290	D60647	Hs.250879	ESTs, Highly similar to CTXN RAT CO	Hydroxyornadase:TM	2.7
420888	AB006713	Hs.100058	dihydropyrimidinase-like 4		2.7
444001	AI740721	Hs.178522	ESTs		2.7
417622	AW298163	Hs.82318	WAS protein family, member 3	W42:TM	2.7
438626	AI198059	Hs.26370	ESTs		2.7
404439			ENSP0000067222:Mitochondrial ZB5	OLF:SS	2.7
446375	NM_004644	Hs.21022	adaptor-related protein complex 3,	Adaptin_N:TM	2.7
420989	AB002372	Hs.323833	synaptobrevin	TM	2.7
419651	NM_007023	Hs.91971	cAMP-regulated guanine nucleotide e	cNMP_binding,DEP,ras,GEF,F	2.7
414562	AW965734	Hs.12195	ESTs, Weakly similar to 2108407A ca		2.7
410865	T16342	Hs.66727	ESTs, Weakly similar to 211613 hypo	IRK	2.7
421146	AI002215	Hs.19993	ESTs, Moderately similar to SERP1		2.7
419087	AB671245	Hs.24835	hypothetical protein FLJ14594	igL,LRRLNRT,LRRCCT,TM:SS	2.7
421499	AZ271438	Hs.236131	homeodomain-interacting protein kin	phnase,Peptidase_M1:TM	2.7
425014	AJ251449	Hs.171939	ESTs	P10,PDZ	2.7

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	448655	AL035289	Hs.21708	hypothetical protein from clone 248	TM,SS	2.7
	424410	W79227	Hs.217162	ESTs		2.7
	447117	A362798	Hs.40183	ESTs		2.7
5	447478	BE518843	Hs.28144	fibrinectin type 3 and SPRY domain-	IK3,SPRY, TM,	2.7
	437645	R20728	Hs.21154	ESTs		2.7
	433698	H24201	Hs.20423	adducin 2 (beta)	Abdoase_J, TM,	2.7
	419701	AA248999	Hs.7913	ESTs		2.7
	410510	AW294625	Hs.64054	potassium voltage-gated channel, su	chMP_binding, ion_trans, PA	2.7
	425869	AB014534	Hs.30898	KIAA0534 protein	IK3,SS	2.7
10	428045	T15465	Hs.18231	thyrotropin-releasing hormone	SS	2.7
	425218	NM_014909	Hs.155182	KOA1036 protein	TM,	2.7
	425558	AF040723	Hs.158300	huntingtin-associated protein 1 (ne	TM,	2.6
	440789	AB007857	Hs.7416	KIAA0397 gene product	TBC, RUN, TM,	2.6
	418423	NM_014732	Hs.301658	KIAA0513 gene product	TM,	2.6
15	452000	AH94722	Hs.278044	ESTs	teclin_c	2.6
	413566	AW504451	Hs.268814	sprexly (Drosophila) homolog 4	SH2, SH3, TM, SS	2.6
	443759	BE390832	Hs.134729	FXYD domain-containing ion transpor	ATP1G1, PLM, MAT8, TM, SS	2.6
	425069	AA687465	Hs.298184	potassium voltage-gated channel, sh	abdo_hel_red	2.6
	425387	AG533657	Hs.249109	mannosyl (alpha-1,3)-glycoprotein		2.6
20	424798	AW016523	Hs.182850	ESTs		2.6
	447455	H38335	Hs.6750	Homo sapiens mRNA for FLJ00068 prot	TM, SS	2.6
	417212	AW952823	Hs.351547	NS1-binding protein	E2_NL2E_C, DNA_mis_repir,	2.6
	432265	BE362679	Hs.235753	SCG10-like protein	Stathmin, TM, SS	2.6
25	417092	C21115	Hs.26512	ESTs, Moderately similar to S23650		2.6
	421091	W22821	Hs.351612	ribosomal protein L26	TM,	2.6
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene	homeobox, CUT, TM,	2.6
	431987	AF243653	Hs.375498	organic cation transporter	sugar, h, TM, SS	2.6
	439151	AW132665	Hs.283110	carbonic anhydrase X	carb_anhydrase, TM, SS	2.6
	424134	AF070637	Hs.140950	hypothetical protein FLJ171313	DUF176, SS	2.6
30	430213	AW993446	Hs.235445	hypothetical protein FLJ21313	GRAM, TM,	2.6
	445354	AA148926	Hs.27836	hypothetical protein FLJ23632	IK3, TM,	2.6
	445084	H38914	Hs.250848	hypothetical protein FLJ14761	TM, SS	2.6
	446236	NM_006293	Hs.301	TYRO3 protein tyrosine kinase	IK3, Ig, kinase, TM,	2.6
	433706	AW947250	Hs.283645	ESTs	PH, RhoGAP	2.6
35	423606	AB011094	Hs.128692	KIAA6522 protein	PH, bZIP, JQ, Sec7, TM,	2.5
	438915	AA280174	Hs.225881	Williams-Beuren syndrome chromosome		2.5
	448923	AL234562	Hs.225884	pedonophyllin	Opicoid, neuropap, SS	2.5
	408115	AB033107	Hs.42796	KAA1281 protein		2.5
	446772	AW254404	Hs.144515	Homo sapiens cDNA FLJ11672 fs, clo		2.5
40	427989	H65525	Hs.40479	glt.yv6900.r1 Scanes melanocyte 2hb	TM, SS	2.5
	435833	BE259178	Hs.41541	thymosin (thymosin) like 4, RNA bin	rme, TM	2.5
	423797	BE259364	Hs.132898	fatty acid desaturase 1	hemc_1, FA_desaturase, TM	2.5
	448277	BE622827	Hs.95466	hypothetical protein FLJ13044	mlio_carr, TM, SS	2.5
	417298	AW665639	Hs.37358	ESTs	K11-domain, TM,	2.5
45	415577	AF257770	Hs.20330	poly(C)-binding protein 4	ig, TM, SS	2.5
	420742	U79251	Hs.99902	opac-binding protein-like adhesion	plasma, LRCT, ig, LRR, LRRN	2.5
	419109	BE169157	Hs.172717	ESTs		2.5
50	TABLE 28C:					
	Play:	Unique number corresponding to an Eos probe set				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA				
		sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495				
	Strand:	Indicates DNA strand from which exons were predicted.				
	NL_position:	Indicates nucleotide positions of predicted exons.				
55	Play	Ref	Strand	NL_position		
	405569	6006906	Plus	99719-99873		
	404439	7139680	Plus	55318-55585		
60	TABLE 29A: ABOUT 362 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE					
	Table 29A lists about 362 genes up-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 28A, except that the ratio of "average" glioma					
	to "average" normal brain was greater than or equal to 3.0, the "average" glioma level was set to the 90th percentile value amongst various glioma specimens, the "average" normal					
	adult brain tissue level was set to the 90th percentile value amongst various non-malignant adult brain specimens, the "average" glioma value was greater than or equal to 50 units.					
	Predicted protein domains are noted.					
65	Play:	Unique Eos probe set identifier number				
	ExAccn:	Exon/Accession number, Genbank accession number				
	UigenetID:	Uigenet number				
	Uigenet Title:	Uigenet gene title				
	Protein Domains:	Predicted Protein Domains				
70	R1:	glioma vs non-malignant adult brain tissue				
	Play	ExAccn	Uigenet ID	Uigenet Title	Protein Domains	R1
	414477	U41635	Hs.78228	amplified in osteosarcoma	kinase, LRR, TM, SS	11.2
	407241	M34516		glt Human omega light chain protein	TM,	10.9
75	408972	AL050100	Hs.49378	DRF2P58000919 protein	TM,	7.0
	417512	H76534	Hs.47226	glycoprotein (transmembrane) mb	PQD, TM, SS	6.9
	414001	AG10347	Hs.103812	ESTs, Moderately similar to ALU1_HU	Gelsolin, VHP, p450	6.3
	428847	AG54833	Hs.98881	ESTs		6.2
	407061	X37748		glt H.sapiens PTX3 gene promoter reg		5.4
80	440020	AA480204	Hs.177131	ESTs		5.4
	406832	AW085990	Hs.63428	ESTs, Weakly similar to Z195_HUMAN		5.3
	406837	R70292	Hs.156110	immunoglobulin kappa constant		5.2
	407607	NM_001887	Hs.37135	crystallin, beta B1	crystallin, TM,	5.1

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	435013	H01923	Hs. 110024	NM_020142 Homo sapiens NADH ubiquin		5.1
	424916	AW067440	Hs.23096	ESTs	mm	5.1
	409659	AW970843	Hs.55682	eukaryotic translation initiation f	:SS	5.1
5	432576	AW157424	Hs.165954	ESTs. Weakly similar to U50027 hypo	mm	5.1
	406621	AS7809	Hs.181125	immunoglobulin lamida locus	igJHSP70.Pxx-GppA1.TM,SS	5.1
	430418	R08852	Hs.30029	heart and neural crest derivatives	HLH	5.1
	414633	AW958444	Hs.112242	normal mucosa of esophagus specific	TM,SS	5.0
	429707	W16631	Hs.211819	matrix metalloproteinase 23B	igPapiladase_M10,TM,SS=	5.0
10	438915	AA200174	Hs.255881	Williams-Bourne syndrome chromosome	Band_7.TM	5.0
	411321	HT1182	Hs.127771	B-cell associated protein	Ribosomal_S13	4.9
	406848	A1264844	Hs.278685	ribosomal protein S18	TNF:TM,SS	4.8
	432505	AF064090	Hs.129708	tumor necrosis factor (ligand) supe	Zn_cerbOpept,Propep_M14,T	4.8
	433848	AF065719	Hs.53764	carboxypeptidase A4	homoelec,TM	4.8
15	431882	NM_001426	Hs.211937	enkephalin homolog	LIM	4.8
	446296	A1355029	Hs.101650	ESTs. Weakly similar to T14171 atax	mm	4.8
	409170	W91994	Hs.16145	ESTs	Lysyl_oxidase,Alkose_epim	4.7
	421155	H87879	Hs.102267	lysyl oxidase	Glyco_hydro_20,Glyco_Jdtd	4.7
	405202	AA236981	Hs.51043	herocaminidase B (beta polypeptide)	:SS	4.7
20	411215	AK001763	Hs.73239	hypothetical protein FLJ110001	C1q,Collagen,TM:SS	4.7
	405463	AW952018	Hs.201398	G-protein coupled receptor interact	cl-C2H2,bZIP	4.7
	445960	A1268399	Hs.140489	ESTs. Weakly similar to LUN1_HUMAN	Ribosomal_S4,S4,IRNA_inL	4.6
	406807	AA507605	Hs.180929	ribosomal protein S3	transmembrane4,TM,SS	4.6
	409190	A0016536	Hs.50984	sarcoma amplified sequence	TM	4.6
25	401699			Target Exon	TM	4.6
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	ig,TM	4.6
	441569	R78196	Hs.25692	Homo sapiens cDNA FLJ11436 fs, cl	Ribosomal_L11;TM	4.6
	406968	AA505445	Hs.300597	immunoglobulin heavy constant gamma	:SS	4.6
	408699	L08505	Hs.182979	ribosomal protein L12	COX8,SHMT,MIF,GST_CEF1G	4.6
30	406663	U24683		immunoglobulin heavy constant mu	:SS	4.6
	427714	AF119850	Hs.2186	eukaryotic translation elongation f	COX8,SHMT,MIF,GST_CEF1G	4.6
	407260	L08096	Hs.163593	gb.Homo sapiens mRNA fragment	Ribosomal_L18ae,TM	4.6
	408803	H42321	Hs.163593	ribosomal protein L18a	HC03_cotransp;TM	4.5
	430397	A0524533	Hs.105607	bicarbonate transporter related pro	proflin;TM	4.5
	414044	BE614194	Hs.75721	profilin 1	TM,SS	4.5
35	424238	AA337017	Hs.137635	ESTs	Armadillo_sq,HEAT,TMS	4.5
	421532	AW136207	Hs.107170	hypothetical protein FLJ22969	transferrin,translat_ry	4.4
	421241	XS1811	Hs.102666	transferrin-like 1	Ribosomal_S17e,PolyA_pot	4.4
	436398	H87136	Hs.5174	ribosomal protein S17	phkinase,ICE_p10,ICE_p0,T	4.4
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and	IL;SS	4.3
40	446921	AD012113	Hs.16530	small inducible cytokine subfamily	:	4.3
	433271	BE521697	Hs.14317	nuclear protein family A, member	:	4.3
	406964	M21305		GENES predicted novel secreted pro	ABCI,TM	4.3
	432191	AA043193	Hs.231186	hypothetical protein, clone Telcho	Glyco_hydro_ase;TM	4.3
45	420890	AA434058	Hs.100071	p-phosphorylconclonase	TM	4.2
	413963	AW962363	Hs.65377	ESTs. Moderately similar to KIAA139	TM	4.2
	406687	K31126	Hs.352054	matrix metalloproteinase 11 (strom	hemopexin,Papiladase_M10,T	4.2
	425157	NM_006227	Hs.283007	phospholipid transfer protein	LBP_BPI_CETP,LBP_BPI_CETP	4.2
	426386	AA748850	Hs.125830	bladder cancer overexpressed prot	TM	4.2
	446480	AK000706	Hs.15125	hypothetical protein FLJ20695	TM	4.2
50	431750	AA514956	Hs.263705	ESTs	cpn60,TCP1	4.2
	428327	AW206236	Hs.28773	ESTs	cystatin,Coprogen_coxidas	4.2
	417342	W40277	Hs.81894	glycophorin C (Gerbich blood group)	TM	4.1
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fs, cl	TM	4.1
55	433170	AB037816	Hs.8962	KIAA1395	TM	4.1
	423084	AU076474	Hs.123178	translocase of inner mitochondrial	TYA,SS	4.1
	407926	AW956382	Hs.59771	ESTs	ATP13F1_PLM_MAT&TM,SS	4.1
	445636	AW105401	Hs.350088	ribosomal protein L28	SEAT,TM,SS	4.0
	418689	A1360033	Hs.375884	hypothetical protein FLJ11029	ubiquitin,TM,SS	4.0
60	405090	AA256696	Hs.333418	FXVY domain-containing ion transp	AT_Jhsp,AT1HLA	4.0
	419092	J05581	Hs.83603	mucin 1, transmembrane	PHM	4.0
	447813	A1394345	Hs.238513	hypothetical protein MGC5442	PDZ_LIM,phkinase	4.0
	456419	A1948626	Hs.171356	ESTs	EF_Ts,UBA;	4.0
	458147	AW752607		gb.L3-CT0214-161299-045-B06 CT0214	ig,TM,SS	4.0
65	443402	U77846	Hs.356316	elastin (supravalvular aortic steno	EPH_inL,InL3,phkinase	4.0
	433436	BE545277	Hs.340999	Ts translation elongation factor, m	TM	4.0
	413095	AW252515	Hs.16145	ESTs	TM	4.0
	412607	Z33642	Hs.74115	immunoglobulin superfamily, member	cpn60,TCP1	4.0
	419913	AW270640	Hs.34455	ESTs	cystatin,Coprogen_coxidas	4.2
	415209	F00183	Hs.172004	Ilfm	TM	4.1
70	439310	AF086120	Hs.102793	ESTs	casein_kappa,phkinase,lg,n	3.9
	421777	BE582088	Hs.768186	HSP-CX37 protein	TM	3.9
	409465	S00590	Hs.252136	ficolin (collagen/fibrinogen domain	Collagen/fibrinogen_C,TM=	3.9
	402241			Target Exon	p450,TM,SS	3.9
	432716	A162964	Hs.205180	ESTs	1RRUPAR_LY6,TM	3.9
75	418140	BE613836	Hs.83551	microtubule-associated protein 2	TM,SS	3.9
	424214	AF110871	Hs.155860	hypothetical protein PR02298	:SS	3.9
	406855	AA902829		gb.hkx2766.s1 NCL_CGAP_GCA Homo sap	hemopexin,Papiladase_M10,T	3.9
	421567	AJ272137	Hs.198265	matrix metalloproteinase 2	SH2_Y,phosphatase	3.9
80	403364			Target Exon	ubiquitin	3.8
	412339	BE151267	Hs.314466	ESTs	TM	3.8
	423007	AA320134	Hs.196029	Homo sapiens mRNA for KIAA1657 prot	SH2P	3.8
	427600	AW963918	Hs.179774	proteasome (prosome, macropain) act	PA2B_alpha,PA2B_beta;	3.8
	405201			Target Exon	milo_carr,SH2,SH3,Alpha_a	3.8

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36906	H95990	Hs.181244	major histocompatibility complex, c	igMHC_L1TMSS	3.8
407319	A174332	Hs.257729	ESTs, Moderately similar to ALU1_HU	rm.Lipoprotein_2	3.8
400290	H18335	Hs.31608	hypothetical protein FLJ20041	Cys_inor	3.8
430240	BE3C0308	Hs.238547	Homo sapiens, clone IMAGE:2905978,	HEAT_1PUS.TM	3.8
442487	AF191019	Hs.8361	hypothetical protein, estradiol-ind	LRFLRRNT1TMSS	3.8
400135	AA311204	Hs.42057	methyltransferase-like 1	Methyltransf_4.TM	3.8
419942	U25138	Hs.93841	potassium large conductance calcium	CaKb.TMSS	3.8
410584	AB011112	Hs.64742	KIAA0540 protein	LTMSS	3.8
405476	NM_004987	Hs.112378	LIM and zinc-finger cell antigen-like	ribosomal_L13cSS	3.7
405874	AW151705	Hs.109042	ribosomal protein L13	7bm_2.03.GPSS locus_gly	3.7
425249	XB1479	Hs.2375	egl-like module containing, mucin-l	FKBP_TPR	3.7
430799	C19035	Hs.164259	ESTs	WD40_TM	3.7
453099	H52087	Hs.31859	thyroid hormone receptor associated	EGF_TOP_KOVR/ribosomal_L14	3.7
427194	X86298	Hs.100371	transcription factor 4, p107b1	Tropomyosin.ACOCX	3.7
444795	A1193356	Hs.160316	ESTs	CLUB/MAM/F5_F8_type_C	3.7
436334	A1741510	Hs.173548	ESTs	RPEB55.SS	3.7
429731	AK001592	Hs.212172	beta-carotene 15,15'-dioxygenase	TSPNp3_3.EGF.Juvin.TM	3.7
426433	L38969	Hs.169875	thrombospondin 3	phkase	3.7
425395	BE151985	Hs.350669	hypothetical protein FLJ23316	myosin_head.IQ.Myoasin_1a1	3.7
406704	M21565	Hs.929	myosin, heavy polypeptide 7, cardiac	Ammonium_transp.FecCD.TM=	3.7
447860	AF193807	Hs.118335	Rhesus blood group, B glycoprotein	mto_carr/homeobox.TMS	3.7
430281	A187842	Hs.237924	CGI-69 protein		3.7
440350	AL117550	Hs.205252	Homo sapiens mRNA; cDNA DKF Zp566P23		3.7
460507	AA020227	Hs.365053	Trp-g8 transient receptor potential		3.7
432078	BE314877	Hs.24553	hypothetical protein FLJ12541 simil	TMSS	3.7
460594	AA613705	Hs.252259	ribosomal protein S3	KF-domain.Ribosomal_S3_C	3.7
425532	AL008726	Hs.118126	proteicase protein for beta-galact	ovine_cantepet.GuP_UDP	3.7
420171	AA483323	Hs.183925	ribosomal protein L35	Ribosomal_L23;	3.6
442265	W28729	Hs.355072	uncharacterized hypothalamus protei	cadherin	3.6
411281	BE392792	Hs.4786	Homo sapiens cDNA FLJ22849 fs, cl	U2L_con.TM	3.6
459557	AW411509	Hs.352557	hypothetical protein PR02121		3.6
414624	BE380320	Hs.23828	3 beta-hydroxy-delta 5-C-22-steroid	sugar_b.Condensation.TM=	3.6
451584	AUK75998	Hs.132760	hypothetical protein MGC157293	hormone_rec.ct-COAT.TM	3.6
445411	AL137255	Hs.12545	hypothetical protein FLJ22699	TMSS	3.6
400785			C110086.1.gp9338070pndp_064687.	TM	3.6
413343	BE392026	Hs.334348	hypothetical protein MGC13045	Kb.TMSS	3.6
427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interf	Kb.TMSS	3.6
427818	AW511222	Hs.193765	ESTs		3.6
449957	D31365	Hs.24220	hypothetical protein	TM	3.6
451529	A1917801	Hs.208541	ESTs	odin	3.6
448528	AU079540	Hs.15243	nuclear protein 1 (120KD)	Hof1_Nbp2_Sun.TM	3.6
431669	AA031675	Hs.268940	t-complex-associated testis express	Tclsr-1.TM	3.6
433350	BE563152	Hs.103382	Homo sapiens cDNA FLJ20944 fs, cl	zf-C3HC1SPRY	3.6
412896	AW804157	Hs.373570	major histocompatibility complex, c	igMHC_C1_beta.TMSS	3.6
414748	RI4429	Hs.209194	ESTs		3.6
409553	AA614553	Hs.252259	hypothetical protein FLJ23059	KH-domain.Ribosomal_S3_C	3.6
457454	AW972234	Hs.126580	ESTs		3.6
429819	AL120751	Hs.211558	eukaryotic translation initiation f		3.6
423309	BE038775	Hs.128702	auth-nucap protein	sushi_HVR.SS	3.6
439802	AA354480	Hs.375594	EBP50-POZ interactor of 64 kD		3.6
453022	AA031499	Hs.118489	ESTs	Amino_oxidase	3.6
434042	A1589941	Hs.8254	Homo sapiens, Similar to tumor dif		3.6
424867	AU024860	Hs.153591	Meis3 (D. melanogaster)-like protei	TMSS	3.6
417298	AW955939	Hs.37958	ESTs		3.6
405943			C5000355.gp4503225rnp_000765.1		3.6
429497	AB028953	Hs.204121	KIAA1030 protein	h3.TM	3.6
426613	U96132	Hs.171260	hydroxyacyl-Coenzyme A dehydrogenas	with_short.TMSS	3.6
423343	AL043021	Hs.12705	ESTs	WDMSS	3.6
458378	AA683904	Hs.89692	TNFRSF1A-associated via death domain	death.TM	3.6
400348	AJ251708	Hs.352588	Target		3.6
404854			Target Exon	SS	3.6
427930	AA417896	Hs.372121	ESTs		3.6
451343	AA382234	Hs.356289	protein tyrosine phosphatase, recep	serpin.SS	3.6
405806	AW088535	Hs.350108	ribosomal protein, large, P0	TM	3.6
406793	AW254291	Hs.5682	guanine nucleotide binding protein	WD40_TM	3.6
414525	C14904	Hs.45184	Homo sapiens cDNA FLJ12284 fs, cl		3.6
419550	AK001545	Hs.93871	hypothetical protein FLJ10183	Glyco_NHc_47.TMSS	3.6
404243			NM_005718.Homo sapiens ring finger	zf-C3HC4_zf_B_box.TMSS	3.4
424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain trans	Ets.SS	3.4
423801	AB21702	Hs.115959	ESTs, Weakly similar to 138022 hypo		3.4
413943	AK204416	Hs.144587	Homo sapiens cDNA FLJ12981 fs, cl	TM	3.4
419558	AW062266	Hs.88131	Fas (TNFRSF3)-associated via death	death.DED-SS	3.4
408930	AA146721	Hs.333486	hypothetical protein FLJ21588	CUE.TM	3.4
403245			Target Exon	HMG_box.SS	3.4
415330	AU077101	Hs.79222	gpi-acyloxidase, beta 1	Glyco_NHc_35.TMSS	3.4
404864			NM_005204.Homo sapiens hypothetical		3.4
441384	AA447849	Hs.288660	Homo sapiens cDNA FLJ2182 fs, cl	7bm_3	3.4
400284	AW935334	Hs.293195	ESTs	RNA_pol_LRNA_pol_L_RacGA	3.4
433669	AL047879	Hs.194251	ESTs, Weakly similar to ALU2_HUMAN	S10_nuclein.TM	3.4
459050	RT9445	Hs.76230	ribosomal protein S10	h3.TM	3.4
422311	AU073515	Hs.114948	cytokine receptor-like factor 1		3.4
408090	AW502034	Hs.287379	ESTs, Weakly similar to T26022 hypo		3.4
428028	U52112	Hs.182018	interleukin-1 receptor-associated k	death.pkinase.TM	3.4

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424213	BE390125	Hs.143187	hypothetical protein	DEAD,holcasc, C.TM,	3.4
154532	BE391767	Hs.79322	glutaminyl-RNA synthetase	TM,SS	3.4
400233		Hs.79322	Eos Control	Ribosomal, S9,	3.4
403252		Hs.79322	Target Exon	tm,SS	3.4
404943	AA074382	Hs.132555	ADAMTS14	ADAMTS14	3.4
426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmic	mm,PABP;TM,	3.4
448222	AI648587	Hs.20725	Mov10 (Mobov leukemia virus 10, m	TM,	3.4
432982	AA531058	Hs.182248	truncated calcium binding protein	OPR,ZZ;TM,	3.4
453814	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	FBPase;TM,	3.4
414826	AA320893	Hs.117052	hypothetical protein FLJ114497	pyr,rdxoc;TM,SS	3.4
427751	AF000152	Hs.355616	conserved gene amplified in osteos	NF;TM,	3.4
416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial	mito_car;TM,	3.4
428046	AAW812795	Hs.337534	ESTs, Moderately similar to 138022	ank	3.4
456575	AAV08369	Hs.191649	ESTs	Myosin_tail	3.4
407366	AF026942	Hs.17518	gbl:homo sapiens ciga33 mRNA, partial	BR	3.4
414738	L24038	Hs.77183	v-rat murine sarcoma 3611 viral onc	kinase,DAG,PE-bind,RBD,T	3.4
456356	M74715	Hs.89560	iduronidase, alpha-L-	Myo_hydro_39,SS	3.3
425628	AA628142	Hs.179951	ESTs, Weakly similar to S28942 prot	EGF_ank,notch,metallo,E	3.3
404113		Hs.179951	NM_024038:homo sapiens Nench	IRF,SS	3.3
20	BE292842	Hs.166120	interleukin regulatory factor 7	PI;SS	3.3
451619	AA018854	Hs.353196	glutathione peroxidase 3 (plasma)		3.3
410225	AAW63894	Hs.12030	ESTs		3.3
422534		Hs.12030	Target Exon		3.3
433750	H15448	Hs.31330	Homo sapiens clone HX00319	GLFV_dehydr,GLFV_dehydr	3.3
421712	AK000140	Hs.107139	hypothetical protein	TM,SS	3.3
433333	AO16521	Hs.71816	v-rat murine thymoma viral oncogene	kinase,Ph;kinase,C	3.3
424915	RZ4755	Hs.23096	ESTs	mm	3.3
406454	AA554714	Hs.187578	Homo sapiens cDNA FLJ11939 fs, clob		3.3
445084	H38914	Hs.250848	hypothetical protein FLJ14761	TM,SS	3.3
446478	AI950021	Hs.370306	ESTs	TM,	3.3
425274	BC281191	Hs.155462	mitochondrion maintenance deficien	MCM;TM,	3.3
456655	AI378736	Hs.111779	secreted protein, acidic, cysteine-	kazal,SS	3.3
438912	AF065843		gbl:Homo sapiens full length insert		3.3
428396	U70539	Hs.184161	exostosin (multiple) 1	Exostosin;TM,SS	3.3
437546	AAW074836	Hs.173984	T-box 1	T-box,WG40;TM,	3.3
410613	BE544206	Hs.173984	gbl:homo sapiens 1 Soares_NFL_T_GBC, S1 H	Ctg_Collagen,cystali	3.3
414561	U27256	Hs.527	myosin-binding protein H	h3,lg;TM,	3.3
422766	AA334108	Hs.155572	heparan sulfate (glucosamine) 3-O-s		3.3
426120	AA326243	Hs.165887	coptine 1	CZ;mm;TM,	3.3
452383	T07090	Hs.27169	ESTs	zf,C2H2,PRK	3.3
456759	AC004923	Hs.155187	unc53 (C.elegans) homolog B	TM,	3.3
409227	AA806165	Hs.130323	Homo sapiens, clone IMaGE.3960432,	NANA	3.3
432649	AA281633	Hs.278586	KIAA1108 protein	TBC;TM,	3.3
446897	AA130350	Hs.25545	hypothetical protein FLJ20898	TM,SS	3.3
446690	AI354717	Hs.223808	ESTs	transmembrane4	3.3
437259	AI377755	Hs.120695	ESTs	MHC_II_alpha;lg	3.3
423461	AB020527	Hs.128827	solute carrier family 17 (sodium ph	sugar_b;TM,	3.3
421563	NM_008433	Hs.105806	granulysin	SS	3.3
453804	AA300284	Hs.35276	KIAA0852 protein	TM,	3.3
428810	AF058236	Hs.153788	nitric oxide synthase 2A (inducible	NH_binding,flavodoxin,FA	3.3
453533	AI452933	Hs.65377	ESTs	EF_TS,UBA,transmembr	3.3
449267	AI638640	Hs.220524	ESTs		3.3
418165	R83599	Hs.6837	ESTs	mito_carr	3.3
446673	NM_016361	Hs.15871	UBAP for lysophosphatidic acid phos	acid_phosphat;TM,SS	3.3
402475		Hs.15871	ubiquitin specific protease 18		3.2
404233		Hs.15871	Target Exon	HT	3.2
406655	M21533	Hs.277477	major histocompatibility complex, c	lg,MHC_2;TM,SS	3.2
414556	AAV975883	Hs.343443	Ribosomal protein L36	Ribosomal_L36;	3.2
450191	AW137243	Hs.248074	ESTs	homeobox;TM,	3.2
435906	AI686379	Hs.110796	SAR1 protein	ar;rac;TM,	3.2
412640	C19341	Hs.73399	thyroid hormone receptor interactor	SH3,FCH;SS	3.2
425662	AA920200	Hs.118397	AE-binding protein 1	Zh_carcOpept;F5_FB_type,C	3.2
431051	AAW81143	Hs.263374	ESTs, Weakly similar to CA15_HUMAN	TM,	3.2
407984	AW134708	Hs.243569	ESTs		3.2
441494	AAW452344	Hs.129977	ESTs		3.2
423114	AI076947	Hs.1614	cholinergic receptor, nicotinic, al	Neur_chan_LBD,Neur_chan_m	3.2
419833	AA281131	Hs.226997	ESTs	WHEP;TR5;PRV4-sym_1b,n	3.2
419036	R70967	Hs.372603	gbyd2Z12a11 Soares fetal liver sp	zona_pellucida;TM,SS	3.2
431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spe		3.2
453094	AA740928	Hs.27396	ESTs	BA	3.2
429589	AI815206	Hs.387544	ESTs	ZonaGubiquitin	3.2
445033	AV552402	Hs.72501	cyclin-dependent kinase inhibitor 2	ank	3.2
446272	BE268912	Hs.14501	hematopoietic cell-specific Lyn sub	SH3,HS1_sep;TM,	3.2
438930	AAW84363	Hs.343261	hypothetical protein AL110115	HLH	3.2
438183	BE283522	Hs.6101	hypothetical protein MGCC378	flavox;TM,	3.2
421310	AAW630087	Hs.203315	trinitrocellulose repeat containing 1	PHD	3.2
409283	R12673	Hs.110156	ESTs		3.2
407115	AA084921	Hs.76230	ribosomal protein S10	S10_glecion;TM,	3.2
401174		Hs.76230	Target Exon	transmembrane4,EF_TS,UBA	3.2
403217		Hs.76230	Eos Control	ras;SS	3.2
408676	AI815189	Hs.57475	sex comb on midleg homolog 1		3.2
418245	AA088767	Hs.83883	transmembrane, prostate androgen in	TM,SS	3.2
403894		Hs.83883	Target Exon	UDPGT	3.2

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414265	BE410411	Hs.75864	endoplasmic reticulum glycoprotein		3,2
451118	A1852095	Hs.60540	ESTs	EGF_vwc,TIL,SS	3,2
426264	BE616678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic	ER_lumen_recept	3,2
437386	A1355686	Hs.144798	Home sapiens mRNA: cDNA DKFZp76Z62H18		3,2
429150	AF120103	Hs.103766	smoothed (Elongation) homology	COX8,SHMT,MF,GST,C,EF1G,	3,2
430379	AF134149	Hs.200395	potassium channel, subfamily K, mem	ion_3rns,TM,SS	3,2
434566	BE265566	Hs.4288	hypothetical protein DKFZp434K046	CuIin,TM	3,2
422166	W72424	Hs.112405	S100 calcium-binding protein A9 (ca	efhand,S_100,TM;	3,2
452493	A1904031	Hs.106826	KIAA1036 protein	PHD,Myr,L2,LOC1_at_hoat,TM	3,2
413100	BE056208	gb.RC1.BT0134.310300-015-b09 BT0314	hypothetical protein SP329	F-box,TM;	3,2
420764	BE250676	Hs.19928	Human DNA sequence from clone CTA-9	Collagen,TM,SS	3,2
421680	AL031186	Hs.289106	Human DNA sequence from clone CTA-9	T1 Ribosomal_SS,TM,SS=	3,1
405738	AA507983	Hs.116265	gb.r130609.5.1 NC_03GAP_AA1	EGF granulin,TB,EB,TM,SS	3,2
434286	AW189075	Hs.61333	calpain 5	Calpain_II,Peptidase_C2,	3,1
438264	T86773	Hs.120232	ESTs	nm	3,1
436819	AA731746	Hs.279513	ESTs	TM;	3,1
456298	R86701	gb.yms809.r1 Soares adult brain N2	ESTs	nm,7tm,1,SNF,TM;	3,1
429457	BE243065	Hs.28081	ESTs		3,1
422205	A1928242	Hs.293438	ESTs, Highly similar to AF198488.1		3,1
414393	AA146855	gb.zo410.10.r1 Stratagene endothela	ESTs		3,1
423369	BE210699	Hs.279513	ESTs	Cys-protease-3C,TM;	3,1
429457	BE243065	Hs.202555	hypothetical protein FLJ22657	TM,SS	3,1
409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha (Sa	ABC_tran,TM,SS	3,1
429615	AF288627	Hs.211562	ATP-binding cassette, sub-family A	TM;	3,1
445519	A163202	Hs.170132	hypothetical protein DKFZ2494	TFIIIS,TM;	3,1
413007	AW550887	Hs.57813	zinc ribbon domain containing, 1	glutin,TM;	3,1
407228	ME5019	Hs.153374	hemoglobin, beta	Sulfatase,TM;	3,1
411573	AB029000	Hs.70823	KIAA1077 protein	ig,MHC,TM,SS	3,1
406654	ME0636	Hs.73085	HLA-G histocompatibility antigen, c	st-RanBPADMZ	3,1
435072	AW592716	Hs.116332	ESTs	SS	3,1
456442	AW451623	Hs.100752	putative c-Myc-responsive	Carb_acyltransf,TM	3,1
445457	AF166793	Hs.12743	cameline O-acetyltransferase	2OG-Fetl_Oxy_rnm,SH3,ras	3,1
448389	AW188950	Hs.345838	ESTs	C1q,Collagen,TM,SS	3,1
458248	BE407379	Hs.108082	ESTs, Weakly similar to T31636 hypo	TM;	3,1
451310	AW252651	Hs.25213	Human DNA sequence from clone RP3-4	Ribosomal_SS	3,1
414688	AF175046	Hs.755301	for protein disulfide isomerase-val		3,1
428379	AA496205	Hs.193700	Home sapiens mRNA: cDNA DKFZp586003	LIM,Ran,BPT,GRIP,TPR,pro,	3,1
425067	BE223071	Hs.169142	ESTs		3,1
410639	BE269047	Hs.65234	hypothetical protein FLJ20596	DEAD,Helicase,C,PRK,AP3;	3,1
413011	AW058115	Hs.821	belgpcn	LRR,LR,PT,SS	3,1
421502	AF111856	Hs.105030	solute carrier family 34 (iodium ph	Ribosomal_L20,Na_PL_cotra	3,1
447164	AF026941	Hs.17518	vitipin; similar to inflammatory i	MoaA_NIB_PqqE,TM;	3,1
414807	X03025	Hs.77597	polo (Drosophila)-like kinase	Ribosomal_L37,aa,phnase,P	3,1
418613	AA744529	Hs.85575	mitogen-activated protein kinase ki	Ribosomal_OH,TM;	3,1
456734	AI655616	Hs.105495	gb.b10162.1 NC_03GAP_L1Q2 Homo sap		3,1
401988	AL096739	Hs.107260	hypothetical protein DKFZp56940523	Ricin_B_beta,Glycos_tra	3,1
437959	A1472068	Hs.375604	KIAA1856 protein	eIF5_eIF2B,W2,TM;	3,1
406784	AA428625	Hs.343443	ribosomal protein L36	Ribosomal_L36;	3,1
406637	U14866	Hs.180495	ribosomal protein L5	Ribosomal_L19;	3,1
451080	H41082	Hs.217183	ESTs		3,1
414875	H42679	Hs.77522	major histocompatibility complex, c	ig,MHC_II_alpha,TM,SS	3,1
416385	U15131	Hs.79265	suppression of tumorigenicity 5	DEMN,deENN,uDENN,TM,SS=	3,1
400981		Hs.152707	Est Control	ig,MHC_II_beta,TM,SS	3,1
412270	AC005262	Hs.73797	guanine nucleotide binding protein	c-Glyphi_eIF,TM;	3,1
456843	BE301883	Hs.152707	glioblastoma amplified sequence		3,1
443071	AL080021	Hs.8896	complement component 1, q subcomp	C1q,Collagen,SS	3,1
426196	BE272095	Hs.167791	reticulocathin 1, EF-hand calcium b	efhand,SS	3,1
424010	AL080188	Hs.131758	Home sapiens mRNA: cDNA DKFZp434A13	caldesin,TM,SS	3,1
439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside	Hami1_ike,TM;	3,1
450761	R75930	Hs.174838	Home sapiens cDNA FLJ14192 ts, do		3,1
418322	AA284196	Hs.64113	cyclin-dependent kinase inhibitor 3	Y-phosphatase,DSPc,TMS	3,1
422396	AW226956	Hs.119000	hypothetical protein FLJ14972	Xink,af-CCCH,G-patch,non	3,1
407904	W44735	Hs.107260	Home sapiens cDNA: FLJ21728 ts, of		3,1
452500	AW373011	Hs.54568	hypothetical protein FLJ22222		3,1
432711	AI202053	Hs.343661	ESTs, Weakly similar to ALUE_HUMAN	WD40	3,1
416788	AA363733	Hs.200921	regenerating islet-derived 1 alpha	lcra,c,TM,SS	3,1
442492	AA528489	Hs.234518	ribosomal protein L23	Ribosomal_L14;	3,1
421210	U80016	Hs.102598	mucosal vascular addressin cell adh	TM,SS	3,0
439429	AF150286	gb.AF150286 Human mRNA from cd34 st	mitochondrial Acyl-CoA Thioesterase	RA,Band_7,MBOT	3,0
447463	AW378685	Hs.19625	SET domain, biallelically 1	Acyl-CoA_hydro,TM	3,0
446332	AA331961	Hs.183487	interferon stimulated gene (20kD)	AngC-TSA,SET,MBD,TM,SS=	3,0
428291	AA530009	Hs.174870	ESTs		3,0
456669	AI570830	Hs.8667	ADAMTS2 (a disintegrin-like and me	Pep_M12B_propap,1,Rep	3,0
452962	AW378055	Hs.253650	Home sapiens, clone IMAGE3535476,	SPRY,af-B_box,af-CNHCA,TM	3,0
430069	A1219263	Hs.122630	ESTs		3,0
451028	AA021258	Hs.286	ribosomal protein L4	Ribosomal_L4,TM	3,0
446021	BE389213	Hs.126830	bladder cancer overexpressed protein	WD40,DUFE;	3,0
434652	AF148713	Hs.13178	gamma-tub, gamma S	crystal,TM	3,0
425829	AL133079	Hs.153752	cell division cycle 25B	Ribosome,SS	3,0
424809	SF8187	Hs.1675	gamma-glutamyltransferase-like acid	G_glu,transpep,TM,SS	3,0
423579	NM_004121	Hs.11538	actin related protein 23 complex,	WD40,TM	3,0
444652	BE513613	Hs.131704	ESTs	CUB,MAM,FS_F8_type_C	3,0
441283	AA926760				3,0

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5	437415	AL137400	Hs.306456	pre-mRNA processing factor 18	Band_41,homone2,Pip18,TM	3.0
	444542	A1151293	Hs.280390	aminopeptidase	NAD_binding,flavodoxin,FA	3.0
	442426	A1373062	Hs.312938	hypothetical protein MGCS370	zf-RanBP,MDM2	3.0
	447010	AL137679	Hs.20000	Home sapiens mRNA; cDNA DKF43402d4	Exonuclease,SS	3.0
	428818	NM_004182	Hs.172791	ubiquitously expressed transcrit	DAF1232,SS	3.0
	445417	A001036	Hs.12880	a clonotype-like and metastable	1_z_Rapamycin,Pap_M12B	3.0
	430482	AF131810	Hs.241545	hypothetical protein	TM,SS	3.0
	427651	AA410292	Hs.104761	ESTs	wnt	3.0
	451876	T63141		gb.y99a12 at Skratogene lung (5372	SH3	3.0
	453562	AL137493	Hs.35945	Home sapiens mRNA; cDNA DKF434B12	ig,TM	3.0
10	452965	A504779	Hs.247325	Human DNA sequence from clone RP11-	C2,PH1,RP43A,effector,zf-	3.0
	441455	AJ271271	Hs.7854	zinc-finger regulated transporter-lik	Zfp,TM,SS	3.0
	452600	A910842	Hs.103381	ESTs	Exp_endo_pho	3.0
	450775	AAS0284	Hs.73853	bone morphogenetic protein 2	TGFa_propeptide,TGF-beta	3.0
	417634	W27202	Hs.82327	putative synthase	GSH_synthase,TM	3.0
	415512	W26544	Hs.278712	Home sapiens cDNA FLJ11074 fls, do		3.0
	410093	AW585558	Hs.299883	ESTs, Weakly similar to KIAA0970 pr		3.0
	412404	AW072995	Hs.86228	TRIAD3 protein		3.0
	443466	BE34123	Hs.321945	IKK-related kinase epsilon; inducib	kinase,ROI1,TM	3.0
20	TABLE 29B:					
	Pkey	Unique Eos probe-set identifier number				
	CAT number:	Eos cluster number				
	Accession:	Conbank accession numbers				
30	Pkey	CAT Number	Accession			
	45147	103020_1	AW645781			
	420355	0_0	AA480292			
	405233	11259_1	BC004324 NM_001020			
			BC007977 M06054			
			BM050628			
			BC829609			
			BC385504			
			BC744451			
			BI829914			
35			BI260556			
			BC395117			
			BE385334			
			BE191416			
			BE668218			
			BE194376			
			BE716213			
			BE714408			
			BE362513			
			AV272221			
45			AV272297			
			BI424171			
			BI428267			
			AW598806			
			BC431252			
			BC392433			
			BE045330			
			BE035810			
			BE716536			
			BE761659			
55			BM049537			
			BC474155			
			BC470729			
			BC479523			
			BC479529			
			BC479530			
			BC479531			
			BC479532			
			BC479533			
			BC479534			
65			BC479535			
			BC479536			
			BC479537			
			BC479538			
			BC479539			
			BC479540			
			BC479541			
			BC479542			
			BC479543			
			BC479544			
75			BC479545			
			BC479546			
			BC479547			
			BC479548			
			BC479549			
			BC479550			
			BC479551			
			BC479552			
			BC479553			
			BC479554			
80			BC479555			
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			BC479560			
			BC479561			
			BC479562			
			BC479563			
			BC479564			

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	404243	5672639	Plus	74695-75123
	403246	7637931	Minus	143547-143654,143741-143800
	404864	5263010	Plus	94495-94561,95055-95195,97396-97505,9760
5	403252	7677983	Plus	102214-102692
	404813	7341740	Plus	97717-97975
	402534	9801051	Plus	58989-59457
	402475	7547191	Plus	65363-65725
	404233	8218045	Minus	84791-85123
10	401174	9438414	Minus	132847-132917
	403694	7197765	Plus	142295-143030,165505-166186,167406-16763

TABLE 30A: ABOUT 282 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUES THAT ARE LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 30A lists about 282 genes up-regulated in glioma compared to non-malignant adult brain tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 28A except that the ratio of "average" glioma to "average" normal adult brain tissue level was greater than or equal to 4.0, the "average" glioma level was set to the 99th percentile value amongst various glioma specimens, the "average" normal adult brain tissue level was set to the 75th percentile value amongst various non-malignant brain tissues, the "average" glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. p, h3, dly, 7m domain, signal sequences, transmembrane domains). Predicted protein domains are noted.

20	Play:	Unique Ecol probe/identifier number	
	ExAcon:	Exemplar Accession number, Genbank accession number	
	Unigene ID:	Unigene number	
	Unigene Title:	Unigene gene title	
25	Protein Domains:	Predicted Protein Domains	
	R1	glioma vs. non-malignant adult brain tissues likely to encode extracellular or cell-surface proteins	
	Play	Accession	Unigene ID
	409688	AA025445	Hs.300697
	407241	M34516	Hs.77183
30	414477	U16135	Hs.76228
	417512	X76534	Hs.82226
	405863	H42321	Hs.153533
	429707	W75631	Hs.211919
	419092	J05581	Hs.89603
35	414738	L24038	Hs.77183
	414384	AA447849	Hs.288960
	406621	X57809	Hs.181125
	410584	AB011112	Hs.64742
	426395	BE15985	Hs.355699
40	425184	BE278288	Hs.155048
	435379	AF134149	Hs.240395
	408972	AL050100	Hs.49378
	446921	AB012113	Hs.16530
	425862	AJ367805	Hs.8587
45	416161	AL047476	Hs.296310
	402290	H18836	Hs.31608
	401699		
	423309	BE066775	Hs.126782
50	427600	AW630318	Hs.179774
	438905	HS9590	Hs.181244
	425335	BE394327	Hs.292627
	413011	AW068115	Hs.821
	446295	AJ355029	Hs.101960
	435396	H97136	Hs.5174
55	435013	H91923	Hs.110024
	431809	AB22488	Hs.333468
	424608	X30695	Hs.151134
	438560	AA481690	Hs.300697
	429297	X32494	Hs.198852
60	404643	AW952018	Hs.201398
	417342	W46277	Hs.81994
	416688	A756246	Hs.76901
	414044	BE514194	Hs.76721
	404864		
65	452127	BE562126	Hs.28081
	412115	AK001763	Hs.73239
	409826	AW551112	Hs.353013
	434343	AW595705	Hs.3804
	427714	AF119850	Hs.2186
70	437259	A377755	Hs.120695
	429212	NM_001504	Hs.186252
	448988	Y07573	Hs.22795
	423505	AF064090	Hs.129708
	413053	AW953263	Hs.65377
	430542	AJ557486	Hs.159122
75	435906	AJ683919	Hs.110796
	429307	AJ076592	Hs.198561
	437388	AL355986	Hs.14478
	415714	NM_002290	Hs.76672
80	430733	AJ076665	Hs.297173
	411296	BE207307	Hs.10114
	441321	H17182	Hs.7771
	446637	T19101	Hs.11494

Protein Domains

IgTM;

TM;

phospho_LRR;TM,SS

PXD;TM,SS

Ribosomal_L18ae;TM

IgPeptidase_M10;TM,SS

SEA;TM,SS

phospho_DAG_PE-bind;RBD;T

7m_3;none

IgHSP70;Pp-GppATM,SS

none

phospho;none

Ig;TM,SS

on_tran;TM,SS

TM;

L3;SS

Pep_M12B_propep;isp_1;Rep

connexin;TM,SS

Cys_inot

TM;

suzh;HYR;SS

PAC2_alpha;PA28_beta;

Ig;MHC;IT;TM,SS

ethand;kazal;af;ras;7m_

LRR;LRRNT;SS

LIM

Ribosomal_S17e;PolyA_pol;

none

TM;SS

60kD_JMP;TM;

Ig

EGF;ANATQ;TIL;spiderint

C1q;CLANAT;TM,SS

TM;

threosyl;SS

prolin;TM;

71;

mm;7m_1;SNF;TM;

SS

none

tbl_recept;ATM;

COX3;SHMT;MIF;GST_C;EF1G;

MHC;IT_alpha;g;none

7m_1;TM;

Neur_chan_LBD;Neur_chan_m

TMF;TM,SS

TM;

Ribosomal_L13;LACT;af;ra

af;TM;TM;

b2P;TM;

none

laminin_EGF;lamrin;G;Tro

laminin_b2P;Apoptoprot

20G;EF;Oxy;TM,SS

Band_7;TM;

EGF;TIL;SS

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449475	A1348027	Hs.108557	hypothetical protein PP105/
442574	BE281191	Hs.155465	minichromosome maintenance deficien
442110	AF113008	Hs.8102	ribosomal protein S20
415209	Q0183	Hs.172004	blin
431849	A1190261	Hs.27151	hypothetical protein from clone 247
421567	AJ272137	Hs.158265	statute methylglucosylase 25
427380	NM_005534	Hs.177559	interferon gamma receptor 2 (infero
431303	AW241605	Hs.253298	ESTs
432396	AW255956	Hs.118500	hypothetical protein FLJ14972
415921	RS4469	Hs.301603	Homo sapiens, clone IMAGE:363890A,
430498	X02910	Hs.241570	tumor necrosis factor (TNF) superfam
449957	D31365	Hs.241220	hypothetical protein
419603	BE262579	Hs.915566	PL6 protein
427588	L25281	Hs.150735	ras homolog gene family, member C
421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph
404854			Target Exon
411281	BE352792	Hs.4786	Homo sapiens cDNA: FLJ22849 fs, cl
414045	NM_002951	Hs.75722	rhodopsin II
431830	Y16645	Hs.2711387	small inducible cytokine subfamily
412096	AW004157	Hs.375570	major histocompatibility complex, c
429305	AF095727	Hs.287832	myelin protein zero-like 1
451698	Y16187	Hs.26580	endothelin converting enzyme-like 1
422687	AW058823	Hs.113026	insulin-like growth factor binding
444542	A1161293	Hs.280380	aminopeptidase
429833	NM_012079	Hs.288627	diacylglycerol O-acyltransferase 4a
456376	AA663904	Hs.89862	TNFRSF1A-associated via death domain
433508	R08865	Hs.111135	major histocompatibility complex, c
456356	M74115	Hs.89560	lysionidase, alpha-L
420486	AF036365	Hs.98303	caveolin 2
425123	AF206274	Hs.154695	phosphomannomutase 2
435912	AA410287	Hs.58293	Homo sapiens, clone IMAGE:3163559,
418424	Y13622	Hs.855087	latent transforming growth factor b
433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ29944 fs, cl
432659	AA281633	Hs.278586	KIAA1108 protein
445417	AK001058	Hs.12680	a disintegrin-like and metalloprote
437408	AL358598	Hs.36506	Homo sapiens mRNA; cDNA DKFZ547808
427349	AA360154	Hs.177415	Finkel-Biskis-Reilly murine sarcoma
418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood
421310	AW630087	Hs.103315	triplehelix repeat containing 1
427869	NM_001363	Hs.2230	epidermal growth factor (ErbB-4) pro
447860	AF193807	Hs.131835	Rhesus blood group, B, glycoprotein
418916	BE392781	Hs.85474	ADP-ribosylation factor 6
425720	AA362294	Hs.293584	hypothetical protein MG031302
418942	U25138	Hs.93841	potassium large conductance calcium
423105			Target Exon
418067	A127958	Hs.83393	cystatin E/M
427863	AF189712	Hs.181002	MLL septin-like fusion
458147	AW752597	Hs.223908	gbl13-CT0214-161259-945-805 CT0214
456799	AC004923	Hs.135187	unc53 (C. elegans) homolog B
427136	AL117415	Hs.173716	a disintegrin and metalloproteinase
458766	AW183618	Hs.55610	solute carrier family 30 (zinc tran
446033	AV652402	Hs.77501	cyclic-dependent kinase inhibitor 2
441281	BE501247	Hs.144084	ESTs
439720	AF935202	Hs.311181	Homo sapiens cDNA: FLJ23230 fs, cl
410184	AW503667	Hs.59545	ring finger protein 15
431760	NM_005317	Hs.268531	granzyme M (lymphocyte met-ase 1)
446999	AF354717	Hs.223908	ESTs
427466	AF026442	Hs.17518	griphimo sapiens c1g33 mRNA, partial
426156	BE244537	Hs.167382	nature-like peptide receptor Algaen
442941	U0167828	Hs.8867	cystine-rich, angiotensin inducer,
451118	AB026096	Hs.63640	ESTs
426357	AW411589	Hs.302527	hypothetical protein PR02121
437016	U016916	Hs.53098	guanine nucleotide synthetase
429447	AB028953	Hs.204121	KIAA1030 protein
444080	369115	Hs.10306	natural killer cell group 7 sequenc
454005	AF031927	Hs.288600	hypothetical protein MG03123
412270	AC005262	Hs.73757	guanine nucleotide binding protein
406729	AA069711	Hs.gm25b11.1	Stratagene fibroblast
404610			Homo sapiens cDNA FLJ11027 fs, cl
422311	AF075515	Hs.114848	cytokine receptor like factor 1
406733	MA4096	Hs.158253	major histocompatibility complex, c
407196	CI11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma
404243			NM_006778.Homo sapiens ring finger
443834	AA741510	Hs.173548	ESTs
446057	AA020227	Hs.360033	Trp-yb transient receptor potential
413661	AA071146	Hs.343354	ribosomal protein L18
414875	H42679	Hs.77522	major histocompatibility complex, c
439730	AF035292	Hs.6654	KIAA0057 protein
406257			Target Exon
434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mR
414861	U27266	Hs.927	myosin-binding protein H
430265	L36033	Hs.237356	stromal cell derived factor 1
429249	X81479	Hs.2375	egf-like module containing, mucin-1

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433541	AW081538	Hs_220324	hypothetical protein FLJ13052	NAD_kinase, TM	4.3
400575			NM_022145 Homo sapiens neuroepitide	7tm_1, TM,SS	4.3
427661	AA410292	Hs_104761	ESTs	wnt,none	4.3
452056	AW955065	Hs_101150	Homo sapiens, clone IMAGE-4054156,	TM	4.3
433669	AL047879	Hs_159251	ESTs, Weakly similar to ALU2_HUMAN	RNA_pol_LRNA_pol_L, RasGA	4.3
422624	BE116678	Hs_76152	KDEL (Ervp-Asp-Glu-Leu) endoplasmic	ER_lumen_recept,none	4.3
421680	ALD31186	Hs_289106	Human DNA sequence from clone CTA-9	Collagen, TM,SS	4.3
422766	AA334108	Hs_155572	heparan sulfate (glucosamine) 3-O-4	none	4.3
437556	AA761430	Hs_351250	ESTs, Moderately similar to S65657	phlase, WD40	4.3
415285	D31887	Hs_89868	KIAA0052 protein	Zip, TM,SS	4.3
453082	H18835	Hs_31568	hypothetical protein FLJ20041	ion_chan, TM,SS	4.2
410693	BE044206		gihoc008.x1 Soares_NFL_T_GBC_S1 H	Clq, Collagen, cystat	4.2
411310	BE065208		gprC1-BT0314-310300-015-509 BT0314	none	4.2
432497	AA551134		ESTs, Moderately similar to ALUJC_HU	none	4.2
423041	BE170842	Hs_123059	chloride channel Kb	CBS, voltage_CLC, TM,SS	4.2
449799	AI143466	Hs_125660	ESTs	none	4.2
436472	AW974567	Hs_86278	TRIAD3 protein	none	4.2
432179	X75200	Hs_2913	EgR3	EPH, htd, tyrosinase, SAM-7	4.2
424488	AK002413	Hs_145227	hypothetical protein FLJ20406	Yank, cf_COOH-C_patch, TM-H	4.2
406809	AF000574	Hs_22405	leukocyte immunoglobulin-like recep	ig, Gemini_mov, TM,SS	4.2
407586	Z37544	Hs_37121	phospholipase C, beta 3 (phosphatid	C2, PI-PLC-Y, PI-PLC-X, TM	4.2
407228	M25079	Hs_155376	hemoglobin, beta	globin, TM	4.2
450900	H51005	Hs_37502	ESTs	none	4.2
410188	AL096739	Hs_107250	hypothetical protein CKF7599-0623	Ricin_B_lectin, Glycos_ira	4.2
458248	BE407379	Hs_100802	ESTs, Weakly similar to T31636 hypo	Clq, Collagen, TM,SS	4.2
420138			NM_006055 Homo sapiens G protein-co	7tm_1, HECT, TM,SS	4.2
432074	AA523248	Hs_149723	ESTs	Y-phosphatase, none	4.2
438852	AA354489	Hs_375594	EBP50-PDZ inter1 of 54 ID	none	4.2
401908			C17000154 g1(12003980)g3AA-G43830.1	TM,SS	4.2
451287	AK002158	Hs_26194	likely homolog of mouse immunity-as	TM	4.2
407904	W44735	Hs_107250	Homo sapiens cDNA: FLJ21278 fls, cl	none	4.1
423694			Target Ecton	UDPGT-	4.1
423461	AB020527	Hs_128827	solute carrier family 17 (sodium ph	sugar_lr, TM	4.1
425603	U52219	Hs_158329	G protein-coupled receptor 50	7tm_1, TM,SS	4.1
421486	AA243499	Hs_104600	hypothetical protein FLJ10134	TM,SS	4.1
414509	AW161311	Hs_76294	CD3 antigen (melanoma 1 antigen)	transmembrane-6, TM,SS	4.1
423313	NM_014269	Hs_126838	a disintegrin and metalloproteinase	disintegrin, Rapolysin, Pe	4.1
421271	AJ020503	Hs_343661	ESTs, Weakly similar to ALU8_HUMAN	WD40	4.1
434652	AF148713	Hs_125830	bladder cancer overexpressed protein	WD40, DUF67	4.1
425952	AB020641	Hs_209646	KIAA1118 protein	Tropomyosin, Exo_endo, phos_ID	4.1
432992	AA531058	Hs_182248	truncated calcium binding protein	OPR_ZZ, TM	4.1
424857	AJ024860	Hs_153591	Not56 (i.e. melanogaster)-like protein	TM,SS	4.1
441455	AJ271671	Hs_7854	zinc/mn regulated transporter-like	Zip, TM,SS	4.1
407045			C11000661.g930801.g9elhp_064667.	TM,SS	4.1
447232	AIW49834	Hs_327	Interleukin 10 receptor, alpha	TM,SS	4.1
450785	AA852713	Hs_108885	Homo sapiens, alpha-1 (VI) collagen	vwa, Collagen, TM,SS	4.1
424027	AW337575	Hs_201591	ESTs	7tm_2, HRM, none	4.1
433587	AF234468	Hs_3736	deio-like 4 homolog (Drosophila)	EGF_DSLER, TM,SS	4.1
437118	AB037857	Hs_303591	CD9 partner 1	none	4.1
411410	R20693	Hs_69954	laminin, gamma 3	laminin, B, laminin_EGF, lam	4.1
413902	AJ076743	Hs_75513	CD36 antigen (collagen type 1 recep	EPF_TOP, CD36, SS	4.1
428938	AC020425	Hs_194660	ceroid lipofuscinosis, neuronal 3,	CLN3, TM,SS	4.1
453094	AA749258	Hs_27355	ESTs	none	4.1
443811	BE384713	Hs_74455	ESTs, Weakly similar to T34482 hypo	hormone_rec, cf_C4, none	4.0
407287	A1678912	Hs_345139	gibz59008.x1 NC1_GASP_G40 Homo sa	ras, cadherin	4.0
428028	U52112	Hs_182018	interleukin-1 receptor-associated k	death_phlase, TM	4.0
426469	BE345205	Hs_184488	folin-2	none	4.0
423114	AJ075497	Hs_1614	chimeric receptor, nicotinic, al	neur_chan_LBD, neur_chan_m	4.0
426858	NM_004182	Hs_172791	ubiquitously-expressed transcript	DUF232, SS	4.0
44626	AA320893	Hs_117062	hypothetical protein FLJ14497	pyr_redox, TM,SS	4.0

TABLE 30B:

Play:	Unique Eos probe/est identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Play	CAT Number	Accession
458147	1030220_1	AW648781 AW648490 AW649062 AW752597 AW752699
406726	0_0	AA069711
410693	1054267_1	BE044206 AW797320 BE161676 AW797336 AW797362
413100	1490226_1	BE05224 BE053168 BE05313 BE065208
432497	852_71	AW814689 RS41314 AA551104 AA77332 AK033094 BE247143

TABLE 30C:

Play:	Unique number corresponding to an Eos probe/est
Ref:	Sequence source. The digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Play	Ref	Strand	Nt_position
401699	3176654	Minus	33285-34084
404864	5253010	Plus	94495-94661, 95055-95195, 97390-97506, 9760

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5	402241	7690131	Minus	125073 125206,130996-131125
	404913	7341740	Plus	97717-97976
	404854	7143420	Plus	14260-14537
	403105	8980016	Minus	145287-145744
	404610	9508956	Minus	89583-89715,90402 90555,91428-91673
10	404243	5672608	Plus	74695-75123
	406257	7417784	Plus	55821-56037
	400575	9886575	Plus	131503-132005
	403138	9211494	Minus	164584-165056,167757-168651
	401938	9688760	Minus	120889-121024
	403694	7107765	Plus	142925-143080,165505-166186,167496-16763
	400785	8131682	Plus	43113-43967

15 TABLE 31A. ABOUT 189 GENES DOWN-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE

Table 31A lists about 189 genes down-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 30A, except that the numerator was set to the 90th percentile amongst various non-malignant brain specimens, the denominator was set to the 90th percentile value amongst various gliomas, the numerator was greater than or equal to 50 units, and the ratio was greater than or equal to 2.5 (i.e. 2½-fold downregulation in brain tumor vs. normal brain).

Play: Unique Ebox probe/identifies number
 Exon: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Protein Domains: Predicted Protein Domains
 RT: non-malignant adult brain tissue vs. glioma

Play	Exon	Unigene ID	Unigene Title	Protein Domains	RT
412524	AA417813	Hs.44208	hypothetical protein FL23153	F420, oxidized, TM, SS	14.5
432874	W54322	Hs.279551	melanoma inhibitory activity	Sp1, TM, SS	8.3
452659	AA216363	Hs.262558	hypothetical protein DKFZ348B044	SCP1, CLOL, TM, SS	8.2
426300	U15979	Hs.169228	delta-like homing (Drosophila)	E GF, laminin, EGF, TM, SS	8.2
447990	BC248281	Hs.20144	small inducible cytokine subfamily	IL8, SS	7.3
439477	W69813	Hs.55042	ESTs, Moderately similar to GF33, HJ	GNF, TFR	7.1
411602	L01406	Hs.767	growth hormone releasing hormone re	7tm, 2HRMT, TM, SS	6.1
417067	AJ001417	Hs.81086	solute carrier family 22 (extraneur	sugar, TM, SS	6.0
426488	X03350	Hs.4	alcohol dehydrogenase 18 (class I),	adh, zinc, TM;	5.9
447656	NM_003726	Hs.1826	src kinase-associated phosphotyrosine	SH3PH, TM;	5.3
435960	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	aldhydease, Hydrolase, TM;	5.2
406837	R70292	Hs.158110	immunoglobulin kappa constant		4.9
410387	A1277367	Hs.47094	ESTs		4.8
432855	AF017988	Hs.278558	scored1, frizzled-related protein 5	Fz, NTR, TM, SS	4.7
441499	AW29233	Hs.101689	ESTs		4.6
421481	AW351972	Hs.104696	KIAA1324 protein	TM, SS	4.6
420255	NM_007269	Hs.1298	membrane metallo-endopeptidase (neu	Peptidase_M13, TM, SS	4.5
407230	AA157857	Hs.182265	keratin 19	filament, bZP, SS;	4.4
412445	X51362	Hs.73933	dispermin receptor D2	7tm, 1TM, SS	4.3
413866	AA133635	Hs.173704	ESTs, Moderately similar to A53599		4.2
415165	AW87604	Hs.78005	complement component 7	ldl_recept, s_sushi, bsp, 1,	4.2
420103	AA382239	Hs.95197	aldehyde dehydrogenase 1 family, me	aldoh; TM;	4.2
428723	AW003069	Hs.183860	ESTs	GN1-2TM, SS	4.1
409081	AJ201027	Hs.50403	T-box 19	T-box, TM;	4.0
407142	AA412535		gluc2g9810.1 Scores_testis_NH1 Hom	Na_sulph_syp, TM;	4.0
414449	AA557660	Hs.76152	ocerin	LRRNT, LRR, LRR, LRRNT	4.0
444794	D12485	Hs.11951	ectonucleotide pyrophosphatase/phos	Somatostatin_B, Endonuclease	3.9
423321	D78761	Hs.96657	hypothetical protein	bsp, 1SS	3.8
401700			Target Exon	TM;	3.8
418807	NM_004944	Hs.88646	deoxyribonuclease I-like 3	Exo_endo_phos; TM, SS	3.8
406746	AA580355	Hs.279860	tumor protein, translationally-coat	TC1P; TM;	3.7
449077	AW252836	Hs.252844	ESTs		3.7
415718	F30631	Hs.200237	ESTs	isoamylase_N	3.7
402449			Target Exon	phkinoase, LRR, LRRCT; TM, SS	3.6
457489	AJ693815	Hs.127179	crylic gene	TM, SS	3.6
406743	AA911568	Hs.279860	tumor protein, translationally-coat	TC1P; TM;	3.6
415950	AL040798	Hs.80552	dermatopontin		3.6
451554	AA74966	Hs.193237	ESTs		3.6
440708	AF038962	Hs.7381	voltage-dependent anion channel 3	Euk_poin, Enterotoxin_A_P	3.5
426095	AZ19023	Hs.89986	ESTs	WD40 none	3.5
406742	AA468291	Hs.279860	tumor protein, translationally-coat	TC1P; TM;	3.5
426343	AK000785	Hs.193480	Homo sapiens, Similar to spin3, c	VHS, EHTH, UIM;	3.4
439457	AF086274		gblHomo sapiens full length insert		3.4
408796	AA688292	Hs.170345	ESTs	hormone_rec_c1-C4	3.4
440659	AF134150	Hs.7327	cydin 1	PMF22, Cladonin, TM, SS	3.4
415042	NM_006759	Hs.77337	UDP-glucose pyrophosphorylase 2	UDCP; SS	3.4
417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group	hormone_rec_c2-C4, none	3.3
445234	AIW137636	Hs.146059	ESTs	14-3-3, none	3.3
430511	BE018156	Hs.2575	cspalin 1, (lmv) large subunit	ehfand, Peptidase_C2, Calpa	3.3
420485	AF218596	Hs.268485	cell death-inducing DFFA-like efflic	7tm, 1, CIDE, N; TM, SS	3.3
413687	AS52318	Hs.100819	ESTs	TM, SS	3.3
429828	BE405038	Hs.194657	cadherin 1, type 1, E-cadherin (epi	cadherin, Cadherin_C, Jern,	3.3
409738	BE222975	Hs.56205	insulin induced gene 1		3.2
442046	AA4074575	Hs.287385	ESTs	c1-C2H2, SET; TM;	3.2
413127	BE065529		gbl-RC3 ET0333-300300-017-a12 ET0333		3.2
429350	A1754634	Hs.131987	ESTs	MAM, TM;	3.2
427980	AA418305	Hs.303205	EST	LRR, none	3.2

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42498	A003043	Hs.149377	hypothetical protein DKFZp761J0424
43584	NM_001290	Hs.4590	LIM domain binding 2
407632			Target Exon
43130	NM_006103	Hs.2719	HE4, epidermis-specific, whey-acid
410636	A008177	Hs.172870	ESTs
42598	N8564	Hs.30212	thyroid receptor interacting protein
435180	N46243	Hs.110373	ESTs, Highly similar to T42626 sect
430319	A0480214	Hs.356075	nirjun 2
439424	A1912498	Hs.53955	hypothetical protein FLJ14596
450693	NM_005744	Hs.15461	mieloid-binding protein 4, hetero
429598	AL1175178	Hs.722009	DKFZP344C128 protein
417677	NM_016055	Hs.82389	CGI-118 protein
443792	A0730073	Hs.204873	ESTs
443661	BE293423	Hs.11889	single lg L1-related molecule
427815	A0037360	Hs.183800	hypothetical protein FLJ20277
458689	NM_002251	Hs.117780	potassium voltage-gated channel, de
464692	AW005115	Hs.161287	ESTs
427706	AW917225	Hs.263800	ESTs, Weakly similar to ALU1_HUMAN
458008	A460314	Hs.123205	ESTs
449708	A094598	Hs.207126	ESTs
410132	NM_003480	Hs.300946	Microfil- associated glycoprotein
422778	Y05267	Hs.132821	flavin containing monooxygenase 2
425260	U31519	Hs.1872	phenylalanine carboxylase 1
453177	AW089509	Hs.223747	ESTs
416781	AF072928	Hs.78977	myobulin related protein 5
447582	BE293520	Hs.18910	prostate cancer overexpressed gene
417365	D56683	Hs.82028	transforming growth factor, beta re
452540	AW161048	Hs.150549	ESTs, Weakly similar to 133697 hyp
430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N10
418127	BE243982	Hs.83532	membrane cofactor protein (CD46, t
404445			Target Exon
423223	A051628	Hs.127007	potassium channel, subfamily K, mem
452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp58M07
427981	BE275986	Hs.181311	asparaginyl-tRNA synthetase
452242	R50956	Hs.159993	glycyltransferase
446232	A176925	Hs.112554	ESTs
444634	AW511088	Hs.197813	ESTs
446889	BE451196	Hs.266958	ESTs
414483	R25513	Hs.10983	ESTs
453500	A1747427	Hs.43125	esophageal cancer related gene 4 pr
419785	TT7104	Hs.53194	protein kinase C, alpha binding pr
427804	AL496554	Hs.180871	phosphoinositide-3-kinase, class 2,
432753	Y11312	Hs.132463	ESTs, Weakly similar to RET2_HUMAN
430699	AW969947	Hs.292718	gb-RC1-OT29-16220-013-a12 OT0029
427842	AW535991	Hs.128113	cytochrome b5 reductase 1 (B5R, I)
432834	F06459	Hs.289113	ESTs
421435	AW972072	Hs.372167	ESTs
402458			C100Z064.gli11993050gAAG42574.1
413035	R57171	Hs.57875	crataegevin 2 (cardiac muscle)
412570	A0033517	Hs.74047	electron transfer-flavoprotein, bet
459439	AW402931	Hs.352411	gb.UH-F8-BK0-abb-a-01-U-1R1 NH_M
438622	L03151	Hs.301596	ESTs, Weakly similar to 565657
417023	AA192278	Hs.301596	ESTs, Weakly similar to A25704 syna
452281	W46280	Hs.55940	Target Exon
403028			polio carrier family 7 (calicic a)
449029	N28985	Hs.22891	FAT1 tumor suppressor (Drosophila) h
425483	AF231022	Hs.156159	gb.Homo sapiens DNA-binding protein
409118	M68357	Hs.59865	non-kinase Cdc42 effector protein
435213	AW002510	Hs.59865	ESTs
443990	AW205085	Hs.35657	ESTs
451698	Y15187	Hs.26880	endothelin converting enzyme-like 1
451713	AK000386	Hs.267997	EHH4 gene
431469	N42424	Hs.124159	ESTs
400396	AF075290	Hs.50964	gap junction protein, alpha 3, 4kD
406684	X16354	Hs.10083	carcinoembryonic antigen-related ce
449874	AA135888	Hs.10083	Homo sapiens, clone IMAGE:4135788,
402213			NM_016593 Homo sapiens intermed
459665	BE157874	Hs.47647	gb.MR0-HT0408-220300-001-N06 HT0408
421823	N40850	Hs.28625	ESTs
422693	BE300073	Hs.273650	tumor protein, transcriptionally-cont
454986	A213322	Hs.101077	ESTs, Weakly similar to T22963 hypo
447075	AW62037	Hs.124740	ESTs, Weakly similar to 158022 hypo
450273	AW296454	Hs.24743	hypothetical protein FLJ20171
434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypo
438972	AB284679	Hs.25640	claudin 3
441379	AW175787	Hs.333481	selenium binding protein 1
421143	AB024536	Hs.102171	immunoglobulin superfamily contain
422558	NM_006420	Hs.118249	brefeldin A-inhibited guanine nucle
428900	AA437189	Hs.352324	Human DNA sequence from clone RP1-6
421153	AF009287	Hs.102238	Homo sapiens clone FB1 C81-B4-the
427074	AS527435	Hs.175889	hepatocellular carcinoma antigen ge
448133	AA723157	Hs.737769	folate receptor 1 (adult)
491158	AF031475	Hs.89648	arginine vasopressin (neurophysin I

AP3TMSS	3.2
LIM_bnd;TM	3.2
lg;TMSS	3.1
wag;TMSS	3.1
TMSS	3.1
PC2;TM	3.1
laminin_GLRRCT;none	3.1
TMSS	3.1
C2;TM	3.1
lncanin,TGF-beta,TGFb_p	3.1
TM	3.1
	3.1
	3.1
TIR;TM	3.1
LRR;none	3.1
ion_trans;TM;SS	3.1
SPRY_zf-B_box;PAAD_D	3.1
	3.0
SCAN_zf-C2H2;none	3.0
	3.0
TMSS	3.0
FMO-like_pyr_redox;TM;S	3.0
PEPOK;TM	3.0
zf-C2H2;none	3.0
	3.0
sugar_tm;TMSS	3.0
TMSS;WD40;TM	3.0
PK;Bis;CH_spectin;Ca_cha	2.9
sush;TMSS	2.9
	2.9
ion_trans;TMSS	2.9
7tm_1;none	2.9
IRNA-sym;2_IRNA;none;IRN	2.9
	2.9
OKS	2.9
TM	2.9
	2.9
TMSS	2.9
Adol;protein;SS	2.9
P2;SS	2.9
C2;P3_P4_kinase;PK3a;P	2.9
lyocatin;SS	2.9
ethand_mio;cap;none	2.8
NAD_binding;FAD_binding_6	2.8
	2.8
TMSS	2.8
Catechol;SS	2.8
ETF_beta;SS	2.8
	2.8
	2.8
	2.8
lysosin;trefoil	2.8
agp_pemases;TMSS	2.8
EGF_cathelin;laminn_QTM	2.8
zf-C2H2_KRAB_zfBED;TM	2.7
TM	2.7
	2.7
Peptidase_M13;TM	2.7
Band_4;TM	2.7
SH3	2.7
connexin;TM;SS	2.7
lg;TMSS	2.7
	2.7
SH3;ethand;C2;PH1;RhoGEF;T	2.7
	2.7
TCIF;none	2.7
TM	2.7
TM	2.7
immune	2.7
	2.7
FMF;P2_Claudin;TM;SS	2.7
TM	2.7
lg;LRR;LRRN;LRRCT;TMSS	2.7
Sec7;none	2.7
SS	2.7
	2.7
ethand;TM	2.6
Folate_rec;MP;TM;SS	2.6
homone;S;homone;SS	2.6

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	448406	AW772298	Hs.21103	Homo sapiens mRNA: cDNA DKFp564B07		2,6
	437175	AW176509	Hs.42346	calcineurin-binding protein calcic	Galactosyl_T, TM, SS	2,6
	435075	RS1094	Hs.12400	ESTs		2,6
	403153			Target Exon		2,6
5	400387	AF133131		double homeobox, 5		2,6
	425940	AB023184	Hs.153890	KIAA0967 protein	PDZ, SS	2,6
	416157	NM_002343	Hs.342874	transforming growth factor, beta re	zona_pellucida, TM, SS	2,6
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALUS_HUMAN	HLH, PAC, PAS, none	2,6
	453247	T80198	Hs.111606	ESTs	wa, Cdc, none	2,6
10	437144	AB022629	Hs.30295	ATP-binding cassette, sub-family A	ABC, Itron, PRK, TM, SS	2,6
	432677	AW974111	Hs.292477	ESTs	Ests, SAM, PNT, none	2,6
	450115	A1591038	Hs.36132	ESTs		2,6
	406337	NM_005269	Hs.7693	C14000021.gq172429/3.khg1BA0439547.1	Papillase_M22	2,6
15	433877	AB023184	Hs.153890	glutamate-associated oncogene homolog	z-Cct2, SS	2,6
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (fundul		2,6
	450493	M83718	Hs.166373	nitric oxide synthase 3 (endothelia	NAD_binding flavodoxin, FA	2,6
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochond	ethand, mko, car, TM, SS	2,6
	446585	AV503387	Hs.25968	ESTs, Weakly similar to I38027 hypo		2,6
	427223	BE280168	Hs.174531	cytochrome c oxidase subunit VIIa	tubulin, FKBP, COX6B, 7tm, 1,	2,6
20	428111	S76517	Hs.2243	8 lymphoid tyrosine kinase	SH2, SH3, pkinase, SS	2,6
	440133	A056255	Hs.133349	ESTs		2,6
	419633	AA133749	Hs.301350	FXD domain-containing ion transpor	ATP1G1, PLM, MATS, TM, SS	2,6
	417103	Z33565	Hs.81218	hypothetical protein MGC25507	TPR, zif-CHC, ALPHO, TM, SS	2,6
25	415100	AA464362	Hs.6748	hypothetical protein PP1665	squash, GDFP, TM, SS	2,6
	449525	A1342493	Hs.24192	Homo sapiens cDNA FLJ200767 fs, cto		2,6
	430937	XS3463	Hs.2704	glutathione peroxidase 2 (gastroni	GSH, P, SS	2,6
	425640	U34651	Hs.159450	cyclin-dependent kinase 5, regula	CKM, activator, TM, SS	2,6
	439021	AA156640	Hs.43881	tetray acid binding protein 3, muscl	lipocalin, none	2,6
	400538			ENSP00000239776-BA425A6.2 (similar	TM, SS	2,6
30	468847	AF146747	Hs.232165	polycythemia rubra vera 1: cell sur		2,6
	408310	AW179023	Hs.191705	gb.FM03-ST0036-17089-01-e08 ST0036		2,6
	433332	A1084065	Hs.20072	myosin regulatory light chain inter	SS	2,6
	419389	A1074951	Hs.319095	ESTs		2,6
35	453145	R63438	Hs.183454	Homo sapiens cDNA FLJ14883 fs, cto	Band, 41:	2,6
	443460	AL050275	Hs.9383	DKFZF98602713 protein	DPPV, N_tern, none	2,6
	421903	AW079640	Hs.1651	ESTs, Weakly similar to S32436 coll	STT3, TM, SS	2,6
	421757	Z20897	Hs.296259	paraoxonase 3	EGF, laminin, EGF, EB, TM, SS	2,6
	428475	AF172940	Hs.184542	CGI-127 protein	SS	2,6
40	424657	AA344719	Hs.236720	gb.EST50501 Gall bladder II Homo sa	Arylesterase, SS	2,6
	432662	AW040958	Hs.236720	amniotic protein		2,6
	427195	W27230	Hs.173912	eukaryotic translation initiation f	TM, SS	2,6
	447770	AB023417	Hs.19545	fizzled (Drosophila) homolog 4	DEAD, helicase, C,	2,6
	456523	A1083658	Hs.50601	hypothetical protein MGC10596	Fz, Fizzled, 7tm, 2, TM, SS	2,6
	451646	T55840	Hs.11762	ESTs	pkinase, none	2,6
45	432506	BE265489	Hs.3123	larval giant larvae (Drosophila) ho	WD40, TM,	2,6
	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38027 hypo		2,6
	441488	AW450935	Hs.7652	hypothetical protein FLJ20312	TM,	2,6
	444659	F18939	Hs.153627	ESTs		2,6
50	452497	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 fs, cl		2,6
	TABLE 31B:					
	Play:	Unique Eos probelet identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
55	Play	CAT Number	Accession			
	439457	23338_1	AF086274 W59434 W59517			
	413127	151610_1	G0407256 BF330633 BF1747375 BE066356 BE066292 BF330900 BF747142 BE066419 BF742510 BE066529 BE066298 BF742516 BF746603			
			BE066274 BF334312			
60	427842	1164138_1	AW936950 AW936961 AA16706 R29415			
	438622	46171_1	L03151 L03155 L03151			
	424657	896375_1	AW953467 AA355077 AA344719			
	TABLE 31C:					
	Play:	Unique number corresponding to an Eos probelet				
	Ref:	Sequence source. The 7-digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA				
		sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.				
	Strand:	Indicates DNA strand from which exons were predicted.				
	NL_position:	Indicates nucleotide positions of predicted exons.				
70	Play	Ref	Strand	NL_position		
	401700	3176554	Minus	35416-35534		
	402449	9799574	Plus	58867-60039 52588-52628 63465-63023 64692		
	402632	9931268	Plus	101166-101419		
75	404445	7599586	Minus	31112-31423		
	402458	9798782	Plus	170478-171134		
	403026	7670577	Minus	114150-114272		
	403213	7630897	Minus	162572-162739 164442-164540		
	403153	9799871	Minus	42232-43389		
80	406337	9213455	Plus	50117-60037		
	400538	9757838	Plus	8752-9822		

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428609	S78187	Hs.153752	cell division cycle 25B	Rhodanese,SS	2.5
408369	R38438	Hs.182675	SLC15A2 Solute carrier family 15 (H	PTR2,TM,	2.5
414561	A1064813	Hs.191555	Homo sapiens amino acid transport s	Aa_trans,TM;	2.5

5 TABLE 32B.
Play Unique Eos preblast identifier number
CAT number Gene cluster number
Accession Genbank accession numbers

10 Play CAT Number Accession
438693 2580163_1 A1526361 AA834879 AA828995
412070 287551_1 BG620657 AW860808 BF904755 AW893260 B1034684 BF963423 BF961550 M86588

15 TABLE 32C.
Play: Unique number corresponding to an Eos preblast
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nil_position: Indicates nucleotide positions of predicted exons.

20 Play Ref Strand Nil_position
402154 8516165 Minus 125299-125494

25 TABLE 33A: ABOUT 798 GENES UP-REGULATED IN KIDNEY CANCER

Table 33A lists about 798 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59880 probes on the Affymetrix/Eos HuO3 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 50th percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 50th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 Play: Unique Eos preblast identifier number
ExAccess: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal tissue

	Play	ExAccn	UniGeneID	Unigene Title	R1
	421471	U05045	Hs.104635	solute carrier family 17 (podium phospho	1007.4
	445178	A1752241	Hs.126314	kidney-specific membrane protein	438.0
35	452401	NM_007115	Hs.26352	tumor necrosis factor, alpha-induced pro	336.4
	421727	Y13163	Hs.107318	kyurenine 3-monoxygenase (kyurenine 3	323.6
	440304	BE159994	Hs.123595	ESTs	295.0
	438878	BE465204	Hs.47448	ESTs	258.8
45	452755	AK035255	Hs.18878	hypothetical protein FLJ121620	258.6
	421155	H87879	Hs.102267	lysoyl oxidase	251.8
	428471	M22440	Hs.170009	transforming growth factor, alpha	224.6
	421478	A1683243	Hs.97258	ESTs	212.6
	424086	A1351010	Hs.102267	lysoyl oxidase	196.2
50	428296	NM_003368	Hs.183572	solute carrier family 22 (organic cation	186.4
	428890	AA393167	Hs.41294	ESTs	183.4
	441031	A1110584	Hs.7645	fibrinogen, B beta polypeptide	174.0
	411642	NM_014532	Hs.71132	neuroisin 1	172.4
	452838	U05011	Hs.30743	preferentially expressed antigen in mel	161.4
55	425984	AA186277	Hs.166363	hypothetical protein DKFZ761C0721	151.0
	438966	AA959074	g0:EST391184 MAGE resequences, MAGP Homo	135.0	
	453165	S74727	Hs.32042	aspartoacylase (aspartoacylase 2, Canavian	134.8
	453160	A1263307	Hs.146228	ESTs	111.8
	452431	U08879	Hs.29489	tol-like receptor 3	106.6
60	423508	AA604267	Hs.129711	hepatitis A virus cellular receptor 1	120.4
	420642	AK001520	Hs.95545	Homo sapiens cDNA FLJ10658 fs, clone NT	112.6
	407875	B98425	Hs.41716	endothelial cell-specific molecule 1 (NO	111.8
	431708	AA68136	Hs.108873	ESTs	109.8
	446460	AA001389	Hs.150164	ESTs	103.6
65	443450	N66045	Hs.133529	ESTs	103.0
	432865	A1753709	Hs.152484	ESTs	101.4
	442438	AA65998	g0:nc26003 s1 NCL_CGAP_Kid5 Homo sapiens	98.8	
	433447	U22195	Hs.3281	neuronal pentraxin II	98.5
	440311	A1733079	Hs.125407	ESTs, Moderately similar to ALUE_HUMAN ;	98.2
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	97.0
	437157	BE048860	Hs.120655	ESTs	94.4
	453319	A186336	Hs.201117	ESTs	91.4
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	90.2
	439169	A1812122	Hs.41095	ESTs	86.6
	431870	AA449902	Hs.105500	ESTs	84.4
	438953	AA828956	g0:cd77068 s1 NCL_CGAP_Ov2 Homo sapiens	83.8	
	445279	B41590	Hs.22245	ESTs	82.4
	451592	A1805416	Hs.213897	ESTs	79.4
	422966	AA648419	Hs.122613	dimethylglycine dehydrogenase precursor	78.8
	423109	M55305	Hs.123655	naniontic peptide receptor Glycylate	78.0
80	415989	AA07700	Hs.111128	ESTs	77.0
	422544	AB018259	Hs.118140	KIAA0716 gene product	74.8
	425878	AA964306	Hs.38085	ESTs, Weakly similar to putative glycine	74.8
	429352	AK001512	Hs.200957	hypothetical protein FLJ10650	73.0

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	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	72.2
	441665	A0301355	Hs.151285	ESTs	71.6
	436094	A1560129	Hs.277523	EST	71.2
5	403345	Y52599	Hs.2561	nerve growth factor, beta polypeptide	69.6
	434440	AA8668	Hs.50873	ESTs	69.0
	440482	AA8668	Hs.50873	ESTs	67.6
	457100	AA417878	Hs.48401	ESTs, Weakly similar to ALUR_HUMAN ALU S	67.0
	420537	AW576153	Hs.252905	gb:EST388262 MAGE resequences, MAGN Homo	65.2
	407905	AW103655	Hs.252905	ESTs	63.2
10	422998	AK000866	Hs.122923	hypothetical protein FLJ20581	61.8
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 f1, clone HE	61.2
	449448	D60730	Hs.57471	ESTs	60.6
	413141	AK000105	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone CO	59.8
	419752	AA204573	Hs.152618	ESTs	58.4
15	446579	AW021260	Hs.134014	prostate cancer associated protein 6	58.2
	408609	AA330431	Hs.640	calciolnin receptor	57.4
	451009	AA013140	Hs.115707	ESTs	56.4
	435610	A1852767	Hs.114157	ESTs, Weakly similar to putative p150 [H	56.2
	411893	R82045	Hs.273709	ESTs	55.4
20	415227	AW821113	Hs.72402	ESTs	55.2
	433659	AW896758	Hs.163925	ESTs	55.0
	450459	AK591193	Hs.299254	ESTs	54.8
	402302	N480256	Hs.1915	nitric hydrolase (prostate-specific memb	53.4
	421831	AA298836	Hs.22026	ESTs	52.4
25	438617	AK023799	Hs.163242	ESTs	52.1
	449101	AA205847	Hs.23016	G-protein-coupled receptor	52.0
	410025	BE220489	Hs.113559	ESTs	51.8
	423685	BE359434	Hs.48753	Homo sapiens mRNA for KIAA1561 protein,	48.0
	436761	AA732217	Hs.294054	ESTs	46.6
30	445424	AB028945	Hs.126956	contactin SH3 domain-binding protein	45.4
	444059	R85743	Hs.75442	albumin	44.8
	442671	A1005668	Hs.134179	EST	44.4
	445657	AW612141	Hs.279575	ESTs	44.3
	452891	N17582	Hs.212875	ESTs, Weakly similar to KIAA0357 [H.sapi	44.0
35	423735	AA330259	Hs.113559	gb:EST33963 Embryo, 12 week H Homo sapi	43.8
	422553	AK597720	Hs.171455	ESTs	43.6
	452461	N78223	Hs.108105	transcription factor	42.6
	408430	S79676	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	42.6
	452240	A1591147	Hs.61232	ESTs	41.7
40	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor I	41.4
	427818	AW294571	Hs.136040	ESTs	41.4
	419287	X51906	Hs.89872	chloride channel 5 (nephrolithiasis 2, X	40.6
	428822	W28418	Hs.301148	potassium voltage-gated channel, Isk-rel	40.2
45	412359	AW857985	Hs.127648	hypothetical protein PR02176	40.0
	434208	T32641	Hs.127648	hypothetical protein PR02176	39.2
	442168	A1253165	Hs.146022	ESTs	38.8
	400792	AA635052	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434C0051 f	38.6
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	38.4
	444743	AA045648	Hs.11817	nucleic (nucleotide diphosphate linked mol	38.4
50	428795	RA5503	Hs.57405	ESTs, Weakly similar to H8698 alpha-1,3	37.6
	406411				37.6
	423657	AL045128	Hs.1691	glucan (1,4-alpha), branching enzyme 1	37.5
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	37.2
	446788	AW570286	Hs.107070	ESTs	37.2
55	441826	AW503603	Hs.129915	phospholipase related	37.0
	409263	AA069573	Hs.50319	ESTs	36.8
	422577	BE464496	Hs.290977	ESTs	36.8
	452249	BE384412	Hs.61252	ESTs	34.8
	435986	AA703156	Hs.187848	ESTs	34.4
60	417236	A1808497	Hs.107037	Homo sapiens cDNA: FLJ23251 fs, clone C	33.8
	440234	AW117264	Hs.126522	ESTs	33.8
	435334	RA4223	Hs.117747	ESTs	33.3
	410153	BE311926	Hs.16630	Homo sapiens cDNA FLJ12691 fs, clone NT	33.2
	424871	NM_004525	Hs.153595	low density lipoprotein-related protein	32.8
65	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp5648222 f	32.4
	423992	AW898292	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564411663 f	32.4
	451050	AW937420	Hs.69562	ESTs	32.0
	449034	AW624049	Hs.17405	gb t41a09.x1 NC1_OCAP_11 Homo sapiens	31.6
70	434539	AW748078	Hs.214410	ESTs	31.0
	431595	AA508196	Hs.23796	gb:gb0007.s1 NC1_OCAP_P16 Homo sapiens	30.6
	449625	NM_014253	Hs.23796	odg (odd) Olfen-m, Drosophila homolog 1	30.5
	448243	AW369771	Hs.177496	small nuclear ribonucleoprotein polypept	30.4
	413573	A1733659	Hs.149089	ESTs	30.2
	421037	AW684808	Hs.197653	ESTs	30.2
75	419353	AK001220	Hs.271369	ESTs	30.2
	416548	H62953	Hs.271369	gb:gb1006.r1 Soares fetal liver spleen	30.2
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	29.6
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	29.6
	459508	R81365	Hs.205956	ESTs	29.2
80	414245	BE148072	Hs.75893	WAS protein family, member 1	28.8
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	28.6
	445925	A1733820	Hs.145664	ESTs	28.4
	412616	AW970584	Hs.291033	ESTs	28.0

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	424638	AM72106	Hs.49303	Homo sapiens cDNA FLJ11663 fls, clone HE	27.6
	445885	A1734009	Hs.127699	KIAA1603 protein	27.6
	410247	AF181721	Hs.61345	RU2S	27.4
5	406414				27.2
	435951	AF269162	Hs.41267	c1orf71 form A-D	27.2
	458480	N73773	Hs.282960	ESTs	27.2
	419648	AB041035	Hs.93847	NADPH oxidase 4	26.4
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	26.3
10	427457	AW779105	Hs.164662	ESTs, Weakly similar to ORF2 consensus	26.0
	446346	AC092025		gb:U75055.v1 Squares_HuHMFu_S1 Homo sapi	26.0
	448595	AB014544	Hs.21572	KIAA0644 gene product	25.8
	419569	A1971651	Hs.91143	jagged 1 (Alagille syndrome)	25.6
	433242	AB040938	Hs.113940	KIAA105 protein	25.6
	453118	AW198449	Hs.252757	ESTs	25.6
15	412209	AW091456		gb:RCD.NN1012.2:70300:031 c07 NN1012 Homo	25.2
	429710	AJ337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fls, clone L	25.2
	444783	AK001468	Hs.62180	anillin (Drosophila Scrp homolog), act	24.6
	436788	AA166908	Hs.259847	ESTs	24.4
	427660	AT111320	Hs.114121	Homo sapiens cDNA: FLJ23228 fls, clone C	24.4
20	419172	AW338625	Hs.22120	ESTs	24.3
	436061	AJ248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fls, clone C	24.2
	413623	AA629721	Hs.246973	ESTs	24.0
	407615	AW753085		gb:PMH.CT07047.15:1299-095-a03 CT0247 Homo	23.8
	452466	N84635	Hs.29964	Human DNA sequence from clone 682115 on	23.8
25	432809	AA565509	Hs.131703	ESTs	23.7
	440102	AI872443	Hs.131190	ESTs	23.6
	451559	AL119880	Hs.128657	ESTs	23.2
	410811	AW805687	Hs.309548	ESTs	23.0
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsul	23.0
30	453628	AW243307	Hs.170187	ESTs	22.8
	401352				22.6
	451581	N52812	Hs.177403	ESTs	22.6
	401976				22.4
	410558	AW105231	Hs.192035	ESTs	22.4
35	416220	N49776	Hs.121773	ESTs	22.2
	424073	U03481	Hs.138959	gap junction protein, alpha 7, 45kD (con	22.0
	444575	AI264847	Hs.22545	Homo sapiens cDNA: FLJ12935 fls, clone NT	22.0
	444144	BE159397	Hs.7736	hypothetical protein	21.8
	438504	AW665281	Hs.224625	ESTs	21.2
40	438157	AA919737	Hs.20160	ESTs	20.8
	429006	AA443143	Hs.50529	Homo sapiens cDNA FLJ13842 fls, clone TH	20.5
	442006	AW675183	Hs.262663	ESTs	20.2
	409569	AW573153	Hs.256216	ESTs	19.8
45	421160	AL080215	Hs.102301	Homo sapiens mRNA: cDNA DKFZ5965J0323 (f	19.8
	404200				19.6
	446591	H44186	Hs.15456	PDZ domain containing 1	19.2
	420218	AW558037	Hs.22437	Homo sapiens cDNA: FLJ23366 fls, clone H	18.9
	408390	AA054222	Hs.40400	ESTs	18.8
50	444038	AW134500	Hs.135077	ESTs	18.8
	446443	AV559082	Hs.134228	ESTs	18.8
	442204	A1635450	Hs.21914	ESTs	18.4
	451177	A1667116	Hs.13034	ESTs	18.2
	453931	AL121278	Hs.25144	ESTs	18.1
55	437212	A1765221	Hs.210775	ESTs	18.1
	431806	AF106114	Hs.270737	tumor necrosis factor (ligand) superfam	18.0
	451659	BE379761	Hs.14248	ESTs, Weakly similar to ALUR_HUMAN ALU S	17.8
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	17.6
	441082	AJ0444804	Hs.202655	ESTs	17.6
60	446259	AA425204	Hs.42278	Homo sapiens cDNA FLJ13391 fls, clone PL	17.6
	423609	AA328348	Hs.218289	ESTs	17.4
	423901	AW628666	Hs.98440	ESTs	17.4
	446364	AB006624	Hs.14912	KIAA0286 protein	17.4
	419983	VC5565	Hs.54030	Homo sapiens mRNA: cDNA DKFZ596E1624 (f	17.0
65	424929	A1640761	Hs.224988	ESTs	17.0
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non recept	17.0
	449122	A631310	Hs.196955	ESTs	17.0
	409519	AA073368		gb:trfR10 r1 Straglene ovarian cancer	16.8
	410947	AK000306	Hs.67055	hypothetical protein FLJ20298	16.8
	418053	AA211493		gb:zn55d06.s1 Straglene muscle 937209 H	16.8
70	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	16.8
	443284	AW026678	Hs.28943	Homo sapiens cDNA FLJ13103 fls, clone NT	16.6
	421002	AF116030	Hs.100932	transcription factor 17	16.5
	419296	AA236115	Hs.120785	ESTs	16.2
75	421659	NM_014459	Hs.106511	proteocalthrin 17	16.0
	417589	T62075	Hs.13911	ESTs	16.0
	446057	AA323227	Hs.149358	ESTs	15.8
	434636	AA083764	Hs.241334	ESTs	15.6
	446797	A1682536	Hs.163495	Homo sapiens cDNA FLJ13608 fls, clone PL	15.6
	443718	AB083580	Hs.221373	ESTs	15.4
80	429748	AW070776	Hs.202661	ESTs	15.2
	443211	AJ128388	Hs.143655	ESTs	15.0
	428911	Z43846	Hs.194478	Homo sapiens mRNA: cDNA DKFZp43401572 (f	14.9
	444692	AW779922	Hs.145047	ESTs	14.8

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445436	A1224105	Hs.151408	ESTs	14.6
408684	R61377	Hs.12727	hypothetical protein FLJ21610	14.5
405943				14.4
406291				14.4
458679	AW975460	Hs.143653	ESTs	14.4
450152	A1138635	Hs.22968	ESTs	14.4
403899				14.2
454450	AW977778		gb:CM2-UM0041-250200-104-002 UM0041 Homo	14.2
451807	W52054	Hs.27099	DKFZP564J063 protein	14.0
429463	AY002919		gb:CM-BT039-101198-051 BT009 Homo sapien	13.8
447495	AW262580	Hs.147674	KIAA1621 protein	13.8
406598				13.6
430939	A1269471	Hs.187018	ESTs	13.4
443215	AW73463	Hs.18443	ESTs	13.4
408034	N26639	Hs.42102	Human EST clone 251800 mariner transpos	13.2
428508	BE252383	Hs.184668	SBB131 protein	13.2
447934	AW631440	Hs.165596	ESTs	13.2
406671	AA129547	Hs.265754	mel proto-oncogene (hepatocycle growth fa	13.1
438190	AW015531	Hs.122147	ESTs	13.0
415511	A1732617	Hs.182262	ESTs	12.9
426920	AA393351	Hs.132121	ESTs	12.8
447311	R37010	Hs.33417	Homo sapiens cDNA: FLJ2206 fs, clone K	12.5
423231	AB013885	Hs.126526	beta-ureidopropionase	12.5
403622				12.4
439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	12.4
422317	NM_001147	Hs.115181	angiotensin 2	12.2
428637	AW971298		gb:EST1201378 MAGE resequences, MAGE Homo	12.2
445717	AW664558	Hs.149332	ESTs	12.2
418413	R95735	Hs.117753	ESTs. Weakly similar to antigen of the m	12.1
405336				12.0
437100	A1761673	Hs.14535	Homo sapiens cDNA: FLJ22314 fs, clone H	12.0
428227	AA321640	Hs.2248	small inducible cytokine subfamily 8 (Cy	12.0
414923	AW445008	Hs.77637	homeo box A4	11.9
432099	AL137424		gb:Homo sapiens mRNA: cDNA DKFZp7161G2123	11.8
43326	A1379486	Hs.159430	ESTs	11.8
432955	AW676207		gb:RC1-DT0029-120100-011-01 DT0029 Homo	11.8
407510	U96191		gb:Human trophoblast hypoxia-regulated f	11.6
432321	AB040926	Hs.143552	KIAA1493 protein	11.6
415651	A107337	Hs.88977	hypothetical protein d511E16.2	11.6
443672	AA323362	Hs.9667	butyrobacillin (gamma), 2-oxoglutarate d	11.4
405600				11.4
418912	NM_000685	Hs.89472	angiotensin receptor 1	11.4
421306	AA806207	Hs.125880	ESTs	11.4
428721	X02158	Hs.2365	erythropoietin	11.4
410265	AJ228672	Hs.87491	ESTs	11.4
450006	A1241555	Hs.60171	ESTs	11.3
435420	A1928813	Hs.59203	ESTs	11.2
449802	AW901904	Hs.23384	hypothetical protein FLJ20147	11.2
424647	W67751	Hs.137308	ESTs	11.0
435758	A1242163	Hs.22670	chromodomain helicase DNA binding protei	11.0
404347				10.8
438664	A1911173	Hs.213722	ESTs	10.8
429125	AA448584	Hs.277004	ESTs	10.7
416590	R02818	Hs.14102	ESTs	10.6
429945	NM_006729	Hs.226483	daphnorus (Drosophila, homolog) 2	10.6
435085	AW130284	Hs.192752	ESTs. Moderately similar to NSD1 protein	10.6
442409	BE208951	Hs.125644	ESTs. Weakly similar to ORF_Y1L0276 [S.c	10.6
452644	AW501405	Hs.201215	ESTs	10.6
448298	AW137134	Hs.187203	ESTs	10.4
404115				10.2
406242				10.2
420757	X78592	Hs.29915	androgen receptor (5Hydroxysteroidene r	10.2
452588	AA881120	Hs.110637	homeo box A10	10.2
457233	A1355009	Hs.221698	ESTs	10.2
416185	AW975861	Hs.291395	ESTs	10.2
446152	A295208	Hs.150208	ESTs	10.1
446258	AF187813	Hs.14637	kidney- and liver-specific gene	10.1
423637	AL137279	Hs.130187	Homo sapiens mRNA: cDNA DKFZp434O1214 (f	10.0
442405	BE465247	Hs.129530	ESTs	9.9
415213	AW746146		gb:PM0-BT034-170100-004-e03 BT0340 Homo	9.8
428440	A9193836	Hs.294008	ESTs	9.8
423305	AA324656	Hs.267590	ESTs	9.8
446929	A1658841	Hs.161354	ESTs	9.8
423811	AW295998	Hs.58095	homeo box C4	9.8
433527	AW235613	Hs.133000	ESTs	9.6
420975	A1167145	Hs.165538	ESTs	9.6
439979	AW0200291	Hs.6823	hypothetical protein FLJ10430	9.5
437303	AA210863	Hs.3532	nemo-like kinase	9.2
417404	NAL_007350	Hs.82101	pleckstrin homology like domain, family	9.2
451621	A175148	Hs.26770	fatty acid binding protein 7, brain	9.2
406952	S82472		gb:Beta-pcd-DNA polymerase beta (exon a	9.2
419699	AA248958	Hs.31246	ESTs	9.2
443740	R56434	Hs.21062	ESTs	9.2

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5	427228	AW537826	Hs.103262	ESTs	8.2
	436961	AW375974	Hs.156704	ESTs	9.2
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	9.1
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	9.1
	424115	AA335497	Hs.253965	ESTs	9.0
10	402045				9.0
	434326	H69125	Hs.133525	ESTs	9.0
	425493	AW363582	Hs.75323	prohibitin	9.0
	447041	BE619186	gb:601472933F1 NIH_MGC_58	Homo sapiens c	8.8
	402395				8.8
15	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	8.8
	423126	AA322245	Hs.290165	ESTs	8.8
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phospholipase	8.7
	456375	AA209647	Hs.8850	a disintegrin and metalloproteinase domain	8.6
	443647	AV553846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	8.6
20	401439				8.6
	449532	W74653	Hs.271593	ESTs	8.5
	452197	A1916269	Hs.109507	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.5
	448450	BE512490	gb:601451854F1 NIH_MGC_66	Homo sapiens c	8.5
	426176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN T	8.4
25	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	8.4
	402621				8.4
	428133	AW167727	Hs.11873	ESTs	8.4
	419503	AA243642	Hs.137422	ESTs	8.4
	452644	AW452616	Hs.212481	ESTs	8.4
30	452259	AA311439	Hs.28707	signal sequence receptor, gamma (translo	8.4
	409895	AA289661	gb:EST112514 Adrenal gland tumor Homo sa		8.3
	418076	R61388	Hs.6724	ESTs	8.3
	402696				8.3
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	8.3
35	413998	AW103607	Hs.243933	ESTs	8.2
	410008	AA079552	gb:dmH12.s1 Stratagene pancreas (93720		8.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564.f1, clone C	8.2
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	8.1
	435496	AW640711	Hs.265398	ESTs, Weakly similar to transmembran	8.0
40	413627	BE182082	Hs.246973	ESTs	8.0
	415713	AW968573	gb:EST380649 MAGE resequences, MAGEJ Homo		8.0
	426695	AW118191	Hs.112729	ESTs	8.0
	452284	AW451426	Hs.252740	ESTs	8.0
	454833	BE141714	gb:QV04HT0101-061099-032-c04 HT0101 Homo		8.0
45	452629	HI15302	Hs.168590	Homo sapiens mRNA; cDNA DKF Zp565A1046 (f	8.0
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	8.0
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	7.9
	454740	T78281	Hs.13226	Homo sapiens clone 25181 mRNA sequence	7.9
	433190	M26051	Hs.3210	min	7.8
50	432777	AA564991	Hs.263477	ESTs	7.8
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.7
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	7.7
	434032	AWX09861	Hs.206692	ESTs	7.7
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236.f1, clone NT	7.6
55	439024	R96966	Hs.35598	ESTs	7.6
	437205	AL110232	gb:Homo sapiens mRNA; cDNA DKF Zp564D0071		7.4
	446030	AF131605	Hs.13544	Homo sapiens clone 24550 mRNA sequence	7.4
	446311	AW007284	Hs.148795	ESTs, Weakly similar to ALUT1_HUMAN ALU S	7.4
	452883	X80331	Hs.150318	ESTs	7.4
60	448253	H25899	Hs.201591	ESTs	7.4
	406030				7.4
	437094	A911516	Hs.127811	ESTs	7.3
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	7.3
	432143	AL040183	Hs.123454	ESTs, Weakly similar to The KIAA0149 gen	7.3
65	409894	AW076118	gb:zmlB06.s1 Stratagene pancreas (93720		7.2
	425151	AA351814	Hs.238678	ESTs	7.2
	448582	AK039880	Hs.94812	ESTs	7.2
	455068	AB07894	Hs.27910	centrosomal protein 2	7.2
	406504				7.2
70	426395	AA477992	Hs.104885	ESTs, Weakly similar to zinc finger prot	7.2
	421102	AW010353	Hs.89217	ESTs	7.2
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKF Zp564N1116 (f	7.1
	410534	AW905138	gb:QV0-NH1071-280406-207-g07 NN1071 Homo		7.1
	415084	M19367	Hs.77899	tropomyosin 1 (alpha)	7.0
75	410274	AA381837	Hs.517672	hypoosmotic-inducible protein 2	7.0
	438416	W56294	Hs.56254	ESTs	6.9
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKF Zp5861823 (f	6.8
	423349	AF010258	Hs.127428	homeo box A9	6.8
	413070	AA126776	gb:zr08c.11.s1 Stratagene lung carcinoma		6.8
80	449261	AW070780	Hs.201918	ESTs	6.8
	459309	AA040520	Hs.109144	ESTs	6.8
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.8
	415462	W52845	gb:zh0005.r1 Soares fetal_liver_spleen_		6.8
	447835	AW951623	Hs.164129	ESTs	6.7
	435663				6.6
	427897	NM_017413	Hs.181060	apelin, peptide ligand for APJ receptor	6.6
	422063	BE156476	gb:QV0-HT0368-040100-082-c05 HT0368 Homo		6.6

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5	455275	AW577806	gb:EST359810 MAGE sequences, MAGE Homo	6.6
	441350	AB020630	Hs.17782 paraneoplastic antigen MA2	6.6
	445575	Z25368	Hs.172004 tln	6.6
	446075	AW451457	Hs.279179 ESTs	6.6
	405963			6.6
10	423045	X53073	Hs.188023 ESTs	6.6
	438456	AW252677	Hs.65099 ESTs	6.5
	420273	AB628664	Hs.197257 ESTs	6.5
	420831	AA260824	Hs.190035 ESTs	6.4
	423739	AA398155	Hs.97909 ESTs	6.4
15	441559	AA938448	Hs.259733 ESTs	6.4
	433999	AA778212	Hs.191869 ESTs	6.4
	439703	AF066538	Hs.198245 ESTs	6.4
	433757	AW498974	Hs.152970 ESTs	6.3
	422095	AB688872	Hs.285956 ceruloplasmin (ferroxidase)	6.3
20	415138	C18356	Hs.78045 tissue factor pathway inhibitor 2	6.3
	448515	H68441	Hs.13528 Homo sapiens cDNA FLJ14054 f5, clone HE	6.3
	443595	AF169312	Hs.9613 PPA(Rgamma) angiopoietin related protein	6.3
	429357	AA779725	Hs.164589 ESTs	6.3
	404939			6.3
25	417071	N58620	Hs.275133 ESTs	6.2
	436209	AW950417	Hs.254020 ESTs, Moderately similar to unnamed prot	6.2
	423111			6.2
	446796	AA147829	Hs.33193 ESTs, Highly similar to AC007228.3 BC372	6.2
	442353	BE379594	Hs.49136 ESTs	6.2
30	451110	AB955040	Hs.301584 ESTs	6.1
	420092	AA814043	Hs.88045 ESTs	6.1
	441801	AW242799	Hs.211874 ESTs	6.0
	407500	U43279	Hs.205225 gb:human nucleoporin nup 36 mRNA, comple	6.0
	450864	R64139	Hs.205225 ESTs	6.0
35	455711	BE095465	gb:RC2-BT0388-230100-012-e11 BT0388 Homo	6.0
	405394			6.0
	436476	AA326108	Hs.53631 ESTs, Weakly similar to enhancer-of-split	6.0
	454392	BE260893	gb:01150677F1 NIH_MGC_19 Homo sapiens c	6.0
	414675	H11257	Hs.295233 ESTs	5.9
40	436767	W73955	Hs.117874 ESTs	5.9
	445495	BE622641	Hs.38489 ESTs	5.9
	428372	AK000684	Hs.183887 hypothetical protein FLJ22104	5.9
	436464	A016176	Hs.269703 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.9
	415910	U23350	Hs.78913 chemokine (C-X3-C) receptor 1	5.8
45	402421			5.8
	417038	T85290	gb:yt330C2.1 Soares fetal liver spleen	5.8
	436461	AW511956	Hs.293261 ESTs	5.8
	440870	AB687284	Hs.150539 Homo sapiens cDNA FLJ13793 f5, clone TH	5.8
	452281	T35590	Hs.28792 Homo sapiens cDNA FLJ11041 f5, clone PL	5.7
50	417280	AW173116	Hs.262206 ESTs	5.7
	437259	AW377555	Hs.120695 ESTs	5.7
	425717	X07282	Hs.171495 retinoic acid receptor, beta	5.7
	443614	AW555386	Hs.7645 fibrinogen, B beta polypeptide	5.7
	450625	AW970107	gb:EST382188 MAGE sequences, MAGE Homo	5.6
55	425305	AA363025	Hs.155572 Human clone 23801 mRNA sequence	5.6
	430371	DE7466	Hs.240112 KIAA0276 protein	5.6
	430459	AW965408	Hs.231951 ESTs	5.6
	427920	Z11502	Hs.181107 annexin A13	5.6
	449318	AW236021	Hs.108788 ESTs, Weakly similar to zeste [D.melanog	5.5
60	407864	AF069291	Hs.40530 chromosome 8 open reading frame 1	5.5
	410754	T63840	gb:yc16b10.1 Sratogene long (537210) H	5.5
	415286	AW240540	Hs.72548 ESTs	5.5
	443297	AW409664	Hs.1331029 ESTs	5.5
	440138	AB033023	Hs.65882 hypothetical protein FLJ10201	5.5
65	441006	AW950587	Hs.76277 C9orf60 protein	5.4
	403348	A0401535	Hs.146030 ESTs	5.4
	446679	AB023951	Hs.296668 Homo sapiens cDNA FLJ11846 f5, clone HE	5.4
	408938	AA059013	Hs.27607 ESTs	5.4
	456411	AA603305	gb:np12d11.1 NCL_CGAP_P3 Homo sapiens	5.4
70	443756	AW095799	Hs.153665 ESTs	5.4
	427232	C03945	Hs.113374 transcription factor EC	5.4
	424574	BE408618	Hs.150748 malonyl-CoA decarboxylase	5.3
	424834	AK001432	Hs.153408 Homo sapiens cDNA FLJ10570 f5, clone NT	5.3
	440589	BE397763	Hs.194478 Homo sapiens mRNA; cDNA DKF Zp43401572 f	5.3
75	425782	U56468	Hs.159525 cell growth regulatory with EF-hand domai	5.3
	450236	AW162998	Hs.24684 KIAA1376 protein	5.3
	418110	R43523	Hs.217754 Homo sapiens cDNA: FLJ22202 f5, clone H	5.3
	427061	AB032971	Hs.173392 KIAA1145 protein	5.2
	413841	K34276	Hs.75576 plasminogen	5.2
80	432258	A052491	Hs.172630 ESTs	5.2
	416805	F13271	Hs.79981 Human clone 23560 mRNA sequence	5.2
	438475	W03856	Hs.13188 ESTs, Highly similar to Gene product wit	5.2
	413305	A052693	Hs.133318 ESTs	5.1
	413303	H68153	Hs.75616 RAS11A, member RAS oncogene family	5.1
	451859	H44491	Hs.252938 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	429826	N83266	Hs.40747 ESTs	5.1
	436032	AA150797	Hs.109276 latexin protein	5.1

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	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, subunit A1	5.1
	436297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	5.1
	421126	M74587	Hs.102122	insulin-like growth factor binding protein 2	5.1
5	440238	AW451970	Hs.159644	paired box gene 2	5.1
	426851	AJ076846	Hs.171653	nuclear receptor subfamily 1, group H, member 1	5.0
	425813	AA364136	Hs.210553	ESTs, Weakly similar to hypothetical protein	5.0
	432328	AIS72739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bisphosphate	5.0
	430682	AW971949	Hs.291252	ESTs	5.0
10	410493	AW779475	gb:RC2-DT0076-110100-031-410 DT0076 Homo sapiens	5.0	
	425222	AW576932	Hs.99164	ESTs	5.0
	446317	AJ287367	Hs.150906	ESTs	5.0
	493506	NM_006153	Hs.54569	NCK adaptor protein 1	5.0
	407768	AW002841	Hs.29475	ESTs	5.0
15	437636	AJ550087	gbrw:CC682x1 NCL_CGAP_Kd12 Homo sapiens	5.0	
	430403	AF135390	Hs.241382	tumor necrosis factor (ligand) superfamily 1, subunit 2	4.9
	426215	AW963419	Hs.155223	stanniocalcin 2	4.9
	448570	AI923944	Hs.30913	ESTs	4.9
	445034	AW253076	Hs.160323	ESTs	4.9
20	410361	BE391804	Hs.67661	guanylate binding protein 1, interferon- γ inducible	4.8
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDNA	4.8
	438492	AW340048	Hs.293188	ESTs	4.8
	446417	AJ299505	gbrq1412x1 NCL_CGAP_Lu2 Homo sapiens	4.8	
	405676	BE541386	gb:hs:352x1 NCL_CGAP_Lu21 Homo sapiens	4.8	
	417269	NM_004851	Hs.17958	coelenterate (3'-phosphoadenylyl) sulfate lyase	4.8
	413795	AL040178	Hs.142003	ESTs	4.8
25	422857	AF016272	Hs.115418	cadherin 16, KSP-cadherin	4.8
	452208	AA024752	Hs.31895	ESTs, Weakly similar to B9 [H.sapiens]	4.7
	427111	DE5641	Hs.21739	Homo sapiens mRNA: cDNA DKFp568151a (f100000)	4.7
	441392	AW451831	Hs.222119	ESTs, Weakly similar to K1C02_HUMAN KERATIN 1	4.7
30	438221	AA737106	Hs.32250	ESTs	4.7
	431956	AA002032	Hs.77245	Homo sapiens cDNA FLJ11170 fs, clone PL11170	4.7
	417355	D13166	Hs.82022	endothelin receptor type B	4.7
	414700	H63202	Hs.38163	ESTs	4.7
35	402739				4.6
	403170				4.6
	443456	NM_003428	Hs.9450	zinc finger protein 34 (HPF2)	4.6
	404880	AF120350	Hs.44532	disulfotulin	4.6
	427899	AA825266	Hs.181062	serum amyloid A1	4.5
40	446302	A285848	Hs.149757	ESTs	4.5
	414812	XZ7255	Hs.17367	monokine induced by gamma interferon	4.4
	424063	NM_002019	Hs.138671	iris-related tyrosine kinase 1 (vascular endothelial growth factor receptor 1)	4.4
	413384	NM_000401	Hs.75334	exotoxins (multiple) 2	4.4
	471298	AW172431	Hs.13012	ESTs	4.4
45	420789	AA670057	Hs.198882	ESTs	4.4
	453558	AA117023	Hs.46478	ESTs	4.4
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	4.4
	451762	AF222980	Hs.26985	disrupted in schizophrenia 1	4.4
	410334	AW979261	Hs.291993	ESTs	4.4
50	457030	A301740	Hs.173381	dihydropyrimidinase-like 2	4.4
	427194	AB944133	Hs.290922	ESTs, Weakly similar to dJ88JB.1 [H.sapiens]	4.3
	410467	X66639	Hs.63287	carbonic anhydrase IX	4.3
	401157				4.3
	432004	BE018302	Hs.2894	placental growth factor, vascular endothelial growth factor	4.3
55	426966	UC2230	Hs.172816	neuregulin 1	4.3
	446115	AJ733075	Hs.252682	ESTs, Weakly similar to S69913 hypertensin	4.3
	424704	AJ263293	Hs.152096	cytochrome P450, subfamily III (arachidonate 15-hydroxylase)	4.2
	446619	AJ076543	Hs.313	secreted phosphoprotein 1 (osteopontin, alpha2)	4.2
	433578	BE336896	Hs.3416	adipose differentiation related protein 1	4.2
60	407065	Y10141	gb:1.sapiens DAT1 gene, partial, VNTR, 384bp	4.2	
	407182	AA312551	Hs.230157	ESTs	4.2
	416565	AW000960	Hs.44970	ESTs	4.2
	442230	BE219088	Hs.279547	ESTs	4.2
	446880	AA533008		gb:cd450R.s1 NCL_CGAP_Lu2 Homo sapiens	4.2
	413802	AW964490	Hs.32241	ESTs	4.2
65	438370	AA843242	Hs.48523	ESTs	4.2
	423231	R31178	Hs.287820	fibronectin 1	4.2
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	4.2
	441484	AA533481	Hs.58972	ESTs	4.2
	411213	AA676939	Hs.65285	neuropilin 1	4.2
70	463005	AW418979	Hs.224502	ESTs	4.2
	407999	AJ126271	Hs.49433	ESTs, Weakly similar to HYPOTHETICAL PRO	4.2
	409770	AW499536	gb:UAF-ER0(p-jc-12-0-UL)1 NH_MGC_5		4.1
	449856	AA203155	Hs.18200	ESTs	4.1
	430806	S69377	Hs.247978	T-cell acute lymphocytic leukemia 2	4.1
	412872	BE063431	gb:RC2-BN0127-240300-011-B05 BN0127 Homo sapiens	4.1	
	430719	AA488988	Hs.293795	ESTs	4.1
	409537	AA323848	Hs.55407	Homo sapiens mRNA: cDNA DKFp434K0621 (f100000)	4.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	4.1
80	446470	H58373	Hs.317494	ESTs	4.1
	440892	AJ008821	Hs.270209	ESTs	4.1
	408830	AK001709	Hs.48403	hypothetical protein FLJ110847	4.1
	419088	AIS38323	Hs.77496	small nuclear ribonucleoprotein polypeptide B	4.1
	416655	AW968613	Hs.79428	BC12/adenovirus E1B 19kD-interacting protein	4.1

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	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sporn re	4.1
	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKF7p56612424 (f	4.1
	455955	AL040421		gb:DKFZp43480714_r1.434 (synonym: htes3)	4.1
5	438859	AI559626	Hs.154973	ESTs, Weakly similar to AF231024.1 probe	4.0
	432279	AW595661	Hs.292943	ESTs	4.0
	441592	AW137071	Hs.127211	ESTs	4.0
	411835	AW301879		gb:U0011021-280400-212-110 NN1021 Homo	4.0
	426384	AI427078		gb:U0011021-280400-212-110 NN1021 Homo	4.0
10	417494	AL133990	Hs.792	ADP-ribosylation factor domain protein 1	4.0
	413583	AL120806	Hs.5888	ESTs	4.0
	415610	L44319		gb:HUMEST11010 Human thymus NSTH11 Homo	4.0
	430009	AA894054	Hs.22242	ESTs	4.0
	448539	W80363	Hs.58446	ESTs	4.0
	438929	AW195515	Hs.233177	ESTs	4.0
15	415000	R82342	Hs.79856	ESTs	4.0
	429516	AI982722	Hs.120845	ESTs	4.0
	459471	AV648003	Hs.194240	ESTs	4.0
	433155	BE21878	Hs.32352	hypothetical protein DKFZp434K1210	4.0
	450445	AA910339	Hs.26216	Homo sapiens cDNA: FLJ22811 fts, clone K	3.9
20	438177	BE327015	Hs.281391	ESTs	3.9
	422438	AA445925	Hs.270895	ESTs	3.9
	450332	AA397658	Hs.60257	Homo sapiens cDNA: FLJ13598 fts, clone PL	3.9
	448511	AI970394	Hs.191075	ESTs	3.9
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	3.9
25	452881	AW135220	Hs.241521	ESTs	3.9
	414729	BE469528	Hs.281901	ESTs	3.9
	428815	AA004585	Hs.19352	ATP-binding cassette, sub-family C (CFTR	3.9
	425908				3.8
30	445452	H52975	Hs.246046	ESTs, Weakly similar to RET1_HUMAN RETIN	3.8
	447961	W32791	Hs.170405	ESTs	3.8
	446539	AB15828	Hs.132501	ESTs	3.8
	401189				3.8
	429548	AW138972	Hs.135288	ESTs	3.8
35	431523	N55759	Hs.153674	ESTs	3.8
	430014	H55354	Hs.182465	actinin, alpha 4	3.8
	427580	H56655	Hs.195308	tryptophan rich basic protein	3.8
	451988	AF263928	Hs.27410	papillomavirus regulatory factor PRF-1	3.8
	437539	AW298000	Hs.141840	ESTs, Weakly similar to S5501 interfero	3.8
40	427510	Z47542	Hs.175312	small nuclear RNA activating complex, po	3.8
	433522	AB211700	Hs.116528	ESTs	3.8
	443843	AV878864	Hs.13528	Homo sapiens cDNA: FLJ14054 fts, clone HE	3.7
	407305	AA715284		gb:U0011021-280400-212-110 NN1021 Homo	3.7
	434613	AI821826	Hs.187786	ESTs, Moderately similar to ALUB_HUMAN I	3.7
	410275	AI554545	Hs.58301	ESTs	3.7
45	422504	AA311407		gb:EST182167 Jurkat T-cells V Homo sapie	3.7
	421013	M62397	Hs.1345	mutated in colorectal cancers	3.7
	437949	U78519	Hs.41854	ESTs	3.7
	431840	AA345058	Hs.2890	POU domain, class 5, transcription facto	3.7
50	429446	AI511773	Hs.67949	ESTs	3.7
	415253	AA948033	Hs.130853	ESTs	3.7
	450205	AI795450	Hs.201500	ESTs	3.7
	439444	AG778652	Hs.54578	ESTs	3.7
	437828	AW975806	Hs.291805	ESTs	3.7
55	453238	AA033991	Hs.293234	ESTs	3.7
	429041	AE005142	Hs.94592	lmo4	3.7
	448458	AW614367	Hs.171054	ESTs	3.7
	435080	AB311760	Hs.155111	ESTs	3.7
	444249	TF3296	Hs.205810	ESTs	3.7
	426595	AW971980	Hs.62402	p21Cdc42Rac1-activated kinase 1 (yeast	3.7
60	417715	AW965687	Hs.86366	ESTs	3.7
	432579	AF043244	Hs.279439	nucleolar protein 3 (apoptosis repressor	3.6
	440046	AA971461	Hs.153469	ESTs, Weakly similar to envelope protein	3.6
	430091	AB032958	Hs.233023	KIAA1132 protein	3.6
	438030	X98427	Hs.122534	ESTs	3.6
65	453496	AA442103	Hs.133084	solute carrier family 2 (facilitated glu	3.6
	446936	AC022663	Hs.151767	oligon (no-interfering, gamma) interferon	3.6
	417860	AW408557	Hs.235498	Homo sapiens cDNA: FLJ14075 fts, clone HE	3.6
	435794	H22108	Hs.13704	ESTs	3.6
	449955	AA164569	Hs.34550	ESTs	3.6
70	411485	AW648125		gb:U0011021-280400-212-110 NN1021 Homo	3.6
	425274	D38122	Hs.2007	lmo4	3.6
	458201	AB959551	Hs.233477	ESTs, Moderately similar to A Chain A, S	3.6
	440987	AA911705	Hs.130229	ESTs	3.6
	425178	H16997	Hs.161027	ESTs	3.6
75	413300	AA150835	Hs.18578	hypothetical protein FLJ21620	3.6
	436091	AA704705	Hs.181044	ESTs, Weakly similar to A Chain A, Human	3.6
	452671	AW961074	Hs.225833	ESTs	3.6
	437222	AL117588	Hs.299963	ESTs	3.6
	437889	AL137723	Hs.5835	Homo sapiens mRNA; cDNA: DKFZp434C08818 (f	3.5
80	4115445	AW505818		gb:U0011021-280400-212-110 NN1021 Homo	3.5
	417499	AI752416	Hs.77326	insulin-like growth factor binding prote	3.5
	439882	AA847856	Hs.124565	ESTs	3.5
	419229	AB27237	Hs.282884	ESTs	3.5

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5	431889	AA521277	Hs 124946	ESTs	3.5
	422660	AW297582	Hs 237062	ESTs	3.5
	415122	D6G708	Hs 22245	ESTs	3.5
	444127	N63620	Hs 13281	ESTs	3.5
	416913	AW534714	gb:R1C1-DT0001-031299-011-a11 DT0001 Homo	3.5	
10	490944	A1T29596	Hs 33033	ESTs	3.5
	453365	AA035211	Hs 17404	ESTs	3.5
	452355	NA54926	Hs 29202	G protein-coupled receptor 34	3.5
	422246	AL119114	Hs 23187	ESTs	3.5
	434131	A655275	Hs 143659	ESTs	3.5
15	425304	AA463844	Hs 31339	fibroblast growth factor 11	3.4
	453775	NM_002916	Hs 35120	replication factor C (activator 1) 4 (37	3.4
	428559	AB001514	Hs 170414	parval basic amino acid cleaving system	3.4
	456311	AA226532	Hs 190016	He 190016	3.4
	420737	L08096	Hs 99999	tumor necrosis factor (ligand) superfamily	3.4
20	448733	NM_005629	Hs 187958	solute carrier family 6 (neurotransmitter	3.4
	401811				3.4
	404021				3.4
	447175	A1365208	Hs 293606	ESTs	3.4
	453743	AL120480		gb:DKFZp761K098_r1 761 (synonym: hamy2)	3.4
25	455070	AW564675	gb:MR1-CT0258-290300-206-a01 CT0258 Homo	3.4	
	419546	AA244199	gb:nc95c95.11 NQ_CGAP_P11 Homo sapiens	3.4	
	449441	A6556940	Hs 196532	ESTs	3.4
	441606	R37263	Hs 21065	ESTs	3.4
	446594	A1311917	Hs 16292	ESTs	3.4
30	428464	A1432572	Hs 184221	ESTs	3.4
	413719	BE439560	Hs 75468	small inducible cytokine subfamily A (Cy	3.4
	427914	AA417350	Hs 20575	ESTs	3.4
	438257	AW474419	Hs 224794	ESTs	3.4
	412642	BE244598	Hs 809	hepatocyte growth factor (hepatoprotein A;	3.4
35	454690	AW546326	gb:MR1-CT0258-140100-203-a10 CT0258 Homo	3.3	
	428046	AW812795	Hs 155381	ESTs, Moderately similar to 130202 hypot	3.3
	407331	A1570416	Hs 99910	phosphofructokinase, platelet	3.3
	440472	AA886169	Hs 169071	ESTs	3.3
	421893	NM_001078	Hs 109225	vascular cell adhesion molecule 1	3.3
40	407397				3.3
	417924	AU077231	Hs 82632	cyclin D1 (PRAD1): parathyroid adenomas	3.3
	410623	AW569302	Hs 253833	ESTs	3.3
	446338	H73444	Hs 394	adrenomedullin	3.3
	441024	AW091530	Hs 137088	ESTs	3.3
45	405257				3.3
	450386	AU077002	Hs 24950	regulator of G-protein signalling 5	3.3
	416992	L24498	Hs 80409	growth arrest and DNA-damage-inducible	3.3
	444471	AB020684	Hs 11217	GAA/G377 protein	3.3
	431899	AA305688	Hs 267895	UDP-Galactose/GlcNAc beta 1,3-galactosyltr	3.3
50	452053	AA447453	Hs 27860	Homo sapiens mRNA; cDNA DKFZp586M0723 f	3.3
	425236	AW067800	Hs 155223	stanniocalcin 2	3.3
	428924	W23824	Hs 173059	ESTs	3.3
	450101	A1644989	Hs 24365	Human hbc547 mRNA sequence	3.2
	425260	L47726	Hs 1870	phenylalanine hydroxylase	3.2
55	443630	A124095	Hs 143273	ESTs	3.2
	415245	N59650	Hs 27252	ESTs	3.2
	405953				3.2
	430812	L10405	Hs 247992	DNA binding protein for surfactant prote	3.2
	418946	A1798841	Hs 132103	ESTs	3.2
60	424750	D09936	Hs 152818	ubiquitin specific protease 8	3.2
	453542	AW979168	Hs 163976	ESTs	3.2
	455860	AW972657	Hs 212739	ESTs	3.2
	430172	AA468591	Hs 181889	ESTs	3.2
	431842	NM_005764	Hs 271473	epithelial protein up-regulated in canci	3.2
65	415121	A6454701	Hs 210589	ESTs	3.2
	435211	AW001581	Hs 80961	polymerase (DNA directed), gamma	3.2
	433727	C16221	Hs 112608	ESTs	3.2
	424897	D63216	Hs 153534	hizzled-related protein	3.2
	414821	M63835	Hs 77424	Fc fragment of IgG, high affinity Ia, re	3.1
70	419830	BE207573	Hs 83321	neurotrophin B	3.1
	417919	A050203	Hs 86379	ESTs	3.1
	430437	A1768801	Hs 169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.1
	409663	A1743750	Hs 65862	ESTs	3.1
	454024	AA953527	Hs 16281	hypothetical protein FLJ23403	3.1
75	424890	L42172	Hs 164078	lipopolysaccharide-binding protein	3.1
	421633	AF121880	Hs 106260	sorting nexin 10	3.1
	436002	R68529	Hs 120967	ESTs	3.1
	437682	AA476652	Hs 94952	Homo sapiens cDNA, FLJ23371 fis, clone H	3.1
	439451	A1086270	Hs 278554	heterochromatin-like protein 1	3.1
80	430183	BE011038	gb:PMG-BN0176-100400-001-g04 BN0176 Homo	3.1	
	428479	Y00272	Hs 184572	cell division cycle 2, G1 to S and G2 to	3.1
	441285	NM_002374	Hs 167	microtubule-associated protein 2	3.1
	456386	W28491		gb:47a1 Human retina cDNA randomly prime	3.1
	451130	A782250	Hs 211347	ESTs	3.1
85	439702	AW065525	Hs 134182	ESTs	3.1
	453331	A1240665	Hs 8895	ESTs	3.1
	428841	AA419430	Hs 104935	ESTs	3.1

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5	448896	A1610700	Hs.103280	ESTs	3.1
	436009	H57130	Hs.120925	ESTs	3.1
	448866	AW372514	Hs.287462	Homo sapiens cDNA FLJ11875 fs, clone HE	3.1
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	418526	BE019020	Hs.85638	solute carrier family 16 (noncarboxylic	3.1
10	401260				3.1
	450705	U50304	Hs.25351	iroquois-class homeodomain protein	3.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ215974 fs, clone H	3.1
	424415	NM_001975	Hs.146580	oncosis 2, (gamma, neuronal)	3.0
	402346				3.0
15	446319	AW207590	Hs.160711	ESTs	3.0
	437927	AF113013	Hs.278919	PROX086 protein	3.0
	407921	A1378617	Hs.23100	Homo sapiens cDNA FLJ12592 fs, clone NT	3.0
	414618	A0204000	Hs.965978	ESTs	3.0
	434398	AA121098	Hs.38338	serum-inducible kinase	3.0
20	440113	A0916332	Hs.188272	ESTs	3.0
	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	428945	AW152803	Hs.90574	ESTs	3.0
	428297	RS4033	Hs.21245	ESTs	3.0
	424405	A076838	Hs.12967	ESTs	3.0
25	411290	AW835544		gb:U44-LT0016-271299-068-03 LT0016 Homo	3.0
	450608	BE464396	Hs.118468	ESTs	3.0
	450965	A373532	Hs.159710	ESTs	3.0
	437653	A1754443	Hs.185851	ESTs	3.0
	429418	A081028	Hs.95283	ESTs	3.0
30	406117				3.0
	415452	R41674	Hs.16491	ESTs	3.0
	419454	AW664873	Hs.87835	Homo sapiens PAC clone RPS-1087M15 from	3.0
	453688	AK381270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C0814 (f	3.0
	408119	W65213		gb:Z2d1.0 Human retina cDNA randomly prim	3.0
35	438338	AL035992	Hs.210278	ESTs	3.0
	412372	RS5998	Hs.118615	ESTs	3.0
	431564	AL080239	Hs.272234	Human DNA sequence from clone GS1250C22	3.0
	403782				3.0
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fs, clone NT	3.0
40	453388	W26557		gb:58d1 Human retina cDNA randomly prime	3.0
	447522	Z2921.0	Hs.20015	hemochromatosis	3.0
	428857	AF008192	Hs.194283	putative GR6 protein	3.0
	406991	S82185		(NONE)	3.0
	423596	AJ224741	Hs.278461	maltrin 3	3.0
45	453502	AW085781	Hs.26270	Homo sapiens cDNA FLJ11588 fs, clone HE	3.0
	414132	AW801235	Hs.48480	ESTs	3.0
	409122	W07089	Hs.297873	ESTs	3.0
	405547				3.0
	422219	AW978073		gb:EST390182 MAGE resequences, MAGO Homo	3.0
50	417227	TS7776	Hs.151094	ESTs	3.0
	448592	N65546	Hs.141706	ESTs	3.0
	421477	A1904743	Hs.104650	hypothetical protein FLJ10252	3.0
	400368	BE779278	Hs.69149	proline-sucrose isomerase phosphatase m	3.0
	453562	AW030255		gb:QV3-NH1024-100500-181-s02 NH1024 Homo	3.0
55	443378	RS7911	Hs.134106	ESTs	3.0
	419348	AA236845	Hs.98274	ESTs	3.0
	439138	AJ742605	Hs.153696	ESTs	3.0
	449547	H53943	Hs.117963	ESTs	3.0
	455180	AW863503		gb:MR3-SN0009-180400-110-c12 SN0009 Homo	3.0
60	444228	AV648612	Hs.282396	ESTs	3.0
	423496	U51963	Hs.129700	tollold-like 1	3.0
	401707				3.0
	419276	BE165009	Hs.134682	Homo sapiens cDNA: FLJ23161 fs, clone L	3.0
	441677	AW271702	Hs.53739	ESTs	3.0
65	459587	AA031956		gb:zkl5e04.s1 Soares_pregnant_uterus_NBH	3.0
	431311	AA502552	Hs.188980	ESTs	3.0
	403206	BE162953	Hs.250528	ESTs, Weakly similar to unnamed protein	3.0
	412685	BE092186		gb:IL2-BT0734-200400-075-H05 BT0734 Homo	3.0
	414752	BE503505	Hs.248689	ESTs	3.0
70	403144				3.0
	407535	X91103		gb:H sapiens mRNA for Hx44 protein.	3.0
	412395	AW547581		gb:RCD-MT0004.140300-331-008 MT0004 Homo	3.0
	407637	AW257944	Hs.242811	ESTs	3.0
	456676	A681882	Hs.270428	ESTs	3.0
75	417066	AA329572	Hs.172004	uim	3.0
	406007				3.0
	416940	N75620	Hs.43157	ESTs	3.0
	433322	H50621	Hs.134156	ESTs	3.0
	406088				3.0
80	416573	R10356	Hs.18865	ESTs, Weakly similar to AC007228.2 BC372	3.0
	423130	AW897586	Hs.21213	ESTs	3.0
	412721	AW183165	Hs.95600	ESTs	3.0
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25KD	3.0
	422692	AF016833	Hs.122785	multisite-glucosylase (alpha-glucosidase)	3.0
	406506				3.0
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	3.0
	422650	D42055	Hs.1565	neural precursor cell expressed, develop	3.0

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400325	M5292	Hs 247924	Homo sapiens endogenous HIV-1 related se	3.0
441078				3.0
449645	A1336596	Hs 156254	ESTs	3.0
446704	A1337228	Hs 197083	ESTs	3.0
427072	H38046		gbyv58c10.r1 Scores fetal liver spleen	3.0

TABLE 33B:

Pkey:	Unique Eos preblast identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Pkey	CAT number	Accession
406715	1005404_1	AW753085 AW753082 AW054744 AW753107 AW753087
408119	100172_1	W56213 HB0655 Z44031 AW054559 R17434
409519	113922_1	AW053589 AA075369
409578	1140976_1	BE041336 AW419449 AW663635
409594	114249_1	AA076118 AA975618 AA076220
409695	114876_1	AA236561 AA076989 AA077628 AA077497
409745	115237_1	AA077091 A1347616 A1341433 A088754 AW0297401 AW960912 AA021874 AA286633 AA150722 BE152363 AW158822 BE152450
409770	1154046_1	AW499536 AW499553 AW052138 AW499537 AW502136 AW501743
410008	116812_1	AA079552 BE142525 BE142527
410049	1172307_1	AW575475 AW573654 AW573655
410534	1207247_1	AW995138 AW753008 R13818 Z43519
410754	1219733_1	TS5840 AW801589 AW801588
411290	1237736_1	AW835440 AW835613 AW835697 AW835703 BE029536 BE029199 114185 1247181_1AW848125 AW848124 AW848203 AW848695
411545	1249130_1	AW848633 AW848693 BE350771
411836	1260610_1	AW852818 AW858363 AW851100
412209	1283610_1	AW901679 AW901875 AW865247 BE011294 BE504813
412359	129085_1	AW901456 AW901450 AW901441
412379	1292475_1	AW837985 AW837938 AA101935 AW837913 AW837935
412685	1321663_1	AW947581 AW947455 AW947544
412872	1333898_1	BE092186 BE092157 AW968699
413070	134815_1	BE006341 BE005307 BE005311
415610	1540554_1	AA126778 AA133984 BE148613 BE063475 AA358219
415713	154859_1	L43119 F12851 T75057
415842	1559554_1	AW865574 AA167225 AA401129
416548	1600181_1	W928491 W92749
416913	1630001_1	HE2953 N76508 N72413
417038	164390_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
418353	171810_1	TS6240 AA152058 TB9159
419213	182860_1	AA211430 AW819789 AW807836
419546	185768_1	AW749145 AW749136 AW749123 AW749130 AA235142
420637	195241_1	AA244199 AA244272 H57440
422063	210852_1	AW976153 AA278945 AA747691
422219	213547_1	BE155476 BE156473 BE156474 BE156475 AA302839
422604	217160_1	AW978073 AW978072 AA087550 AA306567
423735	2314938_1	AA311407 AW958321 N23583 R70050
426384	266211_1	AA330259 AA661806 AA502463 1 AW974533 AA649496
427072	274684_1	AA72078 AA37709 AA858807
428637	293660_1	H30046 W69545 AA387958 H30047
430183	31412_2	AW979268 AA878419 AA431342 AA431628
431595	335512_1	BE010038 AA676833 A1311783 T86895 W88032 BE064393 BE064394 BE157228 BE183262 AW36370 AA552514 T67280 AA03909
432009	34025_1	AA308198 BE142620 A280311 A205616 D61709
437205	434633_1	AL137424 BE007148 T52277
437938	44572_3	AL110232 N54765
438966	467436_1	AW950387 N70208 R97040 N36809 A1308119 AW967677 N53320 A1251473 H59397 AW971573 R97278 W01059 AW967671 AA906598 AA251875
438993	467651_1	A1826051 A1826532 W87891 T85904 U71456 T82631 BE238711 T75102 R34725 AA864922 BE238717 A219788 AA864444 N925758 F15163 AA327794
440680	500172_1	AW867408 AL134043 A0253533 A063346 AW005822 AA488564 AA281144 A1850387 A0550434 A1711336 A6868982 AA328015 AW102598
442438	514269_1	AW871193 A1076323 A1713596 AW1560239 A0633832 A076268 AA988777 AA488992 A1358394 AA103813 A1539542 AA642789 AA856975 AW005512
443646	613545_1	AW61530 AW269790 BE512681 AW726997 AW513601 AW512843 AA044209 AW856538 AA180009 AW861101 AA251669 AA251874
445417	676384_1	AW819225 AW206462 A063338 AW856509 AW276055 A1633006 AW372584 AW008741 AW072629 AW513996 AA232373 AA369739 W75628 N23288
447641	73043_1	H84729 H68052 T52467 A0020258 AA780419 AA551005 W87071 AW613456 A1373032 A564265 F05311 H83486 W37181 W78802 T86956 A002029
448460	76395_1	R87840 AA300207 AW85681 TS3226 F04005
449034	79417_1	AW979074 AA834841 AA828650
450625	84032_1	AA828995 AA834879 A1526361
452463	918300_1	AA903058 AW836693 BE160824 AW608818 AW582699 AW836768
452463	918300_1	AA929595 A151654 R81781 T77332 F07756 F08145 F07647
452463	918300_1	A1292005 AW235762 A151268
452463	918300_1	A1290950 BE259910
452463	918300_1	BE819186 BE264952 R26042
452463	918300_1	BE612405 T05205 AA811817
452463	918300_1	AA024040 AW117770 A1858360
452463	918300_1	AW970107 AA513951 AA010406
452463	918300_1	AA902519 A1902516 A1902516
452463	918300_1	AL120480 AW836446 AW176802
452463	918300_1	AW576207 AW536883 AW000206 N88905
452463	918300_1	BE260843 AA078319 R65057 AW829024 H85811 AA078293
452463	918300_1	AW977778 AW797781 AW797780
452463	918300_1	AW854639 AW854718 AW854718 BE145880 AW854692 BE145866 AW854698 AW854654 AW813335 AW854699
452463	918300_1	AA141714 AA184593 AA860889
452463	918300_1	AW854625 AW854658 AW854716 AW854690 AW864615 AW854624 AW854611 AA184593 AW854652 AW854655 AW854651
452463	918300_1	AW863303 AW863382
452463	918300_1	AW917806 AW887923 AW886321

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5	455362	1284507_1	AW902635	AW902674	BE011167	BE011329	AW902808	AW902651
	455711	1352369_1	BE069465	BE069505				
	456386	1842693_1	W28481					
	456388	1842839_1	W28557					
	456411	185688_1	AA603305	AA244095	AA244183			
	456587	94853_1	AA031956					
	456595	969956_1	AL040421					
10	TABLE 33C							
	Unique number corresponding to an Eos probe/set							
	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunkham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunkham, et al. (1999) <i>Nature</i> 402:489-495.							
	Ref: Indicates DNA strand from which exons were predicted.							
	Strand: Indicates nucleotide positions of predicted exons.							
15	Strand: Indicates nucleotide positions of predicted exons.							
	Pkey	Ref	Strand	NT_position				
	401078	3687273	Plus	105052-105171				
	401157	9438289	Minus	114133-114247,114567-114645				
20	401189	9690246	Minus	93815-95029				
	401260	8076883	Minus	86008-86355				
	401352	9931258	Minus	26064-26208				
	401439	8246737	Plus	92953-94026				
	401707	2951946	Plus	21972-22104				
	401811	6130720	Plus	107002-107209				
25	401976	3095020	Minus	17594-17706,21068-21175				
	402045	7923943	Plus	5964-6128				
	402421	9796341	Minus	46698-46692,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924				
	402596	7238818	Minus	23600-23731				
	402739	9212192	Plus	60456-61019				
30	402921	7981303	Minus	52242-52384,55599-55858,57124-57309,59633-59761,519957-60123				
	403095	8954339	Plus	150025-150240,151564-151690				
	403111	8980970	Plus	175012-175159				
	403144	9454649	Minus	166200-166528				
	403170	9838134	Plus	40955-41356				
	403345	8569726	Plus	77890-78369				
	403346	8569726	Plus	92752-93015				
35	403563	8101139	Plus	2806-3201				
	403622	8569879	Plus	1941-2388,2580-2761				
	403782	8078608	Plus	41326-41633				
40	403787	8099996	Minus	123655-125008				
	403869	7331715	Minus	9144-91350				
	404021	8655966	Plus	192534-193489				
	404115	9621489	Plus	232707-232932				
	404200	6010176	Minus	7066-7210				
45	404347	9839136	Plus	744593-74609				
	404539	6862587	Plus	175318-175476				
	405257	7329310	Plus	73121-73273				
	405336	6094635	Plus	33267-33363				
	405394	6624123	Minus	31900-32373				
50	405517	1054740	Plus	124351-124320,124914-125050				
	405609	5757553	Minus	42814-43010,43583-43763,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51969,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727				
	405908	6789795	Plus	97869-98715				
	405943	6789796	Plus	20605-20812				
55	405953	7960374	Minus	65101-65574				
	405963	8247786	Plus	4056-4699				
	406007	8247802	Minus	13484-13829				
	406030	6312328	Minus	96123-95847				
	406088	9123919	Minus	65772-66270				
60	406117	9142932	Plus	54304-54584				
	406242	7417725	Minus	36736-36951				
	406291	5696274	Plus	9562-9587				
	406411	9256407	Plus	7400-7327				
	406414	9256407	Plus	49593-49850				
65	406504	7711350	Minus	107068-107277				
	406506	7711374	Plus	6843-8077				
	406598	8248614	Plus	56373-56849				
70	TABLE 34A: ABOUT 197 GENES UP-REGULATED IN KIDNEY CANCER							
	Table 34A lists about 197 genes up-regulated in kidney cancer compared in normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 33A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., fn3, ogf, 7m domains). Predicted protein domains are noted.							
	Pkey: Unique Eos probe/set identifier number							
	ExAccess: Exempt/Accession number, Genbank accession number							
75	UniGeneID: UniGene number							
	UniGene Title: UniGene gene title							
	PSDomain: Protein Structural Domain							
	R1: Ratio of tumor to normal tissue							
80	Pkey	ExAccess	UniGeneID	UniGeneTitle	PSDomain	R1		
	421471	U09045	Hs.104635	solute carrier	TM,SS	1007.4		
	452401	NM_007115	Hs.29352	tumor necrosis	TM,SS,Xlink,CUB	336.4		
	421727	Y13153	Hs.107318	lysine-rich 3-mo	TM,SS,Monoxygenase	323.6		

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	426471	M2240	Hs.170009	transforming gr	TM,SS,EGF	224.6
	441031	A1110684	Hs.7645	fibronogen, B b	fibronogen_C	174.0
	411642	NM_014932	Hs.71132	neuroigin 1	TM,SS,Coesterase	172.4
5	452838	U65611	Hs.30743	profermentally	TM	161.4
	429894	AW53277	Hs.155836	hypothetical pr	TM	151.0
	453165	574727	Hs.32042	aspartacylase	TM	134.8
	452431	U88679	Hs.29499	tol-like recep	TM,SS,TIR,LRCT	130.6
	423508	AW504297	Hs.129711	hepatitis A vir	TM,SS,lg	120.4
	407975	XB9426	Hs.41716	endothelial cel	SS,KRBP	111.5
10	415076	NM_000857	Hs.77890	guanylate cycla	TM,guanylate_cyc	97.0
	447046	AA326187	Hs.17170	G protein-coupl	TM,Tm_1	90.2
	423109	M59305	Hs.123655	naturicell pep	TM,SS,ANF_receptor	78.0
	422544	AB018259	Hs.118140	KIAA0718 gene p	TM	74.8
	425352	AK001512	Hs.200097	hypothetical pr	TM	73.0
15	453392	U23752	Hs.32964	SRV (sus delet	TM,HMG_box	72.2
	403345				TM,alpa-amyase	69.6
	430440	X32599	Hs.2581	nerve growth fa	TM,SS,NGF	69.0
	490605	AA330431	Hs.640	calcinin rice	TM,SS,Tm_2	57.4
20	445101	AA905847	Hs.22016	G protein-coupl	TM,Tm_1	52.0
	420686	BE350494	Hs.49753	Homo sapiens mR	TM,Myosin_tail	48.0
	452891	N75582	Hs.212875	ESTs, Weakly st	SS	44.0
	408430	S75876	Hs.44926	dipeptidylpept	TM,SS,DPPIV_N_term,Peptidase_S9	42.6
	415287	XJ1206	Hs.59872	chloride channel	TM,CBS,voltage_CLC	40.6
25	428822	W26418	Hs.301148	potassium volta	TM	40.2
	434208	T32641	Hs.127648	hypothetical pr	TM,SS	39.2
	400792	AA635062	Hs.50094	Homo sapiens mR	TM,BIR,CARD,zf-C3HC4	38.6
	444743	AA045648	Hs.11817	nucle (fructosi	TM,tauT	38.4
	406411				TM,tau,FG-GAP	37.6
	423657	AL045128	Hs.1691	glucan (1,4- α	TM,alpa-amyase	37.5
30	424871	NM_004525	Hs.153595	low density lip	TM,SS,EGF_xd_recept,alpd_recept,b	32.8
	443626	NM_014253	Hs.23796	otz (old Oshen	SHZEGF	32.6
	423200	AA383192	Hs.1616	replication pro	TM,SS	29.6
	422420	U03398	Hs.1524	tumor necrosis	TM,TNF	29.6
	414245	BE148072	Hs.75850	WAS protein lam	TM,WH2	28.8
35	410247	AF181721	Hs.61345	RU25	TM	27.4
	405414				TM,tau,FG-GAP	27.2
	435951	AF269162	Hs.41267	c21orf7 form A-	TM	27.2
	419948	AB041035	Hs.53847	NADPH oxidase 4	TM,SS,Fenic_reduct	26.4
40	446895	AB014544	Hs.21572	KIAA0644 gene p	TM,SS,LRCT,LR	26.8
	415969	AB711651	Hs.51143	jagged 1	TM,SS,DSL,EGF	25.8
	433242	AB040938	Hs.113240	KIAA1505 protei	SS	25.6
	416778	M16505	Hs.79876	steroid sulfata	TM,Sulfatase	23.0
401352					TM	22.6
	404200				SS	19.6
45	445591	H44186	Hs.15456	PDZ domain cont	TM,PDZ	19.2
	431806	AF186114	Hs.270737	tumor necrosis	TM,SS	18.0
	423909	AJ223183	Hs.135194	immunoglobulin	TM,SS,lg	17.6
	446364	AB006634	Hs.14912	KIAA2285 protei	TM	17.4
50	425695	NM_005401	Hs.159238	protein tyrosin	TM,Band_41_Y_phosphatase	17.0
	410947	AK000305	Hs.67055	hypothetical pr	TM	16.8
	421002	AF116030	Hs.100932	transcription f	TM,KRAB,zf-C2H2	16.5
	421659	NM_014469	Hs.106511	protocadherin 1	TM,SS,cadherin	16.0
	458679	AH975460	Hs.143563	ESTs	SS	14.4
406508					SS	13.6
55	428508	BE262383	Hs.184668	SIBI31 protein	TM,PX	13.2
	423321	AB013885	Hs.126926	beta-ureidoprop	TM,SS,ON_hydrolase	12.5
	423217	NM_001147	Hs.115181	angiotensin 2	fibronogen_C	12.0
	428227	AA321649	Hs.22140	small inducible	IL8	12.0
60	414923	AW445008	Hs.77637	homeo box A4	TM,homeobox	11.9
	433321	AB040926	Hs.143552	KIAA1493 protei	SS	11.6
	443672	AA323362	Hs.9667	butyrobetaine (TM	11.4
405609					TM,Myosin_tail,myosin_head	11.4
	411812	NM_000685	Hs.89472	angiotensin rec	TM,Tm_1	11.4
65	449802	AW501804	Hs.23984	hypothetical pr	TM	11.2
	404347				SS	10.8
	425945	NM_006729	Hs.226483	diaphanous (Dp	TM,FH2	10.6
	435085	AW130284	Hs.192752	ESTs, Moderate	TM	10.6
404115					SS	10.2
70	420757	X78592	Hs.99915	androgen recept	TM,Androgen_recap,hormone_rec,zf-C4	10.2
	446298	AF187813	Hs.14637	kidney- and liv	TM,Acetyltransf	10.1
	433703	AA210863	Hs.3532	nerve-like knots	TM,kinase	10.0
	417404	NM_007350	Hs.82101	pleckstrin homo	TM	9.2
	451621	AI879148	Hs.26770	fatty acid bind	TM,SS,lipocalin	9.2
75	402045				TM,SS	9.0
	403955				SS,PAX/homeobox	8.8
401439					TM	8.6
	407721	Y12735	Hs.38018	ducal-specific	TM,kinase	8.4
402921					TM	8.4
80	419503	AA243642	Hs.137422	ESTs	TM	8.4
	432259	AA317439	Hs.28707	signal sequence	TM	8.4
402696					TM	8.3
	400001	NM_001044	Hs.406	solute carrier	TM,SS,SNF	8.1
433190		M26901	Hs.3210	renin	SS,asp	7.8

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	449444	AY618436	Hs.23590	solute carrier	TM,ACT	7.7
	449402	NM_004915	Hs.10237	ATP binding cas	TM,ABC_tran	7.7
	452863	X80031	Hs.150318	ESTs	TM,CA,Colagen	7.4
5	425151	AA351814	Hs.296678	ESTs	TM,SS	7.2
	455068	AB07894	Hs.27910	centrosomal pro	TM,SS	7.2
	465504				TM	7.2
	410274	AA381807	Hs.61762	hypoxia-inducib	SS	7.0
	423349	AF010258	Hs.127428	homoeo box A9	TM,homoeobox	6.8
10	406771	AW732573	Hs.47504	potassium volta	TM,K_1etra,trans	6.8
	445575	Z35368	Hs.172004	tin	TM	6.6
	415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	6.3
	443595	AF169312	Hs.9613	PPAR(gamma) ang	TM,SS,biotinogen_C	6.3
	404539				TM	6.3
	436209	AW850417	Hs.254020	ESTs, Moderat	TM,SS	6.2
15	403111				TM	6.2
	405394				TM	6.0
	454392	BE260893		glt601150677F1	TM,SS	5.0
	415910	U20350	Hs.78913	chemokine (C-X	TM,tm_1	5.9
20	402421				TM	5.8
	425717	X07282	Hs.171495	retinoic acid r	TM,homone_rec,cf-C4	5.7
	427920	Z11502	Hs.181107	annexin A13	TM,annexin	5.6
	407864	AF069291	Hs.40539	chromosome 8 op	TM,FHA,BRCT	5.5
	441066	AW603267	Hs.7327	COI-60 protein	TM	5.4
	422232	D43945	Hs.113274	transcription f	TM,HLH	5.4
25	425782	U66468	Hs.159525	cell growth reg	SS	5.3
	450236	AW152998	Hs.24684	KIAA1375 protei	TM,SS	5.3
	413841	M04275	Hs.75575	plasmaogen	SS,tyrosin,kringle,PA	5.3
	4366132	AA150797	Hs.100275	taxin protein	TM	5.1
	447081	Y13896	Hs.17287	potassium inwar	TM,PK	5.1
30	421125	M74587	Hs.102122	insulin-like gr	SS,thyroglobulin_1,GF	5.1
	426651	AL076546	Hs.171683	nuclear recepto	TM,cf-C4,homone_rec	5.0
	432328	A572739	Hs.195471	6-phospholucifer	TM,PP2C,PCAM	5.0
	409506	NM_005153	Hs.54589	NCK adaptor pro	TM,SH2,SH3	5.0
	410351	BE391804	Hs.62661	guanylate bindi	TM,SS,GBP	4.8
35	453891	AB031751	Hs.36353	Homo sapiens nR	TM	4.8
	447259	NM_004861	Hs.17958	cardiacoside (P	TM,SS	4.8
	422357	AF015272	Hs.115419	cadherin 15_K5	TM,cadherin	4.8
	417355	D13168	Hs.82002	endothelin rece	TM,SS,tm_1,cf-C3HC4	4.7
40	402739				SS	4.6
	443465	NM_003408	Hs.9450	zinc finger pro	TM,RYR2,cf-C2H2	4.6
	403890	AF123050	Hs.44532	diaphanin	TM,ubiquitin,tm_3,ANF_receptor,sushi,tm_1	4.6
	414612	X72755	Hs.77367	monokine induc	SS,IL8	4.4
	424053	NM_002019	Hs.136571	frs-related tyr	TM,SS,kinase,ase	4.4
45	413394	NM_000401	Hs.75334	exostoses (fruit	TM	4.4
	457030	A031740	Hs.173381	dihydroxyimide	TM,SS,Dihydroxyacetate	4.4
	410407	X56839	Hs.63287	carbonic anhydr	TM,SS,carb_anhydrase	4.3
	401157				TM,citrate_synt	4.3
	432004	BE018302	Hs.2894	placental growt	SS,POGF	4.3
	424704	A253253	Hs.152095	cytochrome P450	SS,p450	4.2
50	407065	Y10141		glt11.sapiens DA	TM,SS,SNF	4.2
	411213	AA676939	Hs.59285	neurepin 1	TM,CUB,F5_F8_type_C,MAM	4.2
	430805	S69377	Hs.247978	T-cell acute ly	TM,HLH	4.2
	414696	AF020220	Hs.75918	Niemann-Pick di	TM,SS,Patched	4.1
55	402830	AC011709	Hs.48403	hypothetical pr	TM,LUPP013	4.1
	416655	AW968613	Hs.79428	BCL2adenovirus	TM	4.1
	412494	AL133900	Hs.792	ADP-ribosylatio	TM,art,cf-B_box,cf-C3HC4	4.1
	453195	BE241876	Hs.32352	hypothetical pr	TM	4.0
	428816	AA004986	Hs.193852	ATP-binding cas	TM,ABC_membrane,ABC_tran,COX15-ClaA	3.9
60	401189				TM,SET,PHD,HMG2_box	3.8
	451988	AF263928	Hs.27410	papillomavirus	TM	3.8
	427013	M62397	Hs.1345	mutated in colo	TM	3.7
	420041	AB035142	Hs.94592	Mutho	TM,SS,Glyco_hydrn_1	3.7
	432979	AF043244		nuclear protei	TM	3.6
65	453496	AA442103	Hs.33084	solute carrier	TM,SS,sugar_r	3.6
	446636	AC002563	Hs.15767	citron (rho-int	TM,CNH,DAG_PE_bind,PK,phkase,phkase_C	3.6
	426274	D38122	Hs.2007	tumor necrosis	TM,TNF	3.6
	452355	H54926	Hs.28202	G protein-coupl	TM,tm_1	3.5
	453775	NM_002916	Hs.35120	replication lac	TM,SS,AAA	3.4
	426559	AB001914	Hs.170414	paired basic am	TM,Peptidase_S0P	3.4
70	420737	L08096	Hs.99899	tumor necrosis	TM,TNF	3.4
	446733	NM_005629	Hs.187958	solute carrier	TM,SNF,ABC_tran,sodh,phkase,Ribosomal_1,18ae	3.4
	413719	BE439580	Hs.75498	small inducible	SS,IL15	3.4
	427914	AA417350	Hs.20575	ESTs	TM,GAS2	3.4
	412642	BE244598	Hs.809	hepatocyte grow	kringle,PA,tyrosin	3.4
75	421893	NM_001078	Hs.159225	vascular cell a	TM,SS,ig	3.3
	417924	AF077231	Hs.82932	cyclin D1 (PRAD	TM,cyclin	3.3
	405257				TM	3.3
	450396	AU077002	Hs.24950	regulator of G-	TM,RGS	3.3
80	418992	L24498	Hs.80409	growth arrest a	TM,Ribosomal_L7Ae	3.3
	425236	AW067800	Hs.155223	stannocalcetin 2	SS	3.3
	430812	L10405	Hs.247992	DNA binding pr	TM,SS	3.3
	431842	NM_005784	Hs.271473	epithelial prot	TM,SS	3.2
	424897	D63216	Hs.153884	trizzled-relate	TM,F2,NTR	3.2

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414921	ME3835	Hs.77424	Fc fragment of	TM,SS,lg	3.1
419030	BE207573	Hs.83321	neurexin B	SS	3.1
421633	AF121860	Hs.106260	sorting nexin 1	TM,PX	3.1
411285	NM_002374	Hs.167	microtubule-actin	SS,subunit-binding	3.1
416226	BE119020	Hs.85838	solute carrier	TM,ACT	3.1
401260				TM,SS	3.1
450705	U90304	Hs.25351	iroquinolone-class	TM,homeobox	3.1
424415	NM_001975	Hs.146580	inositolase 2, (gam	TM,SS,enzyme	3.0
403346				TM	3.0
432757	AF113013	Hs.278919	PRO0806 protein	TM	3.0
434368	AA121098	Hs.3838	serum-inducible	TM,kinase,PCLO_box	3.0
424539	LD2911	Hs.150402	activin A recep	TM,Activin_recep,kinase	3.0
406117				SS	3.0
408119	W26713		glt-22d10 Human	TM,SS	3.0
431984	AL080239	Hs.272284	Human DNA seque	TM	3.0
403782				TM	3.0
447922	Z32910	Hs.20019	hemochromatosis	TM,SS,lg,MHC_L,histone,SPRY,zf-B_box,zf-C3HC4	3.0
428857	AF008192	Hs.194283	putative GRP pr	SS	3.0
432936	AJ224741	Hs.279461	matrin-3	SS	3.0
453202	AW085781	Hs.26270	Homo sapiens cD	TM	3.0
405547				TM,SS,ABC_membrane,ABC_tran	3.0
423496	U91963	Hs.129700	tollind-llka 1	TM,SS,EGF,CUB,Asiadin	3.0
401707				SS	3.0
403144				TM,ion_trans,K_1etra	3.0
418375	NM_003081	Hs.84389	synaptosomal-as	TM,NA	3.0
422992	AF016833	Hs.122785	maltase-glucosam	TM,Glyco_hydro_31,Irefol	3.0
406506				TM	3.0
413472	BE242870	Hs.75379	solute carrier	TM,SDF	3.0

30	TABLE 34B:	
	Play	Unique Ecos proteol identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

35	Play	CAT number	Accession
	408119	1040172_1	W69213108055 Z44031 AW954550 R17434
	454392	115882_1	BE200993 AA078319 RB5067 AW803024 HB5811 AA078293

40	TABLE 34C:	
	Play:	Unique number corresponding to an Ecos proteol
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al (1999) Nature 402 489-495
	Strand:	Indicates DNA strand from which exons were predicted.
	NT_position:	Indicates nucleotide positions of predicted exons.

45	Pkey	Ref	Strand	NT_position
	401157	9438289	Minus	114133-114247,114507-114645
	401189	9690246	Minus	90815-90929
	401260	8078883	Minus	89030-89385
50	401352	9531258	Minus	26054-26208
	401439	8246737	Plus	32993-94026
	401707	2551946	Plus	21972-22104
	402045	7523943	Plus	5954-6128
	402421	9798241	Minus	46528-46652,46758-46811,86253-96346,89776-89829,90049-90101,102817-102924
55	402696	7328818	Minus	23600-23731
	402739	9212152	Plus	60456-61019
	402921	7581303	Minus	62442-52384,55599-55838,57124-57309,59533-59761,59957-60123
	403295	8554339	Plus	150025-150240,151554-151699
60	403111	8930970	Plus	175012-175159
	403144	9454649	Minus	166200-166628
	403345	8569726	Plus	77990-78063
	403346	8569726	Plus	92752-93015
	403792	8076698	Plus	41326-41633
65	404115	9621489	Plus	232707-232982
	404200	6010176	Minus	7066-7210
	404347	8638195	Plus	74403-74829
	404539	6862697	Plus	175319-175476
	405257	7328310	Plus	73121-73273
	405394	6624123	Minus	31900-32373
70	405547	1054740	Plus	124381-124520,124914-125050
	405609	5757553	Minus	42814-43010,43083-43783,44863,45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51920,52602-52918,55469
				55601,57111-57307,58163-58296,60215-60332,61482-61727
	406117	9142932	Plus	54304-54584
	406411	9296407	Plus	7400-7527
	406414	9296407	Plus	45333-45850
75	406504	7711360	Minus	107058-107277
	406506	7711374	Minus	6843-8077
	406598	8248614	Plus	56373-56849

80	TABLE 35A: ABOUT 532 GENES UP-REGULATED IN KIDNEY CANCER	
	Table 35A lists about 532 genes up-regulated in kidney cancer compared to normal kidney. These were selected as for Table 33A except using an "average" of the 70th percentile for both the numerator and the denominator and using non-malignant kidney specimens in determining the denominator value.	

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Phy:	Unique Eos. protein identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of tumor to normal tissue			
Phy	ExAccn	UnigeneID	UnigeneTitle	R1
	424704	A263293	Hs.152096	cyclochrome P450, subfamily II (arachi
	426589	AB001914	Hs.170414	palmito basic amino acid cleaving syst
	430879	A179680	Hs.54277	ESTs
10	433447	U28195	Hs.3281	neuronal pentraxin II
	439979	AW500291	Hs.6823	hypothetical protein FLJ10430
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy
	433539	T68943	Hs.189679	ESTs
15	450152	A1138635	Hs.22958	ESTs
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pr
	440304	BE155984	Hs.125395	ESTs
	414821	MS3635	Hs.77424	Fc fragment of IgG, high affinity Ia, m
	421155	H87879	Hs.102267	lysoi oxidase
20	452795	AW392555	Hs.18878	hypothetical protein FLJ21620
	414812	X72755	Hs.77387	monokine induced by gamma interferon
	426471	M22440	Hs.170035	transforming growth factor, alpha
	427897	NM_017413	Hs.181050	apoptic peptide ligand for APJ receptor
	448523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5
	436981	AW375974	Hs.156704	ESTs
	447499	AW267580	Hs.147674	KIAA1621 protein
	430817	A0223799	Hs.153242	ESTs
	430630	AW269920	Hs.2621	cystatin A (stefin A)
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
30	424086	AJ351010	Hs.102267	lysoi oxidase
	426269	AW135042	Hs.155530	interferon, gamma-inducible protein 16
	436478	AA326108	Hs.53531	ESTs, Weakly similar to enhancer-of-spl
	415286	AW249540	Hs.72548	ESTs
	428157	A1738719	Hs.298668	ESTs
35	456804	AJ211545	Hs.139551	caveolin 2
	429400	A571131	Hs.293634	ESTs, Weakly similar to alternatively sp
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma
	433757	A1949974	Hs.152670	ESTs
	400419	AF084545	Hs.81800	chondroitin sulfate proteoglycan 2 (vers
40	428046	AW512795	Hs.155381	ESTs, Moderately similar to 138022 hypot
	411642	NM_014932	Hs.71132	neutrophin 1
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CASH_HUMAN COLLA
	435767	H73505	Hs.117874	ESTs
	427581	NM_014788	Hs.179703	KIAA0129 gene product
45	440019	AW947164	Hs.159841	ESTs
	406671	AA129547	Hs.285754	mat proto-oncogene (hepatocyte growth fa
	447835	AW591623	Hs.164129	ESTs
	448520	AB002367	Hs.21355	doublecortin and Cdk1 kinase-like 1
50	417308	H60720	Hs.81892	KIAA0101 gene product
	432731	R31178	Hs.287820	fibronectin 1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop
	419235	AW470411	Hs.288433	neurotrophin
	426480	NM_001621	Hs.170887	aryl hydrocarbon receptor
55	421485	AA243498	Hs.104800	hypothetical protein FLJ10134
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox
	411110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202.1s, clone H
	425984	AW688277	Hs.165536	hypothetical protein DKFZ761C07121
	423506	NM_002104	Hs.3006	granzyme K (serine protease, granzyme 3,
60	436772	AW975688	Hs.250687	zona pellucida glycoprotein 3A (spem re
	444989	A203334	Hs.160628	ESTs
	426890	AA393167	Hs.41294	ESTs
	437330	AL353544	Hs.501515	Homo sapiens mRNA: cDNA DKFZ761J1112 (f
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30KD
65	446627	A1973016	Hs.15725	hypothetical protein SBB48
	452960	AK001335	Hs.31137	Homo sapiens cDNA: FLJ22681.1s, clone H
	417280	AW173116	Hs.852206	ESTs
	427173	BE385826	Hs.253510	phalloidin-like protein MD0919
	420552	AK000452	Hs.58806	hypothetical protein
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190
	427871	AW992405	Hs.59622	ESTs, Weakly similar to unknown [Hsapie
70	446152	A1290308	Hs.150328	ESTs
	426560	AA381661	Hs.110878	ESTs
	419034	NM_002110	Hs.85055	hemopoietic cell kinase
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855.1 BM-01
75	452281	T63560	Hs.28792	Homo sapiens cDNA FLJ11041.1s, clone PL
	442032	AA457211	Hs.98858	brachyotom adjacent to zinc finger doma
	426075	AW513691	Hs.270149	ESTs
	434358	AA121058	Hs.3838	serum-inducible kinase
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha
80	425702	U56468	Hs.155525	cell growth regulatory with EF-hand doma
	426108	AA622037	Hs.166468	programmed cell death 5
	416000	R82342	Hs.79856	ESTs
	450226	AW162998	Hs.24684	KIAA1376 protein

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5	49679	AB223651	Hs.296668	Homo sapiens cDNA FLJ11846 fs, clone HE	11.6
	441302	AB028690	Hs.77182	paramyosin antigen M2	11.4
	447227	AW771558	Hs.175437	ESTs	11.4
	414004	AA737033	Hs.7155	ESTs, Weakly similar to 2115357A TYKJ pr	11.4
	447956	HE7878	Hs.157695	ESTs	11.3
10	444963	AW364892	Hs.301323	ESTs	11.3
	452638	UE5011	Hs.30743	preferentially expressed antigen in meta	11.2
	426780	BE242284	Hs.172195	adenylate cyclase 7	11.1
	453160	A263307	Hs.146228	ESTs	11.0
	448535	W83263	Hs.58446	ESTs	11.1
15	415323	BE265352	Hs.945	neutrophil cytosolic factor 2 (63kD), chr	11.1
	428508	AW604257	Hs.129711	hepatitis A virus cellular receptor 1	11.0
	408380	AF123050	Hs.44532	diubiquitin	11.0
	448410	AK000227	Hs.21126	hypothetical protein FLJ120220	11.0
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	10.9
20	453165	S74727	Hs.32042	aspartate lyase (aminoacylase 2, Canavan	10.8
	453380	AA679001	Hs.192221	ESTs	10.7
	447183	AI554733	Hs.173182	ESTs	10.7
	438330	AW455572	Hs.257316	ESTs	10.6
	441302	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERAT	10.5
25	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.5
	452862	AW378066	Hs.6687	ESTs	10.4
	431512	BE270734	Hs.2795	lactate dehydrogenase A	10.3
	421478	AB83243	Hs.97298	ESTs	10.3
	413879	AA132961	Hs.212533	Homo sapiens cDNA: FLJ22572 fs, clone H	10.3
30	411800	N36342	Hs.5184	TH1 thiopeptide homolog	10.3
	433862	D85960	Hs.3610	KIAA0205 gene product	10.3
	440594	AW445167	Hs.128036	ESTs	10.2
	414504	AW069181	Hs.293523	ESTs, Weakly similar to transformation-r	10.2
	431211	MB6849	Hs.5566	gap junction protein, beta 2, 29kD (conn	10.2
35	437882	AA176652	Hs.94552	Homo sapiens cDNA: FLJ23371 fs, clone H	10.1
	430097	AS523245	Hs.121616	ESTs	10.1
	425679	AF042944	Hs.278439	nuclear protein 3 (apoptosis repressor	9.9
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cfs	9.9
	424113	AI743880	Hs.12876	ESTs	9.9
40	435861	AA349408	Hs.124675	ESTs, Weakly similar to unnamed protein	9.9
	411937	AW075626	Hs.26107	gbrPC3-PT0028-120200-013-d06 PT0028 Homo	9.9
	439553	AW021103	Hs.6631	hypothetical protein FLJ20073	9.8
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (ca	9.8
	424623	AW563052	Hs.163809	ESTs	9.8
45	410762	AF226513	Hs.66170	HSMAB protein	9.8
	433286	AW675944	Hs.237396	ESTs	9.7
	413795	AL040178	Hs.142003	ESTs	9.6
	434362	AW583709	Hs.268051	ESTs	9.6
	435542	AA697376	Hs.268533	ESTs	9.6
50	433867	HS6801	Hs.260207	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.5
	410339	AI516499	Hs.298288	ESTs	9.5
	462431	U88879	Hs.29499	toll-like receptor 3	9.5
	405121	AB029889	Hs.88500	mitogen-activated protein kinase 8 inter	9.5
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phospholipase	9.4
55	439566	AW975074	Hs.23796	gb:EST1391164 MAGE resequences, MAGP Homo	9.4
	449625	NM_014253	Hs.23796	ozd (odd Ozten-m, Drosophila) homolog 1	9.4
	441028	AW081530	Hs.137088	ESTs	9.3
	445980	AF070526	Hs.13426	Homo sapiens clone 24787 mRNA sequence	9.2
	433001	AF217513	Hs.279905	clone HQ0310 PR00310p1	9.2
60	440074	AA863045	Hs.198057	ESTs, Weakly similar to T00050 hypothet	9.2
	421669	NM_014459	Hs.106511	protocadherin 17	9.2
	434542	AW758310	Hs.61260	hypothetical protein FLJ13164	9.1
	427283	AI115786	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	9.1
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	9.1
65	419441	AW022731	Hs.274368	Homo sapiens mRNA, cDNA DKF2p586f1524 f	9.0
	407836	AA045281	Hs.266175	phosphoprotein associated with GEMs	9.0
	431941	AK001106	Hs.272227	Homo sapiens cDNA FLJ20899 fs, clone CO	9.0
	446450	AW013559	Hs.150164	ESTs	8.9
	452998	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.9
70	407975	HS8456	Hs.41716	endothelial cell-specific molecule 1 (NO	8.9
	437259	AA371755	Hs.126655	ESTs	8.7
	420275	AA256796	Hs.31178	ESTs	8.7
	439599	AI133076	Hs.5354	hypothetical protein FLJ12716	8.7
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.6
75	435994	AW076677	Hs.180011	ESTs	8.6
	418893	AT752878	Hs.87409	transoxiposin 1	8.6
	425770	NM_014363	Hs.159492	specific ataxia of Charlevoix-Saguenay (s	8.6
	456249	AA206144	Hs.82508	HRHFB2206 protein	8.6
	437672	AW748265	Hs.5741	flavohemoprotein b5-b5R	8.6
80	430268	AK000717	Hs.237480	hypothetical protein FLJ20730	8.5
	417225	AA815048	Hs.24078	Homo sapiens cDNA FLJ12649 fs, clone NT	8.5
	432566	AK001942	Hs.4863	Homo sapiens cDNA FLJ11090 fs, clone PL	8.4
	447574	R76886	Hs.15922	gb:Y64003 x1 Sources placenta NbzHP Homo	8.4
	447850	AB019268	Hs.15922	SEC23A (carnitine) related gene fami	8.3
	429526	AE2540	Hs.205353	ectonucleoside triphosphate diphosphohyd	8.3
	437177	AF227905	Hs.105794	UDP-glucose:glycoprotein glucosyltransfer	8.3
	445784	AF231555	Hs.146065	ESTs	8.3

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	454024	AA993527	Hs.15281	hypothetical protein FLJ23403	8.3
	443885	H81805	Hs.15284	ESTs	8.3
	403713		Hs.74122	caspase 4, apoptosis-related cysteine pr	8.3
	433376	A293361	Hs.90978	granzyme A (granzyme 1, cytotoxic T-lym	8.2
5	419450	NM_006144	Hs.37494	ESTs	8.2
	444670	H50373	Hs.238936	ESTs	8.2
	408761	AA057254	Hs.31463	KIA0281 gene product	8.2
	453033	AA325869	Hs.7153	calumenin	8.1
	441224	AL020864	Hs.106932	ESTs	8.1
	441689	A123705	Hs.190489	ESTs	8.1
	440283	A172892	Hs.208710	ESTs	8.1
	429598	AA811257	Hs.153026	SWAP-70 protein	8.1
	424775	AB014540	Hs.26204	KIAA1205 protein	8.0
	451292	AB037716	Hs.24789	ESTs	8.0
15	453951	A1678235	Hs.44257	Homo sapiens mRNA; cDNA DKF7p76202215 f	8.0
	416200	A1188972	Hs.290191	ESTs	7.9
	431087	H12723	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	7.9
	432328	A572739	Hs.155848	ESTs	7.9
20	419474	AW968619	Hs.293504	ESTs, Moderately similar to ALU1_HUMAN A	7.9
	418342	BE002723	Hs.4947	Homo sapiens cDNA: FLJ22584 fs, clone H	7.9
	408088	AW157022	Hs.130229	ESTs	7.9
	413719	BE42680	Hs.75468	Interleukin 13, clone H	7.9
	440587	AA911705	Hs.126229	ESTs	7.9
	412448	L12564	Hs.73895	tumor necrosis factor receptor superfam	7.9
	415737	AA167626	Hs.118743	ESTs	7.9
	412569	DB7458	Hs.75990	KIAA0282 protein	7.8
	424247	X14008	Hs.234744	lysine (renal amyloidosis)	7.8
	453331	A1240665	Hs.8885	ESTs	7.8
30	421991	NM_014818	Hs.110488	KIA0590 protein	7.8
	443450	N59045	Hs.133529	ESTs	7.8
	431876	AA521183	Hs.208978	ESTs	7.7
	432582	A523817	Hs.168457	ESTs	7.7
	445800	AA126419	Hs.301632	ESTs	7.7
	424636	AA453734	Hs.10158	ESTs	7.7
	432134	AB16762	Hs.122583	Homo sapiens cDNA: FLJ21934 fs, clone H	7.7
	446873	A1564436	Hs.30724	ESTs	7.7
	400753	AA535662	Hs.50094	Homo sapiens mRNA; cDNA DKF7p434005 t5 f	7.7
	436051	A1248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fs, clone C	7.7
40	442028	A1238437	Hs.48945	ESTs	7.7
	442760	BE012897	Hs.10097	ESTs, Weakly similar to KIAA1205 protein	7.7
	442152	R39246	Hs.239566	Homo sapiens cDNA FLJ13495 fs, clone PL	7.7
	427944	AA417878	Hs.48401	ESTs, Weakly similar to ALU8_HUMAN ALU 5	7.7
	414646	AA363776	Hs.501	CD48 antigen (B-cell membrane protein)	7.6
45	407634	AWG16568	Hs.307280	ESTs, Highly similar to AF241831 f intra	7.6
	416372	AA311633	Hs.84316	restoration protein A1 (FMO)	7.6
	434666	AF151103	Hs.112259	T cell receptor gamma locus	7.6
	442432	BE093659	Hs.38178	Homo sapiens cDNA: FLJ23468 fs, clone H	7.6
	408418	AW963857	Hs.44743	KIAA1435 protein	7.6
	418805	A182920	Hs.227513	ESTs	7.5
	425354	U50207	Hs.155535	complement component 3a receptor 1	7.5
	408743	AL110246	Hs.47367	hypothetical protein from EUROMIMAGE 78.36	7.5
	444836	A1569825	Hs.173504	ESTs, Weakly similar to JC5238 galactosyl	7.5
55	421810	A102718	Hs.108530	hypothetical protein FLJ10855	7.4
	432753	NM_014075	Hs.278915	PRKQ553 protein	7.4
	420061	AW024937	Hs.29410	ESTs	7.4
	432865	AF33709	Hs.152484	ESTs	7.4
	419570	AW973068	Hs.182553	ESTs	7.4
	430172	AA468591	Hs.161885	ESTs	7.4
	446343	AW771414	Hs.8314	ESTs	7.4
	424125	M31668	Hs.1735	inhibin, beta B (activin B beta polypep	7.4
	453818	BF256832	Hs.10711	Homo sapiens cDNA FLJ13445 fs, clone PL	7.4
	447046	AA326187	Hs.17170	G-protein-coupled receptor 4	7.4
	410577	X91911	Hs.64636	glioma pathogenesis-related protein	7.3
	452240	A591147	Hs.61232	ESTs	7.3
	450375	AA098447	Hs.8850	a disintegrin and metalloproteinase doma	7.3
	422631	BE218918	Hs.118163	hypothetical protein FLJ10888	7.3
	450205	A1215748	Hs.11356	ESTs	7.3
	437212	A1765021	Hs.210775	ESTs	7.3
	440193	AW002312	Hs.7037	pallid (mouse) homolog, pallidin	7.2
70	417022	NM_014737	Hs.80905	Ras association (RACGAP-5) domain fam	7.2
	451818	AB119018	Hs.80337	gltb3401.x1 NCL_CGAP_K65 Homo sapiens	7.2
	453013	AA031407	Hs.2540	gltb315g12.r1 Scarsa_pregnant_alumna_NH4	7.2
	430105	X70267	Hs.26770	cholinergic receptor, nicotinic, alpha p	7.2
75	451621	AB179148	Hs.78045	nitric acid binding protein 7, brain	7.2
	442438	AA495998	Hs.78045	gltb32803.x1 NCL_CGAP_K65 Homo sapiens	7.2
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	7.2
	407305	AA715284	Hs.35403.1	NCL_CGAP_B5 Homo sapiens	7.2
	452814	AB027790	Hs.55016	hypothetical protein FLJ21935	7.2
	426028	NM_001110	Hs.122828	a disintegrin and metalloproteinase doma	7.2
	443452	A1054890	Hs.171176	ESTs	7.2
80	422060	R20953	Hs.75613	CD36 antigen (collagen type I receptor,	7.2
	434096	AW657958	Hs.75825	pleomorphic adenoma gene-like 1	7.1
	443616	A1033516		gltb3405c.x1 Scarsa_fetus_kidney_Nb2H8	7.1

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5	458725	AW970192	Hs.171942	ras responsive element binding protein 1	7.1
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	7.1
	412783	BE276738	Hs.74578	DEADH (Asp-Glu-Ala-AspHis) box polypep	7.1
	435664	A0302007	Hs.209819	ESTs	7.0
	431708	AW69136	Hs.108873	ESTs	7.0
10	426501	AW043782	Hs.293616	ESTs	7.0
	453548	AL079993	Hs.75442	albumin	7.0
	426555	AW971980	Hs.62402	p21Cdc42/Rac1-activated kinase 1 (yeast	7.0
	412450	AWR03564	Hs.286839	Homo sapiens cDNA: FLJ22528 fls, clone H	7.0
	431556	AF016028	Hs.260039	surfactin (Kcs onco gene associated gene	6.9
15	420018	U56387	Hs.94376	propionin convertase subtilisin/kallikrein 1	6.9
	418986	AI123555	Hs.81796	ESTs	6.9
	432860	AT34116	Hs.136355	ESTs	6.9
	427472	AA522539	Hs.131250	transposon-derived Buxs3 transposase-1	6.9
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.9
20	414737	AI160386	Hs.125087	ESTs	6.9
	420479	AW183695	Hs.186572	ESTs	6.9
	437656	NM_000246	Hs.30075	MHC class II transactivator	6.9
	414217	AJ305298	Hs.279838	Homo sapiens cDNA: FLJ21855 fls, clone L	6.9
	431870	AW449902	Hs.105500	ESTs	6.9
25	415788	AW628686	Hs.78851	KIAA0217 protein	6.9
	432066	AI299658	Hs.237825	signal recognition particle 72kD	6.9
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21559 fls, clone C	6.8
	401539				6.8
	412782	AI195211	Hs.173044	ESTs	6.8
30	416058	LI08955	Hs.78995	MADS box transcription enhancer factor 2	6.8
	437205	AI110232		gbrHomo sapiens mRNA; cDNA DKFZp64020271	6.7
	458814	AA498957	Hs.170061	ESTs	6.7
	452106	AI141031	Hs.21342	ESTs	6.7
	413249	AF167160	Hs.75251	DEADH (Asp-Glu-Ala-AspHis) box binding	6.7
35	420910	AL004437	Hs.100522	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	6.7
	445527	W05694	Hs.83286	ESTs	6.7
	424063	NM_002019	Hs.138571	lms-related tyrosine kinase 1 (vascular	6.7
	421977	W94157	Hs.110185	ribosomal protein L26 homolog	6.7
	430280	AA361253	Hs.237868	interleukin 7 receptor	6.7
40	415989	A267700	Hs.111123	ESTs	6.7
	418026	BE379277	Hs.83213	fatty acid binding protein 4, adipocyte	6.6
	425295	AA431365	Hs.37251	ESTs	6.6
	438619	AB032773	Hs.0341	TU1281-TV protein	6.6
	424916	AW867440	Hs.23096	ESTs	6.6
45	429697	AW296451	Hs.24505	ESTs	6.6
	408741	M73720	Hs.546	carboxypeptidase A3 (musl cell)	6.6
	403549				6.6
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	6.6
	435798	BE395289	Hs.12720	olig IE-transporter	6.6
50	447217	BE465754	Hs.17778	neurospilin 2	6.6
	453070	AK001465	Hs.31575	SEC8, endoplasmic reticulum translocon	6.6
	410276	A1554545	Hs.08301	ESTs	6.6
	435391	AA704693	Hs.58394	ESTs	6.6
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11543 fls, clone HE	6.5
55	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	6.5
	448789	BE339108	Hs.22051	Homo sapiens mRNA; cDNA DKFZp4340119 (tr	6.5
	425331	AW962128	Hs.22245	gbrEST174201 MAGC resequencing, MAGC Homo	6.5
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fls, clone PL	6.5
	444880	AW118683	Hs.154150	ESTs	6.5
60	434131	A185875	Hs.143659	ESTs	6.5
	446658	A1440137	Hs.164989	ESTs	6.5
	408150	BE620274	Hs.43112	Homo sapiens mRNA; cDNA DKFZp434B1820 (f	6.5
	403790				6.5
	417129	AI381800	Hs.143275	Homo sapiens cDNA FLJ13233 fls, clone OV	6.5
65	452119	AE655378	Hs.33461	ESTs	6.4
	437336	BE140398	Hs.21621	hypothetical protein DKFZp7620076	6.4
	458946	AA009116	Hs.42311	ESTs	6.4
	452110	T47667	Hs.28005	Homo sapiens mRNA; cDNA DKFZp564G2463 (f	6.4
	445318	AW238021	Hs.108788	ESTs, Weakly similar to zeste (D.melanog	6.4
70	403308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.4
	402474				6.4
	430712	AW044647	Hs.196284	ESTs	6.4
	415299	AA276330	Hs.83968	integin, beta 2 (antigen CD18 (p55), ly	6.4
	432683	AW935441	Hs.10475	ESTs	6.4
75	423764	AF054589	Hs.132733	ESTs	6.4
	409571	AA504249	Hs.187585	ESTs	6.4
	401600	BE247276	Hs.151787	US snRNP-specific protein, 116 kD	6.4
	415076	NM_008057	Hs.77890	guanylate cyclase 1, soluble, beta 3	6.4
	432925	AA878324	Hs.193734	ESTs	6.4
80	427528	AAJ07143	Hs.179565	mitochondosome maintenance deficient (S,	6.4
	453994	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fls, clone NT	6.4
	430335	D80007	Hs.239499	KIAA0185 protein	6.3
	453370	AA76523	Hs.182356	ESTs, Moderately similar to translation	6.3
	421327	AA837295	Hs.186802	ESTs	6.3
	450554	AJ245587	Hs.25275	Kruppel-type zinc finger protein	6.3
	413497	BE177661		gbrRC1-HT0598-020300-011 h02 HT0598 Homo	6.3
	445279	RA1900	Hs.22245	ESTs	6.3

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5	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	6.3
	421252	AA765930	Hs.130878	ESTs	6.3
	432140	AK000044	Hs.278688	hypothetical protein FLJ100397	6.3
	434203	BE263677	Hs.283558	hypothetical protein PRO10855	6.2
	419436	AA971639	Hs.15036	ESTs, Highly similar to AF161358.1 HSPCO	6.2
10	430287	AW182459	Hs.125759	ESTs, Weakly similar to tumor suppressor	6.2
	409690	W45353	Hs.94942	ESTs, Highly similar to ATF3 [H.sapiens]	6.2
	420101	AV505029	Hs.95180	Homo sapiens mRNA; cDNA DKFZp434A205 (l	6.1
	425809	AZ49107	Hs.769901	ESTs	6.1
	417259	AV903838	Hs.81900	chondroitin sulfate proteoglycan 2 (vers	6.1
15	448030	N30714	Hs.20161	HDCME31P protein	6.1
	442571	C06338	Hs.165454	ESTs	6.1
	421702	AF133339	Hs.102506	eukaryotic translation initiation factor	6.1
	415558	AA85143	Hs.125719	ESTs	6.1
	408042	AL049233	Hs.42244	Homo sapiens mRNA; cDNA DKFZp564A023 (f	6.1
20	438086	AA306519	Hs.301167	Homo sapiens cDNA: FLJ21545 fls, clone C	6.1
	427390	AA42163	Hs.256231	Homo sapiens cDNA: FLJ23111 fls, clone L	6.1
	440749	W72235	Hs.7332	Homo sapiens mRNA; cDNA DKFZp61E0323 (f	6.0
	448822	BE149845	Hs.289038	Homo sapiens cDNA: FLJ20994 fls, clone C	6.0
	434806	AA382523	Hs.105689	ESTs	6.0
25	435185	AA689490	Hs.289109	dimethylarginine dimethylaminohydrolase	6.0
	452225	AL339743	Hs.28514	Homo sapiens mRNA; cDNA DKFZp434H092 (f	6.0
	432415	T16971	Hs.289014	ESTs	6.0
	436345	AA873008	Hs.121572	ESTs	6.0
	439451	AF096270	Hs.278554	heterochromatin-like protein 1	6.0
30	434674	AA531679	Hs.136955	ESTs	6.0
	429653	NM_005955	Hs.211981	metal-regulatory transcription factor 1	6.0
	446822	AB037794	Hs.18229	KIAA1373 protein	6.0
	423590	AV952412	Hs.65874	ESTs	6.0
	440426	AV798295	Hs.123218	ESTs	6.0
35	423246	AL119114	Hs.22102	ESTs	5.9
	420982	AV575180	Hs.100729	KIAA0622 protein	5.9
	435008	AF150262	Hs.162898	ESTs	5.9
	420052	AA814043	Hs.88945	ESTs	5.9
	444484	AA022126	Hs.11260	hypothetical protein FLJ11264	5.9
40	410193	ALJ13292	Hs.59757	zinc finger protein 281	5.9
	450534	AV570189	Hs.25132	KIAA470 gene product	5.9
	440146	AV014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fls, clone K	5.9
	425361	AA359533	Hs.132221	Homo sapiens cDNA: FLJ21401 fls, clone MA	5.9
	428174	BE74450	Hs.154078	KIAA261 protein	5.9
45	458287	AA987596	Hs.12867	ESTs	5.9
	433793	AV975999	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	5.8
	443278	W47481	Hs.293798	ESTs	5.8
	419983	W05696	Hs.94020	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	5.8
	410361	BE391804	Hs.62361	guanylate binding protein 1, interferon-	5.8
50	415714	NM_002290	Hs.78672	laminin, alpha 4	5.8
	421889	N87820	Hs.106826	hypothetical protein	5.8
	431176	AA028984	Hs.250662	ESTs	5.8
	443837	AA94825	Hs.9894	spindle pole body protein	5.8
	410623	AV958932	Hs.293833	ESTs	5.8
55	421298	AV1172431	Hs.13012	ESTs	5.8
	443652	AV029507	Hs.161102	ESTs	5.8
	433043	W57554	Hs.125019	ESTs, Highly similar to KIAA0896 protein	5.8
	439444	A277652	Hs.54578	ESTs	5.7
	428698	AA852773	Hs.297539	ESTs, Weakly similar to T17344 hypotheti	5.7
60	411928	AA888624	Hs.19121	actin-related protein complex 2, alpha	5.7
	442242	AV647808	Hs.90424	Homo sapiens cDNA: FLJ23285 fls, clone H	5.7
	417315	AA080042	Hs.105450	ribosomal protein S24	5.7
	422544	AA018259	Hs.118140	KIAA0716 gene product	5.7
	412584	XS4870	Hs.74085	Alu segment on chromosome 12 (unique) 24	5.7
65	433605	AV564027	Hs.15331	Homo sapiens MY-REN-35 antigen mRNA, par	5.7
	419425	BE778367	Hs.63190	KIAA0141 gene product	5.7
	457292	AI921270	Hs.214178	Homo sapiens cDNA: FLJ14251 fls, clone OV	5.7
	457100	AA411878	Hs.48401	ESTs, Weakly similar to ALUS_HUMAN ALU S	5.7
	436995	AI160115	Hs.118112	ESTs	5.7
70	426283	NM_033837	Hs.160139	lysine aminase (L-lysine hydrolase)	5.7
	441518	AV161697	Hs.294150	ESTs	5.7
	448807	AV571940	Hs.7549	ESTs	5.7
	449656	AA002008	Hs.188633	ESTs	5.7
	435211	AV89347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	5.7
75	430440	XS2599	Hs.2561	neuro growth factor, beta polypeptide	5.7
	413561	BE242639	Hs.75425	ubiquitin associated protein	5.7
	441633	AV958544	Hs.112242	ESTs	5.7
	427080	AA396118	Hs.97579	ESTs	5.6
	418260	U29926	Hs.83918	adenosine monophosphate deaminase (iso	5.6
80	432267	AA000872	Hs.274227	Homo sapiens cDNA: FLJ10010 fls, clone HE	5.6
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet)-ac	5.6
	430253	AK001514	Hs.236844	hypothetical protein FLJ10852	5.6
	455447	AF212223	Hs.259109	hypothetical protein P15-2	5.6
	434623	AB023163	Hs.4014	KIAA0946 protein; Hoxan13n interacting	5.6
	420642	AK001520	Hs.99545	Homo sapiens cDNA: FLJ10658 fls, clone NT	5.6
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.6
	420875	AB55727		g0 B5F12.x1 NC_CGAP_GCS Homo sapiens	5.6

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422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	5.6
452046	AB018345	Hs.27657	KIAA0802 protein	5.6
408911	AW294772	Hs.98321	Homo sapiens cDNA FLJ114103 fs, clone MA	5.6
414844	AA296874	Hs.17494	deoxyguanosine kinase	5.6
414698	U13632	Hs.79351	potassium channel, subfamily K, member 1	5.6
430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	5.6
430339	W28608	Hs.238625	integral membrane protein 2B	5.6
420153	N22120	Hs.75277	hypothetical protein FLJ13910	5.6
420892	AW675076	Hs.172599	nuclear phosphoprotein similar to S. cer	5.5
441568	AU33322	Hs.127176	ESTs	5.5
414575	H11257	Hs.295323	ESTs	5.5
419529	U90268	Hs.93810	cerebral cavernous malformations 1	5.5
438613	C25569	Hs.243122	hypothetical protein FLJ13067 similar to	5.5
453064	RA0334	Hs.301395	Homo sapiens cDNA: FLJ21264 fs, clone C	5.5
433409	AZ278802	Hs.25561	ESTs	5.5
407094	AF000574	Hs.22405	leukocyte immunoglobulin-like receptor,	5.5
425234	AW152225	Hs.165909	ESTs	5.5
447644	AW951622	Hs.108546	Homo sapiens cDNA FLJ12534 fs, clone NT	5.5
411853	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	5.5
446534	A307356	Hs.175226	ESTs	5.5
452355	N54926	Hs.29202	G-protein-coupled receptor 34	5.5
434715	BE005346	Hs.116410	ESTs	5.5
440486	BE243813	Hs.1212	hypothetical protein PP1044	5.5
444826	AW167613	Hs.248	mitogen-activated protein kinase kinase	5.5
419172	AW338626	Hs.22120	ESTs	5.4
444831	AW552066	Hs.75131	general transcription factor IIA	5.4
413940	AK33205	Hs.15914	ESTs	5.4
410480	R97457	Hs.63884	cadherin 13, (H-cadherin (heart))	5.4
447072	D61594	Hs.17279	lysosomal sulfotransferase 1	5.4
434261	AF129755	Hs.117772	ESTs	5.4
453382	U23752	Hs.32864	CRY (sex determining region Y)-box 11	5.4
445175	AW62981	Hs.300846	ESTs	5.4
411213	AA678938	Hs.69285	neuropilin 1	5.4
412530	AA765268	Hs.265273	Homo sapiens cDNA FLJ13346 fs, clone Ov	5.4
422667	H25642	Hs.133471	ESTs	5.4
434064	AL450445	Hs.180758	hypothetical protein PR00082	5.4
429688	BE245169	Hs.211610	CLUG triplet repeat, RNA-binding protein	5.4
452060	W29980	Hs.153612	ATP-binding cassette, sub-family F (GCN2)	5.4
419093	AB040554	Hs.112885	ESTs	5.4
436287	AW450538	Hs.180115	ESTs	5.4
406257				5.4
431154	AW971228	Hs.290259	ESTs	5.4
415511	A1732617	Hs.182362	ESTs	5.4
419175	AW270037	Hs.179507	KIAA0779 protein	5.3
494117	BE410100	Hs.40388	receptor-related protein complex 1, sigma	5.3
423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fs, clone C	5.3
409995	AW960597	Hs.30184	ESTs	5.3
414911	NM_000107	Hs.77602	damage specific DNA binding protein 2 (4	5.3
455716	BE012633		gln-DNA-BTG047:280100-099+07 BT0407 Homo	5.3
430598	AK001164	Hs.247112	hypothetical protein FLJ10902	5.3
419985	H66373	Hs.15973	ESTs, Highly similar to BA393116.3 (h-sa	5.3
428753	AW938252	Hs.192527	hypothetical protein FLJ20251	5.3
423059	NM_062837	Hs.123641	protein tyrosine phosphatase, receptor I	5.3
404176				5.3
431475	AI567869	Hs.287316	ESTs	5.3
406825	Y13647	Hs.119597	stearoyl-CoA desaturase (delta-9-desatur	5.3
405475				5.3
430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	5.3
446183	AA354991	Hs.14222	Homo sapiens mRNA: cDNA DKFZp761P019 (fr	5.3
417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	5.3
433029	NM_014322	Hs.279926	opsin 3 (encephalopodin)	5.3
442837	AU22082	Hs.50492	ESTs	5.3
437140	AA312799	Hs.283689	activator of CREM in testis	5.3
409899	AW361666	Hs.49500	KIAA0746 protein	5.3
417355	D13168	Hs.82002	endothelin receptor type B	5.3
407361	AA744622	Hs.292645	ESTs, Weakly similar to ALUS_HUMAN:ALU S	5.3
437734	AA983951	Hs.180284	ESTs	5.3
452234	AW084176	Hs.223296	ESTs	5.3
423057	AW961597	Hs.130816	ESTs	5.3
439593	BE073597	Hs.124883	ESTs	5.3
444501	AJ003816	Hs.150819	ESTs	5.3
416406	DB6961	Hs.79299	ipoma HMICG fusion partner-like 2	5.2
427164	AB037721	Hs.173871	KIAA1300 protein	5.2
416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine poly	5.2
445212	AA745568	Hs.292645	gln:BT047+11 NCBI:GAP:CLT1 Homo sapiens	5.2
412420	AL036568	Hs.73853	bone morphogenetic protein 2	5.2
416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lym	5.2
406615	AA833930	Hs.268036	RNA isopentenylpyrophosphate transferas	5.2
451418	BE387790	Hs.28369	hypothetical protein FLJ20287	5.2
425322	U63030	Hs.155637	protein kinase, DNA-activated, catalytic	5.2
451196	AW983959	Hs.232042	ESTs	5.2
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	5.2
428024	AA593731	Hs.75613	CD36 antigen (collagen type I receptor,	5.2

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	426593	AW207440	Hs.155973	degenerative spermatocyte (homolog Dros	5.2
	451149	AL047595	Hs.10283	ESTs	5.2
	429458	BE161832	Hs.252689	ESTs	5.2
5	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor 1	5.2
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ2037 fs, clone CO	5.2
	417696	BE241624	Hs.62401	CD68 antigen (p80, early T cell activat	5.2
	442991	BE281238	Hs.8856	hypothetical protein FLJ20424	5.2
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	5.2
10	438955	A227786	Hs.164875	ESTs	5.1
	438552	AS21310	Hs.283365	ESTs, weakly similar to ALUS_HUMAN ALU S	5.1
	424856	U52014	Hs.153527	Homo sapiens pTMS mannin-like transpo	5.1
	445563	AW873606	Hs.149006	ESTs	5.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA: cDNA DKF2p566C1723 (I	5.1
	426567	AK000812	Hs.58574	similar to proline-rich protein 48	5.1
15	429530	AL131101	Hs.59508	Homo sapiens mRNA: cDNA DKF2p434O0921 (I	5.1
	455510	AA422025	Hs.143640	ESTs, weakly similar to hyperpolarizatio	5.1
	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	5.1
	438146	Z35842	Hs.57548	ESTs	5.1
	422430	AF112481	Hs.128501	RAD54, S. cerevisiae; homolog of, B	5.1
20	421533	AF121960	Hs.106250	sorting nexin 10	5.1
	447197	R36075	Hs.158875	glyh88001 s1 Soares placenta Nb2HP Homo	5.1
	436943	AA773838	Hs.5353	craspase 10, apoptosis-related cysteine p	5.1
	456210	NA5129	Hs.152875	ESTs	5.1
	411853	RE2845	Hs.273789	ESTs	5.1
25	432331	W27862	Hs.274368	Homo sapiens mRNA: cDNA DKF2p566H524 (I	5.1
	414566	AF002020	Hs.75918	Mannmann-Pick disease, type C1	5.1
	426822	W78950	Hs.228523	ESTs	5.1
	444269	AI990348	Hs.146220	ESTs	5.1
	437204	AL110216	Hs.12285	ESTs	5.1
30	443180	R15875	Hs.70945	ESTs	5.0
	431510	AA580682	Hs.112264	ESTs	5.0
	445312	BE087853	Hs.120601	cd-DNA-BT0681-200400-181-NOS BT0681 Homo	5.0
	448870	AI672487	Hs.15423	hypothetical protein HDGM04P	5.0
	430462	AI584156	Hs.105640	ESTs	5.0
35	457452	AW972675	Hs.1364766	MAGE resequences, MAGL Homo	5.0
	426387	NM_007018	Hs.57437	centrosomal protein 1	5.0
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.0
	426874	N67325	Hs.247132	ESTs	5.0
	415746	AW687943	Hs.127216	Homo sapiens cDNA FLJ13465 fs, clone PL	5.0
40	434237	AF119308	Hs.235516	hypothetical protein PRO2295	5.0
	410274	AA381807	Hs.51762	hypoxia-inducible protein 2	5.0

TABLE 35B:

Key:	CAT number:	Accession:	Unique Eos probaset identifier number
			Gene cluster number
			Genbank accession numbers
50	411537	1266219_1	AW876624
	413497	1733771_1	BE177661 H06215 BE144709 BE144829
	420625	196789_1	AI855727 AI687881 AI02122 AA810877 228718 T16711 AA651703 AL047264 BE000621 R68736 AW992695 AI768764 AW271284 AW914653
			AC088551 AW050146 R93609 AW467031 A099966 AI371871 AI126182 AI564756 AI361460 AI358914 AI419231 AI439733 R87059 AA528054
			AW088970 AW008695 RB6842 AI719136 R97752 AW196262
55	425331	250109_1	AW92128 AA353353 AA427363
	437205	43463_1	AL110232 N94765
	438966	467436_1	AW979074 AA834841 AA828650
	442438	542469_1	AA985998 AB916584 RB1761 T77332 F07756 F08149 F07547
	443161	561385_1	AC083316 AI344631 A281853
	446312	671114_1	BE087853 AI296184
60	447197	711623_1	R36075 AI366546 R36167
	447974	745643_1	R76885 AI453674 R77049
	448212	755099_1	AI75658 AW969013
	451818	887271_1	AI815018 R08492 W27615
65	453013	94390_1	AA031407 N85751 AW974119 AA031408 AA572965
	455715	1352655_1	BE070263 BE070195 BE070265 BE070202 BE070233 BE070399 BE070203
	457452	133381_1	AW972675 AA541366 AA523039
	407305	312857	AA715294

TABLE 35C:

Key:	Ref:	Strand	Unique number corresponding to an Eos probaset
			Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
			sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
			Indicates DNA strand from which exons were predicted.
			Indicates nucleotide positions of predicted exons.
75	401539	8072433	Minus 62026-62608
	402474	7547175	Minus 5326-53628,55755-55920,57530-5775
	403549	8081591	Minus 137150-137362
	403713	6512831	Minus 152769-153155
80	403790	8084957	Minus 87826-87947,89835-90002
	404176	9931122	Plus 52685-52800
	405257	7326130	Plus 73121-73273

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405475 1931025 Plus 1548-1702

TABLE 36A: ABOUT 169 GENES UP-REGULATED IN KIDNEY CANCER

Table 36A lists about 169 genes up-regulated in kidney cancer compared to normal kidney that are likely to be extracellular or cell-surface proteins. These were selected as for Table 35A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. Ig, Fc, Ig, 7tm domains). Predicted protein domains are noted.

Key: Unique Ecos protease identifier number
 ExAcc: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor to normal tissue

Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
424704	A1263263	Hs.152096	cytochrome P450	SS,p150	40.9
426559	AB001914	Hs.170414	paired basic am	TM,Peptidase_S8,P	35.6
458079	A1796570	Hs.54277	EST	TM	34.6
446921	AB012113	Hs.16530	small inducible	SS,Ig	26.9
452401	NM_007115	Hs.29352	tumor necrosis	TM,SS,Tink,CUB	24.8
414821	M63635	Hs.77424	Fc fragment of	TM,SS,Ig	23.4
414812	X72755	Hs.73767	monokine inducible	SS,Ig	22.1
425471	M22440	Hs.170309	transforming pr	TM,SS,EGF	21.3
445523	NM_000579	Hs.54443	chemokine (C-C	TM,7tm,1	20.7
428227	AA321649	Hs.2248	small inducible	IL8	19.6
456804	AA421645	Hs.135951	caveolin 2	TM,Caveolin	17.5
411642	NM_014032	Hs.71132	neurigin 1	TM,SS,Colesterolase	17.2
427581	NM_014788	Hs.175703	KIAA0179 gene p	TM	15.6
448520	AB002367	Hs.21355	doubecortin an	TM,kinase	14.8
417308	H60720	Hs.81892	KIAA0101 gene p	TM	14.8
421566	NM_003039	Hs.1325	early growth reg	TM	14.6
427603	BE242587	Hs.119651	hematopoietic	TM,JC-CP2H	14.4
425984	AW836277	Hs.165636	hypothetical pr	TM	14.2
432606	NM_002104	Hs.3065	granzyme K (ser	TM,SS,lypsin	14.1
458809	AW972512	Hs.20595	sin-3-associated	SS	13.7
446627	AW973016	Hs.15725	hypothetical pr	TM	13.6
452560	AK001335	Hs.31137	Homo sapiens cD	TM,N_Y_phosphatase	13.3
420552	AK000452	Hs.98806	hypothetical pr	TM,SS	13.0
425188	AK002022	Hs.155071	hypothetical pr	TM	12.6
419034	NM_002110	Hs.89555	hemopoietic cel	TM,kinase,SH2,SH3	12.3
442532	AA457211	Hs.8858	bromodomain arj	TM,bromodomain,PHD	12.3
434398	AA121098	Hs.3838	serum-inducible	TM,kinase,POLO_box	12.2
450506	NM_004460	Hs.418	fibroblast act	SS,DPFV_N_term,Peptidase_S9	12.1
425782	U56468	Hs.155025	cell growth reg	SS	12.0
425108	AA627037	Hs.165469	progranulin cell	TM,DFP12	11.9
450236	AW162998	Hs.24684	KIAA1376 protei	TM,SS	11.7
452838	U65011	Hs.30743	preterminality	TM	11.2
456780	BE242784	Hs.172159	acylglutamate cyc	TM,guanylate_cyc	11.1
415323	BE263352	Hs.949	neutrophil cyto	TM,SH3,TFR	11.0
423508	AW604297	Hs.127911	hepatitis A vir	TM,SS,Ig	11.0
408390	AF123050	Hs.44532	dubiquitin	TM,ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1	11.0
446410	AK000227	Hs.21126	hypothetical pr	TM	11.0
451277	AK031123	Hs.26176	hypothetical pr	TM	10.8
453165	S74727	Hs.32042	aspartylcarboxylase	SS,TB,EGF	10.8
418036	Z37976	Hs.83337	latent transfer	SS,TB,EGF	10.5
431512	BE270734	Hs.2795	lactate dehydro	TM,Ikh	10.3
433962	B09560	Hs.3610	KIAA0205 gene p	TM,SS	10.3
431211	M68949	Hs.5966	gap junction pr	TM,connexin	10.2
432579	AF043244	Hs.278439	nuclear prote	TM	10.0
439653	AW021103	Hs.6631	hypothetical pr	TM,SS	9.9
428682	NM_000346	Hs.2316	SRY (sex-determ	TM,HMG_box	9.8
410162	AF226563	Hs.56170	HSP90 B protein	SS,AFMYND	9.8
452431	U88879	Hs.29459	tol-like recep	TM,SS,TIRLR,RCCT	9.5
405121	AB028989	Hs.88500	mitogen activat	SS,vwa,vwd,TIL,Cys_invol,wvc	9.4
449626	NM_014253	Hs.23796	otz (odd Oct2n	SH2,EGF	9.4
427659	NM_014459	Hs.2105511	procalcitonin 1	TM,SS,calcitonin	9.2
427593	AL119796	Hs.174185	actinucleotide	TM,SS,Phosphodiester,Somatostatin_medi_B	9.1
407975	X89426	Hs.41716	endothelial cel	SS,IGFBP	8.9
413554	AA319146	Hs.75426	secretogranin 1	TM,SS,Granin	8.6
418653	A1750875	Hs.87409	thrombospondin	EGF,TSPN,bsp_1,bsp_3,wvc	8.6
427672	AW142065	Hs.5741	fibronectin-protei	TM,heparin_1,oxidized_hsp,CytL_reductase	8.6
430268	AK000737	Hs.237480	hypothetical pr	TM,SS	8.5
447850	AB018208	Hs.19822	SEC24 (S. cerev	TM	8.4
435717	AF227503	Hs.105794	UDP-glucose 4-ep	TM,Glyco_transfer_8	8.3
433376	A245361	Hs.74122	caspase-4, apop	TM,ICE_p10,ICE_p10,CARD	8.2
419490	NM_005144	Hs.90708	granzyme A (gra	TM,SS,lypsin	8.2
453033	AA325869	Hs.31463	KIAA0281 gene p	TM	8.2
432328	A1572739	Hs.155471	6-phosphogluco	TM,BPFX,PGAM	7.9
431719	BE435980	Hs.75498	small inducible	SS,Ig	7.9
412448	L12964	Hs.72055	tumor necrosis	TM,SS,TNFR,c6	7.9
424247	X14008	Hs.234734	lysosomal (renal	SS,Iys	7.8
421991	NM_014918	Hs.110498	KIAA0290 protei	SS	7.8
400793	AA635062	Hs.50094	Homo sapiens mR	TM,BIR,CARD,JC3H4	7.7

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414646	AA353778	Hs.901	CD48 antigen (B	TM,lg	7.6
418372	AA311833	Hs.84318	replication pro	TM	7.6
408418	AW963897	Hs.44743	KIAA1435 prot	TM,WD40_FYVE	7.6
423534	UK0207	Hs.158935	complement comp	TM,Tim_1	7.5
432753	NM_014075	Hs.278915	PROS1 protein	TM,kinase	7.4
447046	AA326187	Hs.17170	G-protein-coupl	TM,Tim_1	7.4
410577	X91911	Hs.64639	glioma pathogen	TM,SCP	7.4
422631	BE218919	Hs.118793	hypothetical pr	TM	7.3
417022	NM_014737	Hs.80905	Ras association	TM,RA	7.2
430105	X70297	Hs.2540	cholesterol me	TM,nour_chan	7.2
451621	A0879148	Hs.26770	fatty acid bind	TM,SS,lipocalin	7.2
415138	C18356	Hs.78045	tissue factor p	Kunitz_BPTI,G-gamma	7.2
426028	NM_001110	Hs.172628	a disintegrin a	TM,SS,disintegrin,Proteolysin	7.2
434095	AW962658	Hs.75825	plasmaoncytic ad	TM,zf-C2H2	7.1
425423	NM_012446	Hs.168833	single-stranded	TM	7.1
417283	BE276738	Hs.74578	DEAD(H) (Asp-Glu	TM,dsm,helicase_C	7.1
431556	AF016028	Hs.260039	sarcospan (Kras	TM	6.9
420018	U55387	Hs.54376	proprotein conv	TM,SS,Peptidase_S8,P	6.9
444042	NM_004915	Hs.10237	ATP-binding cas	TM,ABC_tran	6.9
432665	NM_000246	Hs.3076	MHC class II tr	TM,LRR	6.9
430066	A0236659	Hs.237825	signal recognit	TM,TPR	6.9
401539				TM,SS,zf-B_box,zf-C3HC4,Lysyl_oxidase	6.8
419058	L08895	Hs.78995	MADS box transc	TM,SRF1T	6.8
413249	AF167160	Hs.75251	DEAD(H) (Asp-Glu	TM,SAP	6.7
424063	NM_002019	Hs.139871	trms-related tyr	TM,SS,kinase,Ig	6.6
418026	BE379727	Hs.83213	fatty acid bind	TM,SS,lipocalin	6.6
438619	AB032773	Hs.6341	TUJ1B1-LY prote	TM	6.6
408741	M03720	Hs.646	carboxypeptid	SS,Zn_carbOpept,Proper_M14	6.6
403549				TM,kinase	6.6
435798	BE396289	Hs.12720	eIF-4E-transport	TM	6.6
435070	AK001485	Hs.31575	SEC63, endoplasm	TM,SS,DnaJ	6.6
452802	BE245374	Hs.27842	hypothetical pr	TM,SS,Acyltransferase	6.6
437396	BE140396	Hs.21621	hypothetical pr	TM	6.4
402474				TM,Peptidase_C1	6.4
401800	BE347275	Hs.151787	U5 snRNP-specif	TM,SS,HECT	6.4
415076	NM_000857	Hs.77890	guanylate cycl	TM,guanylate_cyc	6.4
403336	D80007	Hs.239499	KIAA0185 prot	TM,S1	6.3
434203	BE262677	Hs.283558	hypothetical pr	TM	6.2
430287	AW182459	Hs.125799	EGT4, Weakly si	TM,SS	6.2
417259	AW028638	Hs.81800	chondroin sul	TM,Tim,lecfin_c,sushi,EGF,Ig	6.1
421202	AF193339	Hs.102506	eukaryotic tran	TM,SS	6.1
452235	A1039743	Hs.28514	Homo sapiens snR	TM	6.0
429563	NM_005955	Hs.211581	metal-regulator	TM,zf-C2H2	6.0
444844	AK002126	Hs.11280	hypothetical pr	TM	5.9
410193	AJ132592	Hs.559767	zinc finger pro	TM,zf-C2H2	5.9
425381	AA356933	Hs.132221	Homo sapiens cD	TM	5.9
410381	BE391804	Hs.62861	guanylate bindi	TM,SS,GBP	5.9
415714	NM_002290	Hs.78672	laminin, alpha	TM,SS,laminin,G_laminin_EGF	5.8
421889	N07920	Hs.106826	hypothetical pr	TM,SS,PHD	5.8
443837	A0984625	Hs.9884	spindle pole bo	SS	5.8
422544	AB018259	Hs.118140	KIAA0716 gene p	TM	5.7
412584	X54870	Hs.74085	DNA segment on	TM,lecfin_c	5.7
410425	BE278587	Hs.83510	KIAA0741 gene p	TM	5.7
423025	NM_003937	Hs.169139	cytokeratin 16	TM	5.7
439440	X52589	Hs.2581	nerve growth fa	TM,SS,NGF	5.7
413551	BE242639	Hs.75425	ubiquitin assoc	TM,SS,UBA	5.6
418250	U23926	Hs.83918	adenosine Monop	TM,SS,deaminase	5.6
419839	U24577	Hs.93334	phospholipase A	SS	5.6
430253	AK001514	Hs.236844	hypothetical pr	TM	5.6
450447	AF212223	Hs.25010	hypothetical pr	TM,ANF_receptor,guanylate_cyc,kinase	5.6
414020	NM_001294	Hs.75703	small inducible	SS,I3	5.6
414844	AA296874	Hs.77494	deoxyguanosine	SS,dNK	5.6
416488	U33632	Hs.79351	potassium chan	TM	5.6
430512	AF182294	Hs.241578	U6 snRNA-associ	SS	5.6
419929	U90288	Hs.53810	cerebral cavern	SS,ank,Band_41	5.5
407084	AF000574	Hs.22405	Immunocyte immu	TM,SS,Ig	5.5
411653	AF070579	Hs.71168	Homo sapiens cI	TM,SS,Ab_trans	5.5
452895	N54928	Hs.29202	G-protein-coupl	TM,Tim_1	5.5
404886	BE243513	Hs.7212	hypothetical pr	TM	5.5
444825	AW167613	Hs.248	mitogen activat	TM,SS,kinase	5.5
440702	DE1584	Hs.17279	lysozyme	SS	5.5
453392	U23752	Hs.32964	SRY (sex determ	TM,HMG_box	5.4
411213	AA676939	Hs.65285	neurospilin 1	TM,CUB,F5_F8_type_C,MMAM	5.4
429888	BE245189	Hs.211610	CUG triplet rep	TM,urn	5.4
455267				TM	5.4
414811	NM_000107	Hs.77602	damage-specific	TM,WD40	5.3
430698	AK001764	Hs.247112	hypothetical pr	TM	5.3
428763	AW939252	Hs.192527	hypothetical pr	TM,SS	5.3
456525	Y13647	Hs.119597	stearoyl-CoA de	TM,Desaturase	5.3
455475				TM,sugar_tr	5.3
430180	AA331406	Hs.75456	A kinase (PRK)A	TM	5.3
417381	AF164142	Hs.82042	solute carrier	TM,can_ur_pernasee	5.3
433029	NM_014322	Hs.279526	opsin 3 (enkeph	TM,Tim_1	5.3

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417355	D13168	Hs.82002	endothelin receptor	TM,SS,7tm_1,zf-C3HC4	5.3
412420	AL035666	Hs.73853	bone morphogen	SS,TGF β ,propeptide,TGF-beta	5.2
416975	NM_004131	Hs.1051	granzyme B (gr)	SS,grysin	5.2
451418	BE307390	Hs.26369	hypothetical pr	TM	5.2
425322	U03630	Hs.155337	protein kinase	TM,MCM,FAT,FATC,PI3_KH_kinase	5.2
415910	U02050	Hs.78913	chemokine (C-X3)	TM,7tm_1	5.2
428593	AW207440	Hs.185973	degenerative sp	TM	5.2
417696	BE241624	Hs.82401	CD69 antigen (p)	TM,hectin_c	5.2
442991	BE201238	Hs.8896	hypothetical pr	TM	5.2
420467	AK000812	Hs.98974	similar to prel	TM	5.1
412676	NM_000165	Hs.74471	gap junction pr	TM,connexin	5.1
423430	AF112481	Hs.128501	RAD54, S. cerev	TM,SNF2_N_helicase_C	5.1
421633	AF121860	Hs.106269	sorting neuron 1	TM,PK	5.1
438943	AA773838	Hs.5365	caspase 10, apo	TM,ICE_p10,ICE_p20,DED	5.1
414696	AF020200	Hs.76918	Niemann-Pick d	TM,SS,Platched	5.1
446312	BE087853	Hs.	gb:OV1-BT0681-2	TM	5.0
420397	NM_007018	Hs.57437	cytoskeletal pro	TM	5.0
410274	AA381807	Hs.61762	heparin-induced	SS	5.0

20 TABLE 36B*
Pkey: Unique Eos probest identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

25	Pkey	CAT number	Accession
	446312	671114_1	BE087853 A1286184

30 TABLE 36C:
Pkey: Unique number corresponding to an Eos probe
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosomes 10, 22" Dunham, et al. (1999) *Nature* 402:489-495.
Strand: indicates DNA strand from which exons were predicted.
Nt_position: indicates nucleotide positions of predicted exons.

35	Pkey	Ref	Strand	Nt_position
	401539	B072433	Minus	62038-6308
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	403549	8081591	Minus	137150-137362
40	405257	7325010	Plus	73121-73273
	405475	1931025	Plus	1548-1702

45 TABLE 37A: ABOUT 280 GENES DOWN-REGULATED IN KIDNEY CANCER
Table 37a lists about 280 genes significantly down regulated in kidney cancer compared to normal kidney. These were selected as for Table 35A, except that the numerator and denominator were switched.

Pkey: Unique Eos probest identifier number
ExAccess: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of normal to tumor tissue

55	Pkey	ExAccess	UnigeneID	Unigene Title	R1
	425280	L47726	Hs.1870	phenylethanol hydroxylase	59.20
	446535	A1769774	Hs.209831	ESTs, weakly similar to ALU1_HUMAN ALU S	48.14
	440243	BE301029	Hs.226422	ESTs	42.54
	431657	A1345227	Hs.105448	ESTs, Weakly similar to S34037 hypotheti	40.14
	441120	A632015	Hs.164482	ESTs	34.56
	432468	AA551010	Hs.216640	ESTs	33.16
	416854	H40164	Hs.80296	Purkinje cell protein 4	32.06
60	438452	A1220911	Hs.288959	Homo sapiens cDNA: FLJ20920 fls, clone A	29.54
	414523	AU076533	Hs.76353	sorcin (or cysteine) proteinase inhibit	28.26
	430259	NM_016829	Hs.283021	chloride intracellular channel 5	28.16
	446795	A1797713	Hs.156471	ESTs	27.23
	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	26.98
65	432128	A127221	Hs.117037	ESTs	26.54
	448178	A478462	Hs.170789	ESTs	25.42
	438039	D14538	Hs.111	fibroblast growth factor 9 (gla-activat	23.99
	425770	A1948618	Hs.150178	ESTs	23.78
	428839	A1677796	Hs.82302	ESTs	23.04
70	431124	AF284221	Hs.59506	doublet exon and mab 3 related transcript	22.39
	413333	N74028	Hs.73257	fibroblast growth factor 1 (acidic)	22.28
	437575	AW954355	Hs.35529	ESTs	22.14
	451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKF Zp564C1416 (f	22.12
75	447350	A1375572	Hs.172634	ESTs	20.40
	425920	AL049977	Hs.152226	claudin 8	20.30
	446793	AI420213	Hs.149722	ESTs	19.48
	425075	AA506324	Hs.1852	acid phosphatase, prostate	19.10
	418318	U47132	Hs.84072	transmembrane 4 superfamily member 3	18.74
	420130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKF Zp751G02121 (18.56
80	441560	F13368	Hs.7988	Homo sapiens clone 23738 mRNA sequence	17.40
	434980	U02388	Hs.101	cytochrome P450, subfamily IV, polypept	17.30
	406667	M12523	Hs.75442	albumin	17.06
	414502	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKF Zp564B1264 (f	16.54

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	119021	MI5881	Hs.1137	urmodulin (uronic acid, Tamm-Horsfall gly	16.11
	119081	AW246890	Hs.65425	calbindin 1, (29kd)	15.84
	43324	R44013	Hs.164225	ESTs	15.68
5	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	15.46
	436637	AI783629	Hs.26796	ESTs	15.16
	448406	AW772268	Hs.21103	Homo sapiens mRNA; cDNA DKFZp6648076 (H	14.52
	434874	N62448	Hs.135506	ESTs	14.46
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	13.84
	453685	AL110309	Hs.153222	gb.DKFZp664L0278_r1364 (synonym: hbr2)	13.48
10	451939	U04545	Hs.27311	single-minded (Drosophila) homolog 2	13.24
	436624	T94257	Hs.5241	fatty acid binding protein 1, liver	13.05
	428931	AA594579	Hs.58967	ATPase, H(+)-transporting, lysosomal, no	12.97
	424823	NM_006226	Hs.153222	phospholipase C, epsilon	12.65
	431713	AK000388	Hs.267997	SH2G gene	12.66
15	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	12.36
	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	12.32
	425707	AF115402	Hs.11713	ET4-like factor 5 (ets domain transcript	11.52
	440504	AB948966	Hs.130017	ESTs, Weakly similar to VATX_HUMAN VACUO	11.66
	417275	XG5378	Hs.81849	parvalbumin	11.48
20	410929	H47233	Hs.30643	ESTs	11.40
	427167	A123607	Hs.99196	ESTs	11.34
	445591	A471806	Hs.148039	ESTs	11.30
	443622	AI911527	Hs.11805	ESTs	11.23
	438935	H40655	Hs.31564	ESTs	11.16
25	434841	AW075485	Hs.286049	phosphoserine aminotransferase	11.00
	415539	AF333881	Hs.72472	ESTs	10.84
	434981	H43545	Hs.289564	ESTs	9.76
	421688	AK000307	Hs.106825	hypothetical protein FLJ20300	9.74
	407280	AI241296	Hs.145609	ESTs	9.71
30	427969	NM_001963	Hs.2230	epidermal growth factor (beta-urogastron	9.61
	442446	AF733144	Hs.12861	ESTs	9.52
	442208	AA964002	Hs.45154	ESTs	9.51
	410467	AF102546	Hs.63531	dachshund (Drosophila) homolog	9.35
	425469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	9.32
35	418068	AW971155	Hs.253902	ESTs, Weakly similar to prol-4 hydroxy	9.31
	459147	H46143	Hs.110373	ESTs	9.20
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fs, clone H	9.16
	410247	AF181721	Hs.61345	RU2S	9.10
40	430593	AA744550	Hs.136345	ESTs	9.08
	457411	AW085981	Hs.130053	ESTs	8.99
	443790	NM_003500	Hs.9796	acyl-Coenzyme A oxidase 2, branched chain	8.92
	435024	AB63518	Hs.127743	ESTs, Weakly similar to V-ATPase G-subunit	8.76
	424551	AW023337	Hs.5422	glycoprotein M6B	8.74
45	450448	AI703356	Hs.169946	GATA-binding protein 3	8.50
	426255	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	8.31
	431820	AW410408	Hs.271167	L-pipecolic acid oxidase	8.28
	451027	AW519204	Hs.40808	ESTs	8.10
50	435623	R07856	Hs.16355	ESTs	8.06
	426669	AA449013	Hs.99203	ESTs	8.02
	438199	AW016531	Hs.122147	ESTs	7.94
	442176	AA983764	Hs.128910	ESTs	7.94
	450164	AA239923	Hs.32098	ESTs	7.86
55	448627	AW18475	Hs.7343	ESTs	7.85
	445779	AA253104	Hs.189267	ESTs	7.82
	407178	AA195551	Hs.104106	ESTs	7.68
	426966	AA83134	Hs.159125	ESTs	7.68
	445659	AW300508	Hs.149229	ESTs	7.50
60	403204				7.46
	448037	AW195634	Hs.170401	ESTs	7.30
	413689	AW452831	Hs.258811	osmometer protein complex, subunit gamma	7.26
	446863	AF720140	Hs.151079	ESTs	7.26
	424626	AA344368	Hs.126427	ESTs	7.25
	403381				7.16
65	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	7.12
	432102	AW015906	Hs.130730	ESTs	7.12
	442415	AA173892	Hs.7956	ESTs	7.10
	453698	AA037615	Hs.42746	ESTs	7.02
	415003	M11437	Hs.77741	kininogen	6.95
70	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	6.92
	457883	X89631	Hs.150318	ESTs	6.88
	409621	AF197672	Hs.46638	chromosome 11 open reading frame 8	6.76
	410781	AI375672	Hs.165028	ESTs	6.74
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.65
	441031	AI110684	Hs.7645	fibronogen, B beta polypeptide	6.65
75	451099	RS2795	Hs.25864	interleukin 13 receptor, alpha 2	6.64
	437553	AB25936	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHILOR	6.63
	445286	U03886	Hs.264	GS2 gene	6.54
	408427	AY194270	Hs.177236	EST	6.52
80	410442	U73424	Hs.10786	pepck(1) Coenzyme A carboxylase, beta p	6.46
	457901	J03258	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) re	6.46
	420205	AA256395	Hs.88156	ESTs	6.42
	441364	AW40466	Hs.126830	ESTs	6.36

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	475649	U03930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose)	6.34
	405373				6.32
	431372	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	6.32
5	440094	AI651558	Hs.270372	ESTs	6.27
	442764	AI762254	Hs.131122	ESTs	6.21
	424433	HW0607	Hs.9278	ESTs	6.20
	415025	AW070791	Hs.72307	ESTs	6.16
	428927	AA441837	Hs.90250	ESTs	6.16
10	439145	H67346	Hs.269187	ESTs	6.06
	424683	N87519	Hs.271796	ESTs	6.04
	415314	N88802	Hs.5422	glycoprotein M6B	5.94
	424025	AI701852	Hs.301296	ESTs	5.90
	445911	AI958587	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	5.89
	417332	AW972717	Hs.268402	Homo sapiens cDNA: FLJ25111 E8, clone C	5.86
15	440102	AI672443	Hs.131150	ESTs	5.84
	429509	AF002746	Hs.210863	cell adhesion molecule with homology to	5.82
	411656	AF106564	Hs.71346	neurofilament 3 (150kD medium)	5.82
	446224	AW440551	Hs.13308	ESTs	5.74
20	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	5.72
	438802	N34486	Hs.170504	ESTs	5.72
	412452	AA215731	Hs.283446	ESTs, Weakly similar to ALAT_HUMAN ALANI	5.70
	445911	AW418497	Hs.145583	ESTs	5.66
	446328	AA861527	Hs.243989	ESTs	5.66
25	424020	AF055084	Hs.153692	KIAA0686 protein	5.61
	410530	M25809	Hs.54173	ESTs, Highly similar to VAB1_HUMAN VACUO	5.60
	425907	AA365752	Hs.155965	ESTs	5.60
	426523	AW974540	Hs.50826	ESTs	5.58
	429918	AW873985	Hs.115303	ESTs	5.58
30	408369	R38438	Hs.182575	solute carrier family 15 (H+peptide tra	5.56
	446163	AA028880	Hs.25252	Homo sapiens cDNA FLJ13603 fs, clone PL	5.56
	427358	AW393020	Hs.20415	chromosome 21 open reading frame 11	5.52
	418504	BE159718	Hs.85335	Homo sapiens mRNA: cDNA DKFZp564D1462 (f	5.51
	440666	AA302550	Hs.192742	Homo sapiens cDNA FLJ12785 fs, clone NT	5.50
35	432286	AW327432	Hs.255843	ESTs	5.48
	451236	AI767406	Hs.207026	ESTs, Weakly similar to B95205 transcrip	5.46
	422746	NM_004884	Hs.119513	cyclopain 3	5.43
	416426	AA180256	Hs.210473	ESTs, Weakly similar to GEL3_HUMAN GELSO	5.37
	414449	AA557650	Hs.76152	deocatin	5.36
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.34
40	451635	TE3943	Hs.209715	ESTs, Weakly similar to ALUT_HUMAN ALU S	5.32
	424556	W16801	Hs.179	nuclear receptor subfamily 3, group C, m	5.22
	408604	D61408	Hs.21925	ESTs	5.18
	465676	AA287443		gb:z52c10.r1 NCL_CGAP_CCB1 Homo sapiens	5.18
45	433212	BE218049	Hs.121820	ESTs	5.16
	452114	U22687	Hs.8236	ESTs	5.14
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fs, clone K	5.14
	443005	AI027184	Hs.200918	ESTs	5.14
	408554	AA836381	Hs.7323	ESTs	5.12
50	438649	TE2070	Hs.291991	ESTs	5.10
	425343	AW000785	Hs.195480	exon 3	5.08
	452223	AA425467	Hs.8035	ESTs	5.10
	446925	AW974605	Hs.176669	ESTs	5.09
	407694	AW063476	Hs.275080	ESTs	5.08
55	414664	AA501775	Hs.66255	Homo sapiens HSPC311 mRNA, partial cds	5.06
	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodulin-depende	5.04
	435343	AW194962	Hs.195028	ESTs	5.04
	419150	T26618	Hs.89640	TEK tyrosine kinase, endothelial (venous	5.04
	442317	AI915599	Hs.129525	ESTs	5.02
60	404319				5.02
	433637	AW024214	Hs.135405	ESTs	4.92
	440205	T86950	Hs.188465	ESTs	4.83
	432029	D31628	Hs.2889	4-hydroxyphenylpyruvate dioxygenase	4.80
	453125	AW779544	Hs.115457	Homo sapiens cDNA: FLJ22655 fs, clone H	4.80
65	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	4.78
	439750	AI339053	Hs.57564	Homo sapiens mRNA full length insert cDN	4.75
	443633	AI031290	Hs.9654	similar to pregnancy-associated plasma p	4.74
	448950	AW302858	Hs.187333	ESTs	4.69
	422237	M13149	Hs.1458	histidine-rich glycoprotein	4.64
70	442476	AF069475		gb:AF069475 Homo sapiens as trocytoma fib	4.64
	431130	NM_006103	Hs.2719	epitidymis-specific, whey-acidic protein	4.58
	440624	AF017587	Hs.7306	secreted intronless-related protein 1	4.56
	403046				4.51
	450638	R65841	Hs.28653	ESTs	4.48
75	455887	BE154173		gb:PM1-H10340-201299-004-f12 HT0340 Homo	4.47
	453500	AI478427	Hs.43125	ESTs	4.40
	405701				4.37
	476657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.37
	451032	W03692	Hs.25832	Homo sapiens mRNA: cDNA DKFZp564P116 (f	4.37
	476700	AA371876	Hs.234786	KIAA0707 protein	4.35
80	418826	AI655499	Hs.161712	ESTs	4.34
	447754	AW073310	Hs.153633	Homo sapiens cDNA FLJ11412 fs, clone MA	4.32
	438209	AL129659	Hs.6111	KIAA0307 gene product	4.23
	404559				4.22

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5	413272	AA121923	Hs.293256	ESTs	4.21
	423058	M25620	Hs.123107	kallikrein 1, renal/pancreas/salivary	4.19
	416982	J05401	Hs.80691	crealine kinase, mitochondrial 2 [parcom	4.18
	445512	A1241246	Hs.148903	EST	4.17
	445177	A1215070	Hs.16135	ESTs	4.16
	444475	BE513134	Hs.247474	Homo sapiens cDNA: FLJ21032 fs, clone C	4.14
	420702				4.09
	439285	AL133916	Hs.298998	ESTs	4.02
10	429521	A082336	Hs.130874	Homo sapiens cDNA: FLJ14181 fs, clone NT	3.99
	450723	AW294454	Hs.247473	hypothetical protein FLJ20711	3.97
	435311	AL031224	Hs.33102	transcription factor AP-2 beta (activat	3.94
	452620	AA436504	Hs.119286	ESTs	3.92
	428642	X91220	Hs.158462	solute carrier family 12 (sodium/chlorid	3.91
	435884	AJ070143	Hs.192698	ESTs	3.90
15	416889	AW250318	Hs.80396	mat, T-cell differentiation protein	3.89
	419677	N77342	Hs.21851	Homo sapiens cDNA: FLJ12900 fs, clone NT	3.88
	431958	X63629	Hs.2677	cadherin 3, type 1, P-cadherin (placenta	3.84
	455844	AJ264155	Hs.152581	CDP-diacylglycerol synthase (phosphatida	3.82
	442305	A080660	Hs.129205	ESTs	3.82
20	439453	D17056	Hs.268599	Homo sapiens cDNA: FLJ20920 fs, clone A	3.81
	407198	H91679	Hs.2754	glx-yv04607 s1 Soares fetal liver spleen	3.80
	431441	U81961	Hs.75576	sodium channel, nonvoltage-gated 1 alpha	3.77
	413941	M24276		plasma/monog	3.77
	431161	AA493591	gb.h01210 s1 NC1_CGAP_Thy1 Homo sapiens		3.76
25	428544	AA430034	Hs.191511	ESTs	3.74
	453903	AW299606	Hs.232777	ESTs	3.74
	434061	AW024973	Hs.263575	HFD009 protein	3.73
	444805	AB007859	Hs.12017	KIAA0439 protein; homolog of yeast ubiq	3.73
	440080	AW051597	Hs.143707	ESTs	3.71
30	440230	A1732970	Hs.126246	ESTs	3.70
	428135	AJ279246	Hs.192857	NPH52 gene (prodicin)	3.68
	421832	NM_016098	Hs.108725	HSPC90 protein	3.66
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	3.65
	453055	AW291436	Hs.31917	ESTs	3.65
35	450696	A054223	Hs.18626	Homo sapiens cDNA: FLJ23191 fs, clone L	3.59
	440232	A076626	Hs.112554	ESTs	3.59
37	432099	U20760	Hs.272429	calcium-sensing receptor (hypothetic	3.57
	412924	A264671	Hs.164166	ESTs	3.56
40	411366	H45377		gb-y-m99h03.r1 Soares adult brain ZB5H5	3.56
	431103	A57289	Hs.44	pleiotrophin (protein binding growth fac	3.55
	413752	BE161807		gb-IR3-HT0446-300300-203-h01 HT0446 Homo	3.53
	416298	NM_003891	Hs.1011	protein Z, vitamin K-dependent plasma gl	3.53
	423603	AB007880	Hs.129883	KIAA0420 gene product	3.53
45	436610	AW611912	Hs.120414	ESTs	3.50
	425935	AB032559	Hs.161700	KIAA1133 protein	3.48
	403625				3.47
	425210	AA084679	Hs.155150	ribonuclease P (14kD)	3.45
	430168	AW968343	Hs.300896	ESTs, highly similar to AF128113 1 prom	3.42
50	448877	A552696	Hs.253313	ESTs	3.40
	456566	A554303	Hs.359892	Homo sapiens cDNA: FLJ12775 fs, clone NT	3.38
	414725	AA768791	Hs.120355	Homo sapiens cDNA: FLJ13148 fs, clone NT	3.37
	453574	A1767947	Hs.50841	ESTs, weakly similar to kullien (M.musc	3.32
	438535	L09078		glc-Homo sapiens mRNA fragment	3.31
55	414040	N59513	Hs.321271	ESTs	3.30
	451416	AW531469	Hs.203213	ESTs	3.30
	444564	A167877	Hs.143716	ESTs	3.29
	408001	AA046458	Hs.95296	ESTs	3.29
	405666	VC0495	Hs.75442	albumin	3.24
60	421750	AK000758	Hs.107872	hypothetical protein FLJ20761	3.24
	445337	NM_013280	Hs.12523	fibronectin leucine rich transmembrane p	3.23
	423968	AF098277	Hs.136529	solute carrier family 23 (nucleobase tra	3.21
	427209	H05609	Hs.92423	KIAA1505 protein	3.20
	403442				3.20
65	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.19
	425548	AA890023	Hs.1906	prolactin receptor	3.17
	414502	AL133721	Hs.224680	ESTs	3.16
	427811	M81657	Hs.180684	carboxypeptidase B1 (tissue)	3.14
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	3.11
	433942	AW272166	Hs.123465	ESTs	3.11
70	408992	AL040127	Hs.34074	dipeptidylpeptidase VI	3.10
	448819	A109190	Hs.198372	ESTs	3.10
	423041	BE170842	Hs.123123	chloride channel Kc	3.10
	454554	AW847505		gb-RCD-CT0210-260999-021-c10 CT0210 Homo	3.10
	406664	L34041	Hs.25478	glycerol-3-phosphate dehydrogenase 1 (c	3.10
75	449650	AW296292	Hs.199751	ESTs	3.08
	427450	AB014526	Hs.178121	KIAA0626 gene product	3.08
	454788	AW820691		gb-RCS-CT0300-300100-012-H06 ST0300 Homo	3.06
	444895	A0674383	Hs.301192	ESTs	3.06
	457782	M5403		gb-yv40g05 s1 Soares fetal liver spleen	3.05
80	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	3.05
	427041	A063661	Hs.97557	ESTs	3.01
	434788	AF154121	Hs.102867	sodium-dependent high affinity dicarboxy	3.01
	419003	T78640	Hs.268595	ESTs	3.01

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TABLE 37B:			
Key:	Unique Eos probaset identifier number		
CAT number:	Gene cluster number		
Accession:	Genbank accession numbers		
Play	Accession		
411356	1240273_1 H45377 H21137 AW838640		
417352	1385338_1 BE161807 BE161584 BE161700 BE161748		
431161	328713_1 AA463291 AA829120 AA533792		
431322	331543_1 AW970622 AA503009 AA502958 AA502969 AA502805 T92188		
438535	45946_1 L05078 L03145 L00904 L05098 L03165 L08102		
442476	543547_1 AF069475 AF069477 AF069476		
453685	977734_1 AL110309 AW088119 H42681		
454554	1223842_1 AW847505 AW811792 BE061442 BE061433 AW847506 AW806959 AW806996 BE061436 BE061430 BE142460 BE145499 AW806954 AW809156		
	AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431		
	BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142455 BE142459 BE142462 AW864330		
	AW854333 BE061434 BE061437 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998		
	BE061745 BE061753		
454788	1234694_1 AW820691		
455887	1380836_1 BE154173 BE154098 BE154096		
456576	201378_1 AA287443 AA419385 BE084078 AJ478347		
457782	402555_1 NS4493 AA679039 BT9505		
407198	H91679		
TABLE 37C:			
Key:	Unique Eos probaset identifier number		
Ref:	reference g ID		
Strand:	strand identification		
NI_position:	chromosomal nucleotide position		
Play	Ref Strand NI_position		
402072	6117363 Plus 71963-72128		
403046	3540153 Minus 55707-55859,56365-56511		
403204	7622922 Plus 16214-16439		
403381	9438267 Minus 26009-26178		
403442	7210003 Plus 174560-175270		
403625	8569879 Plus 6551-7111		
404319	9211467 Plus 54436-54608		
404569	8748853 Minus 73499-73551,89575-89739		
405373	2076718 Plus 21294-21575		
405701	4263751 Plus 93243-93364		
TABLE 38A: ABOUT 860 GENES UP-REGULATED IN KIDNEY CANCER COMPARED TO NORMAL ADULT TISSUES			
Table 38A lists about 860 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/HuEos H03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 50th percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 70th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.			
Key:	Unique Eos probaset identifier number		
ExAccn:	Exemplar Accession number, Genbank accession number		
Unigene ID:	Unigene number		
Unigene Title:	Unigene gene title		
RT:	Ratio of tumor to normal adult tissues		
Play	ExAccn Unigene ID Unigene Title RT		
435013	H91923 Hs.110024		15.71
447768	X86400 Hs.19520	Hs.19520.FXYD domain-containing ion tran	14.07
445178	A1792241 Hs.129614	Hs.129614.kidney-specific membrane prote	12.56
432642	AF083920 Hs.16039	Hs.16039.chordin 2	12.41
443585	AF168312 Hs.9613	NM.016105.Homo sapiens angiotensin-like	11.77
413719	BE439680 Hs.75498	NM.004591.Homo sapiens small inducible c	10.39
436878	BE465204 Hs.47448	Hs.47448.ES1s	10.18
440304	BE189984 Hs.125395	Hs.125395.ES1s	9.95
407065	Y10141		9.58
413049	NM_002151 Hs.823	NM_002151.Homo sapiens hepsin (transmemb	9.51
425983	AK000226 Hs.165619	Hs.165619.mucin and cadherin-like	8.88
423161	AL049227 Hs.124776	Hs.124776.Homo sapiens mR: cD DKFZp644N1	8.77
403069	AF241254 Hs.178098	Hs.178098.angiotensin I converting enzym	8.45
416768	AA363723 Hs.1023	NM.002903.Homo sapiens regenerating tale	7.94
423357	AF016272 Hs.115418	NM.004062.Homo sapiens cadherin 15, KSP-	7.78
420737	L08096 Hs.59899	NM.001252.Homo sapiens tumor necrosis fa	7.78
409745	AA077391	AA077391.7814E12 Chromosome 7 Fetal Brai	7.74
413936	AF113676 Hs.297681	NM.000295.Homo sapiens seipin (or crystal	7.32
426582	AV060038 Hs.2056	Hs.2056.UDP glycosyltransferase 1 family	7.20
406851	AA609784 Hs.352392	Hs.352392.major histocompatibility compl	7.03
419508	AW997938 Hs.90786	Hs.90786.ATP-binding cassette, sub-famil	6.57
428553	AA306610 Hs.348183	NM.003823.Homo sapiens tumor necrosis fa	6.36
436895	AF037335 Hs.5338	NM.001218.Homo sapiens carbonic anhydras	6.31
431842	NM_005764 Hs.271473	NM_005764.Homo sapiens epithelial protei	6.20
430014	H59354 Hs.374303	Hs.374303.hypothetical protein MGC20576	6.20
423803	NM_005709 Hs.132945	NM_005709.Homo sapiens PDZ-73 protein (P	6.19

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5	412939	AW411491	Hs.75269	NM_005412	Homo sapiens serine hydroxymethyl	3.80
	409162	HQ5530	Hs.50868	NM_002655	Homo sapiens solute carrier fa	3.79
	427715	BE245274	Hs.180428	Hs.180428	KIAA1181 protein	3.78
	412006	AW451618	Hs.290216	Hs.290216	ESTs	3.77
	430413	AW042182	Hs.241302	NM_002685	Homo sapiens small inducible c	3.74
10	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
15	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
20	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
25	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
30	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
35	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
40	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
45	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
50	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
55	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
60	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
65	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
70	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
75	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74
80	446391	BE397753	Hs.14623	NM_005332	Homo sapiens interferon, gamma	3.71
	427282	AF191225	Hs.114309	Hs.114309	apolipoprotein L1	3.71
	420747	BE294407	Hs.59910	Hs.59910	phosphotransferase, platelet	3.76
	414875	HA2679	Hs.77522	NM_006120	Homo sapiens major histocompat	3.75
	411793	AW362987	Hs.88474	Hs.88474	prostaglandin-endoperoxide synth	3.74

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5	430396	D49742	Hs.241363	NM_004132 Homo sapiens hyaluron binding	3.23
	424456	AA341017	Hs.25649	Hs.25649: hypothetical protein FLJ20898	3.23
	452303	R27257	Hs.57734	Hs.57734-G protein-coupled receptor like	3.22
	425390	A092634	Hs.156114	NM_004648 Homo sapiens protein tyrosine	3.21
	416333	NM_012201	Hs.78979	NM_012201 Homo sapiens golgi apparatus p	3.19
10	409091	N25764	Hs.25644	Hs.25644: tumor necrosis factor receptor	3.19
	428055	A053406	Hs.157313	Hs.157313: ESTs	3.18
	422616	BE300330	Hs.118725	NM_012248 Homo sapiens selenophosphate s	3.18
	439318	AW037046	Hs.6527	Hs.6527: G protein-coupled receptor 56	3.17
	422640	AA59293	Hs.118005	NM_001353 Homo sapiens O-dephosphatase taut	3.17
15	409636	AK001691	Hs.57655	Hs.57655: ductin 2	3.16
	432001	AW903849	Hs.173840	Hs.173840: similar to endothelial cell-s	3.16
	451154	AA015879	Hs.33536	Hs.33536: ESTs	3.16
	424722	U84722	Hs.76236	NM_001795 Homo sapiens cadherin 5, type	3.16
	402256	W25945	Hs.8173	Hs.8173: hypothetical protein FLJ10803	3.15
20	428593	AW207440	Hs.155973	NM_003676 Homo sapiens degenerative sper	3.15
	410026	A1912061	Hs.55016	Hs.55016: EPS8-related protein 2	3.15
	445333	BE537461	Hs.44278	Hs.44278: RAB17, member RAS oncogene fami	3.14
	440143	AF039304	Hs.20478	NM_000891 Homo sapiens csnol1 lipofuscin	3.14
	432307	AA320134	Hs.196029	Hs.196029 Homo sapiens mRNA for KIAA1657 p	3.14
25	416511	NM_006762	Hs.79356	NM_006762 Homo sapiens Lysosomal-associ	3.14
	439237	AW408158	Hs.318953	ESTs. Weakly similar to Z195_H	3.13
	446899	NM_005397	Hs.15426	NM_005397 Homo sapiens polydiphenyl-lik	3.13
	413016	N49813	Hs.75615	NM_000483 Homo sapiens apolipoprotein C-	3.13
	434398	AA121098	Hs.3838	NM_006522 Homo sapiens surm-inducible k	3.12
30	441263	AA527670	Hs.131704	ESTs	3.12
	418945	BE246762	Hs.84949	NM_000698 Homo sapiens arachidonic 5-lipo	3.12
	418458	AA332941	Hs.85026	NM_000235 Homo sapiens lipase A, lysosom	3.12
	408989	AW361566	Hs.49500	Hs.49500: KIAA0746 protein	3.11
	436906	H59590	Hs.181244	Hs.181244 major histocompatibility compl	3.11
35	411089	AA456454	Hs.355702	Hs.355702: ESTs. Weakly similar to AC008	3.11
	432990	AL336071	Hs.279889	NM_003201 Homo sapiens tumor necrosis fa	3.11
	425009	X58288	Hs.154151	NM_002845 Homo sapiens protein tyrosine	3.10
	434601	A078554	Hs.42658	Hs.42658: Homo sapiens cD FLJ30167 fra	3.10
	430603	AA148164	Hs.247280	Hs.247280: chromosome 20 open reading fra	3.10
40	413672	BE156336	Hs.353632	ESTs. Moderately similar to h	3.10
	404687	AA687138	Hs.38972	NM_005727 Homo sapiens tetraspan 1 (TSPA	3.09
	414586	AA306160	Hs.16488	NM_002298 Homo sapiens lymphocyte cyto	3.08
	423712	W46802	Hs.81898	Hs.81898: disabled homolog 2, mitogen-res	3.08
	438552	AJ245820	Hs.53100	NM_010410 Homo sapiens type 1 transmembr	3.06
45	443634	T08958	Hs.297214	Hs.297214: hSPC141 protein	3.06
	426437	BE076537	Hs.108985	NM_004223 Homo sapiens ubiquitin-conjug	3.06
	437679	NM_014214	Hs.5753	NM_014214 Homo sapiens inositol(myo)-l	3.05
	422262	AL022315	Hs.113987	NM_006498 Homo sapiens lectin, galactosi	3.06
	410480	R07457	Hs.53694	NM_001257 Homo sapiens cadherin 13, H-c	3.05
50	435818	AA700553	Hs.368614	Hs.368614: ESTs	3.05
	418883	BE387036	Hs.1211	NM_001611 Homo sapiens acid phosphatase	3.05
	453613	F06938	Hs.374476	Hs.374476: ESTs	3.05
	408351	AE62351	Hs.172148	Hs.172148: ESTs	3.05
	432378	AL137596	Hs.274295	Hs.274295: hypothetical protein FLJ23563	3.04
55	407949	W21874	Hs.247057	ESTs. Weakly similar to 210926	3.04
	418090	U57059	Hs.83429	NM_003810 Homo sapiens tumor necrosis fa	3.04
	433165	AA578904	Hs.292437	Hs.292437: ESTs	3.03
	425809	AA373262	Hs.57958	Hs.57958: EGF-TM7-1: integrin-related pro	3.03
	443884	N20617	Hs.194397	Hs.194397: ESTs. Moderately similar to 22	3.03
60	447831	AA332993	Hs.164115	Hs.164115: ESTs	3.02
	413278	BE563085	Hs.833	NM_005101 Homo sapiens interferon-stiml	3.02
	418870	AF147204	Hs.89414	Hs.89414: chemokine (C-X-C motif), recept	3.01
	456376	AA553904	Hs.85862	Hs.85862: TNFRSF1A-associated via death d	3.00
	409736	BE246502	Hs.5598	Hs.5598: sama domain, immunoglobulin dom	3.00
65	444416	AA583085	Hs.11155	NM_016494 Homo sapiens hypothetical cell	2.99
	406656	MA16714	Hs.89943	Hs.89943: transketolase (Wernicke-Korsako	2.99
	408326	AW516005	Hs.84298	Hs.84298: CD74 antigen (invariant polypep	2.99
	418707	U97502	Hs.87497	Hs.87497: butyrophilin, subfamily 3, memb	2.99
	421742	AW970004	Hs.107528	NM_016108 Homo sapiens androgen induc	2.99
70	408824	AW515981	Hs.84298	Hs.84298: CD74 antigen (invariant polypep	2.99
	453605	AF151815	Hs.4973	NM_016580 Homo sapiens hypothetical prot	2.98
	410491	AA465131	Hs.64001	Hs.64001: Homo sapiens clone 25218 mR seq	2.98
	427648	A376722	Hs.180062	NM_004159 Homo sapiens proteasome (proso	2.98
	411125	AA151647	Hs.68877	NM_000101 Homo sapiens cytochrome b 245,	2.98
75	455550	A224458	Hs.324037	Hs.324037: hypothetical protein FLJ20896	2.98
	429373	NM_014894	Hs.200594	NM_014894: Homo sapiens KIAA0605 gene pro	2.98
	445701	AF055581	Hs.13131	NM_005475 Homo sapiens lymphocyte adapt	2.97
	414649	A872727	Hs.76753	NM_000118 Homo sapiens endoglin (Olfet-R	2.97
	444207	A058004	Hs.374415	Hs.374415: ESTs	2.97
80	433225	AA452604	Hs.126359	NM_005206 Homo sapiens Thy-1 cell surf	2.97
	407792	A077715	Hs.39384	NM_014344 Homo sapiens four jointed box	2.97
	445707	A248720	Hs.114390	Hs.114390: ESTs	2.96
	452888	AW555454	Hs.39542	NM_004923 Homo sapiens cyclin-B2 (EFNB2)	2.96
	418478	U83945	Hs.1174	Hs.1174: cyclin-dependent kinase inhibito	2.95
	411441	AL042355	Hs.70202	Hs.70202: WD repeat domain 10	2.95
	443426	AF098158	Hs.9329	Hs.9329: chromosome 20 open reading frame	2.94
	450876	AF189062	Hs.285976	Hs.285976: LAG1 longtermly assurance homol	2.94

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425309	AA374095	HS.10562	HE.10862:Home sapiens cDc FL23231 fs.	2.94
425421	L11669	HS.15875	NM_001201:Home sapiens tetracycline tran	2.93
449879	H03573	HS.287830	HE.287830:Home sapiens cDc DP2-243E1	2.93
451450	B43626	HS.18313	HE.103313:Hupred like zinc finger prot	2.93
451450	AA014520	HS.30168	HE.30168:Home sapiens cDc K220 prot	2.93
457499	W69171	HS.334814	HE.334814:hyothetical protein FLJ14668	2.92
443987	AW163123	HS.10071	NM_016551:Home sapiens terven transmembr	2.92
425399	BC550182	HS.375142	HE.375142:RAGE-like protein, 3 mouse h	2.92
415906	A517357	HS.288741	HE.288741:Home sapiens cDc FL22265 fs.	2.92
425399	BC49225	HS.21638	HE.009113:Home sapiens zinc finger prot	2.91
451527	AF022813	HS.26518	NM_003271:Home sapiens transmembrane 4 s	2.91
425356	BC244879	HS.155939	NM_000541:Home sapiens inositol polyphos	2.91
427480	AW062287	HS.3011175	NM_008272:Home sapiens rare nucleotid C3	2.91
424761	AF024601	HS.16585	HE.000354:Home sapiens gastrin-2 (PKN2)	2.90
417176	BC517025	HS.256567	HE.256697:histidine rich-motifin C2	2.89
406659	AA595163	HS.271477	HE.271477:major histocompatibility comp	2.89
451144	AA695803	HS.61712	HE.61712:Home sapiens cDc FLJ15548 fs. c	2.89
425399	BC373003	HS.17999	HE.17999:Home sapiens cDc FL22265 fs.	2.89
425399	BC382756	HS.165992	NM_000615:Home sapiens sulfate carrier t	2.88
456974	M12529	HS.169401	NM_000041:Home sapiens apolipoprotein E	2.88
421174	L20968	HS.83566	HE.83566:Rho GDP dissociation inhibito	2.88
446955	AB115581	HS.12299	HE.12299:Home sapiens cDc FL22265 fs.	2.87
421384	NM_004428	HS.133554	NM_004428:Home sapiens ephrin-A1 (EP1).	2.87
427700	AA362294	HS.180383	NM_001946:Home sapiens dual specificity	2.87
410668	BC373994	HS.159651	NM_016829:Home sapiens hypothetical prot	2.87
414143	AA747596	HS.160999	HE.160999:ESTs. Weakly similar to F7885	2.87
414143	AF123636	HS.301352	HE.301352:ESTs. Weakly similar to F7885	2.86
443949	AK82386	HS.352579	HE.352579:Home sapiens, chromosome 20 p	2.86
436997	AA741511	HS.137323	HE.137323:ESTs	2.86
446143	BC245342	HS.306079	NM_013336:Home sapiens protein transport	2.86
414143	D11989	HS.62003	HE.62003:Home sapiens cytochrome type B	2.86
410885	AW206135	HS.267659	NM_000113:Home sapiens vav 3 oncogene (V	2.86
436997	AA745033	HS.130315	HE.130315:ESTs	2.85
436997	AF298627	HS.211592	NM_005020:Home sapiens ATP-binding casse	2.85
425399	BC245651	HS.437618	HE.437618:Home sapiens cDc FL22265 fs.	2.85
436997	AA589498	HS.5302	NM_006149:Home sapiens lectin, galactosi	2.84
419625	UP1616	HS.182885	NM_004556:Home sapiens nuclear factor of	2.84
439941	AI326460	HS.18272	HE.18272:cysteine carrier family 3s, memb	2.84
456496	BC281959	HS.52010	NM_004077:Home sapiens gamma glutamyl	2.84
427217	AF115554	HS.115554	HE.115554:Home sapiens cDc FL22265 fs.	2.84
436997	AF035622	HS.6854	HE.6854:KIAA0108:protein	2.83
427217	BC465574	HS.17778	HE.180372:Home sapiens transmembrane 2 (NRP	2.83
429343	AA043021	HS.127075	HE.127055:similar to HYPOTHEICAL_42.1	2.83
427217	AF10519	HS.16788	HE.16788:Home sapiens cDc FL22265 fs.	2.83
415523	AL042003	HS.206847	NM_001119:Home sapiens cytoskeleton (paral	2.83
436968	AW01277	HS.302634	HE.302634:orfz homolog 8 (Drosophila	2.83
415523	Y00285	HS.76473	NM_00089:Home sapiens insulin-like like	2.83
456550	AF077012	HS.285852	HE.285852:Home sapiens cDc FL22265 fs.	2.82
406949	AA159216	HS.55505	HE.55505:hyothetical protein FLJ20442	2.82
415523	M21533	HS.271477	HE.271477:major histocompatibility comp	2.82
456655	BC283932	HS.949	NM_000433:Home sapiens neutrophil cytop	2.82
443195	BC146226	HS.153063	HE.153063:Home sapiens cDc FLJ14201 fs.	2.82
425399	AA248418	HS.164077	HE.164077:ESTs	2.82
450708	AA358065	HS.350685	HE.350685:Home sapiens cDc FLJ30634 fs.	2.82
432681	AA034377	HS.203860	HE.203860:Home sapiens cDc FLJ30207 fs.	2.82
425399	AF076037	HS.124051	NM_005653:Home sapiens Rink-associated	2.82
415523	AA161311	HS.16294	HE.101780:Home sapi	2.82
415523	AA010692	HS.25291	HE.252812:HERV-H1:LTR-associated ?	2.82
417321	AW116787	HS.81972	HE.81972:SHC (Grb1 oncology 2 domain cont	2.82
415995	NM_004573	HS.33558	NM_004573:Home sapiens phosphogluco	2.82
425399	BC200107	HS.17602	HE.17602:Home sapiens cDc FL22265 fs.	2.82
456625	CT5094	HS.334514	HE.334514:chromosome 6 open reading fram	2.82
407893	BC408359	HS.4362	HE.4362:1:Home sapiens protein ABC2305	2.82
425399	BC287341	HS.145629	HE.1454029:BNH1: protein Hsc4	2.82
415906	AF242911	HS.334791	HE.334791:Home sapiens cDc FL22265 fs.	2.82
423462	AA034349	HS.184634	HE.184634:Home sapiens cDc FL22265 fs.	2.82
425399	BC327096	HS.105097	NM_003258:Home sapiens thymidine kinase 1,	2.82
427581	NM_016748	HS.179703	HE.179703:Home sapiens inositol motif	2.82
425457	AW138558	HS.134873	HE.134873:carboxypeptidase M	2.82
425399	BC203124	HS.350447	HE.350447:Home sapiens cDc FL22265 fs.	2.82
425188	AA020052	HS.155471	HE.155021:chromosome 20 open reading fra	2.82
425399	AF151020	HS.180022	NM_010456:Home sapiens hypothetical prot	2.82
425333	AW384710	HS.132696	HE.132696:Home sapiens cDc FLJ13589 fs.	2.82
425399	BC357473	HS.355733	HE.355733:Home sapiens cDc FL22265 fs.	2.82
425333	AW138420	HS.136578	HE.136578:hyothetical protein FLJ22969	2.82
405502	AJ284121	HS.72821	HE.72821:regulator of C-peptide signaling	2.82
444981	AA565398	HS.12820	HE.12216:form endothelial factor C	2.82
439219	AJ3363	HS.41332	HE.41332:ESTs	2.82
439219	AJ3321	HS.80291	NM_006403:Home sapiens enhancer of flam	2.82
425399	BC302645	HS.162459	HE.162459:ESTs	2.82
425399	AF067391	HS.28985	HE.28985:ESTs. Weakly similar to putati	2.82
411218	AA676939	HS.629654	NM_003851:Home sapiens cDc FL22265 fs.	2.82
425399	NM_000545	HS.72950	NM_000545:Home sapiens cDc FL22265 fs.	2.82
425399	BC302645	HS.162459	HE.162459:ESTs	2.82

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425345	AI077297	Hs.155894	NM_002827 Homo sapiens protein tyrosine	2.69
428923	BE047698	Hs.188785	Hs.188785-ESTs	2.69
427923	AW274357	Hs.301406	Hs.301406/hypothetical protein PP3501	2.69
446644	NM_003272	Hs.15791	NM_003272 Homo sapiens transmembrane 7 s	2.68
417445	135956	Hs.107614	Hs.107614-DNF P25681171 protein	2.68
416207	NM_014745	Hs.79077	NM_014745 Homo sapiens KIAA0233 gene pro	2.68
420372	AW960049	Hs.293560	Hs.293560 gene overexpressed in acrocyt	2.68
420542	NM_009095	Hs.1321	NM_009095 Homo sapiens coagulation facto	2.67
425069	AA687465	Hs.298184	Hs.298184 potassium voltage-gated channel	2.67
416558	AW082266	Hs.81131	NM_003624 Homo sapiens Fas (TNFRSF5)-ass	2.67
426511	MQ2483	Hs.168383	NM_000201 Homo sapiens intercellular adh	2.66
406701	AA780613	Hs.62954	Hs.62954/tenin, heavy polypeptide 1	2.66
431681	AK000378	Hs.267565	Hs.267565/hypothetical protein FL20331	2.66
412833	AW960547	Hs.296267	Hs.296267/rhomboid protein S19	2.66
433101	AW572317	Hs.12082	Hs.12082-TIGAI1	2.66
414774	X02419	Hs.77274	NM_002658 Homo sapiens plasminogen activ	2.66
427868	AC360119	Hs.181013	NM_002629 Homo sapiens phosphoglycerate	2.66
413929	BE001689	Hs.75617	Hs.75617 collagen, type IV, alpha 2	2.66
424712	AL119442	Hs.103864	Hs.183804/eukaryotic translation initiat	2.66
422048	NM_012445	Hs.288126	NM_012445 Homo sapiens spondin 2, extrac	2.65
431350	AI192528	Hs.164537	Hs.164537-ESTs	2.65
450184	W31096	Hs.237617	Hs.237617/speckle-type protein 9	2.65
419285	D31887	Hs.89898	Hs.09898/PA10052 protein	2.65
414217	AI309298	Hs.279838	Hs.279838 Homo sapiens cD: FLJ23165 fts,	2.64
451253	H48299	Hs.26126	NM_006804 Homo sapiens claudin 10 (CLDN1	2.64
435965	AW997484	Hs.5003	Hs.5003-SLIT-ROBO Rho GTPase-activating	2.64
432381	AU754655	Hs.278441	NM_014534 Homo sapiens KIAA0015 gene pro	2.63
415782	AA168345	Hs.123177	Hs.123177/hypothetical protein BC011405	2.63
430223	NM_002514	Hs.235936	NM_002514 Homo sapiens nephroblastoma ov	2.63
417526	AA568906	Hs.82240	NM_004177 Homo sapiens syntaxin 3A (STX3	2.63
409956	AW103364	Hs.177	NM_002192 Homo sapiens inhibin, beta A [2.63
409843	R85337	Hs.24030	NM_001680 Homo sapiens solute carrier fa	2.62
417389	BE260964	Hs.82045	NM_002931 Homo sapiens midkine (neurtre	2.62
446312	BE087853	Hs.171802	Hs.171802 Homo sapiens, clone IMAGE:3956	2.62
435059	AC034770	Hs.4756	Hs.4756 flap structure-specific endonuc	2.62
417920	SA1483	Hs.82827	NM_004037 Homo sapiens adenosine monopho	2.62
435702	AC033647	Hs.121001	Hs.121001 Homo sapiens, clone MGC-4552 I	2.62
429599	AV547015	Hs.349256	Hs.349256/paired immunoglobulin-like rec	2.62
419938	AU076772	Hs.1279	NM_001733 Homo sapiens complement compon	2.62
450584	AR94740	Hs.25891	NM_005858 Homo sapiens receptor (calcitri	2.61
421753	BE314826	Hs.107911	Hs.107911/ATP-binding cassette, sub-fam	2.61
443577	AI078033	Hs.171710	Hs.171710/ESTs, Weakly similar to ALU8_H	2.61
453886	R66282	Hs.20247	Hs.20247-ESTs	2.61
421883	X55079	Hs.1437	NM_000152 Homo sapiens glucosidase, alph	2.60
440457	BE387553	Hs.21291	Hs.21291/granule cell differentiation pr	2.60
410295	AA741357	Hs.356624	Hs.356624-ESTs	2.59
420679	X57152	Hs.99853	NM_001436 Homo sapiens fibrinogen (FBL	2.59
451558	NM_001089	Hs.26530	NM_001089 Homo sapiens ATP-binding case	2.59
444672	Z55636	Hs.11659	Hs.11669/tenin, alpha 5	2.59
400669	AA93591	Hs.78146	Hs.78146/platelet/endothelial cell adhes	2.59
426194	T50872	Hs.2001	Hs.2001/thromboxane A synthase 1 (plate	2.59
421814	L12350	Hs.108623	NM_003247 Homo sapiens Thrombospondin 2	2.59
456371	S78625	Hs.89695	Hs.89695 insulin receptor	2.59
429098	AF032429	Hs.196176	NM_001358 Homo sapiens enoyl Coenzyme A	2.59
414443	AU077268	Hs.76144	NM_002609 Homo sapiens platelet-derived -	2.59
428484	AF104032	Hs.184601	NM_003486 Homo sapiens solute carrier fa	2.59
453309	AI791809	Hs.32549	NM_003218 Homo sapiens desmin, beta 1	2.59
417867	AU076581	Hs.74637	NM_003217 Homo sapiens testis enhancin g	2.58
432827	Z56126	Hs.3109	Hs.3109/Rho GTPase activating protein 4	2.58
412669	AW880841	Hs.96908	NM_006030 Homo sapiens p53-induced prote	2.58
412115	AK001163	Hs.73239	Hs.73239/hypothetical protein FLJ11901	2.58
452866	R26869	Hs.268076	Hs.268076 Homo sapiens cD: FLJ21243 fts	2.57
435129	AI381659	Hs.267086	Hs.267086-ESTs	2.57
424482	BE788621	Hs.149155	NM_003374 Homo sapiens voltage-dependent	2.57
410494	N36364	Hs.64016	NM_000313 Homo sapiens protein S (alpha)	2.56
433895	AZ87912	Hs.3638	NM_004834 Homo sapiens mitogen-activated	2.56
424566	R31337	Hs.12111	Hs.12111-ESTs	2.56
417640	C00657	Hs.82353	NM_005404 Homo sapiens protein C recepto	2.56
442622	NM_000435	Hs.8546	NM_000435 Homo sapiens Notch homolog 3 (2.56
430346	AK000331	Hs.797941	Hs.295741/reinoblastoma-associated fact	2.55
419344	US0625	Hs.277445	Hs.277445/diacylglycerol kinase, zeta (IQ)	2.55
426500	NM_014638	Hs.170156	NM_014638 Homo sapiens KIAA0450 gene pro	2.55
408048	NM_007203	Hs.42322	NM_007203 Homo sapiens A kinase (PRKA) anc	2.55
450700	AW732799	Hs.25348	NM_005860 Homo sapiens follicle-stim-like	2.54
417018	M16338	Hs.82087	NM_002260 Homo sapiens v-jes-1 Yamauchi	2.54
419378	Z54922	Hs.90078	Hs.90078/methylenetetrahydrofolate transp	2.54
422451	AA310753	Hs.42491	Hs.42491-ESTs, Moderately similar to hyp	2.53
435906	AI686379	Hs.110796	Hs.110796/SAR1 protein	2.53
402031				2.53
417819	AW291587	Hs.82733	NM_007361 Homo sapiens nidogen 2 (NID2)	2.53
427380	NM_005534	Hs.177559	NM_005534 Homo sapiens interlamin gamma	2.52
426385	AF112213	Hs.184062	Hs.184062/chromosome 20 open reading fra	2.52
430600	AI825880	Hs.5985	Hs.5985/non-kase Cdc42 effector protein	2.52

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5	43813	AA876372	Hs.93861	Homo sapiens mRNA cDNA Zfp67009	2.24
	427458	AB003364	Hs.22083	ESTs, Weakly similar to UCHL1 pr	2.24
	454294	AB000734	Hs.50640	NM_003745 Homo sapiens JAK binding prote	2.24
	407192	AA690200	Hs.366318	Hs.366318 ESTs	2.23
	427571	T11923	Hs.1940	NM_018853 Homo sapiens crystallin, alpha	2.23
10	456437	AB04228	Hs.115185	ESTs	2.23
	413019	BE281604	Hs.75140	NM_002337 Homo sapiens low density lipop	2.23
	418882	BE550964	Hs.89399	Hs.89399 ATP synthase, H+ transporing,	2.23
	435284	AA879470	Hs.96649	Homo sapiens cDNA FLJ11482, clone	2.23
	429630	AA65289	Hs.211573	NM_005529 Homo sapiens leucine sulfide p	2.23
15	427620	AK000436	Hs.175791	RA820, member RAS oncogene fam	2.22
	421917	AB028943	Hs.109445	Hs.109445 hypermethylated in cancer 2	2.23
	416616	BE5964	Hs.334873	carboxypeptidase M	2.23
	407232	X04526	X04526	Human liver mRNA for beta-subunit s	2.23
	423798	AF047133	Hs.132904	Hs.132904 solute carrier family 4, spoli	2.23
20	466755	AW451473	Hs.16134	NM_005950 Homo sapiens serine/threonine	2.22
	452885	AJ524046	Hs.119567	Hs.119567 ESTs, Weakly similar to ALU1_H	2.22
	431393	AW971493	Hs.134269	Hs.134269 ESTs, Weakly similar to 200459	2.22
	431890	X17033	Hs.271936	NM_002033 Homo sapiens integrin, alpha 2	2.22
	428782	X12830	Hs.193400	NM_000565 Homo sapiens interleukin 6 rec	2.22
25	468006	NM_004403	Hs.13530	NM_004403 Homo sapiens deafness, autosom	2.22
	436418	AJ245874	Hs.4245	Hs.4245 chromosome 11 hypothetical prote	2.21
	423869	BE430301	Hs.134022	NM_006688 Homo sapiens C19orf145 facta	2.21
	437730	AW071687	Hs.239176	Hs.239176 nucleolar growth factor 1 r	2.21
	444020	R92962	Hs.35052	ESTs	2.21
30	413882	AA132973	Hs.184492	Hs.184492 Homo sapiens mRNA cDNA Zfp66780	2.21
	412654	AJ093480	Hs.374319	ESTs	2.21
	446888	Y08763	Hs.22765	NM_004661 Homo sapiens gamma-aminobutyri	2.21
	426841	AJ052358	Hs.131741	ESTs	2.21
	408196	AL034548	Hs.43627	NM_006943 Homo sapiens SRY (sex determin	2.20
35	457711	AK000461	Hs.26980	Hs.26980 oral eye syndrome chromosome reg	2.20
	414325	AA251929	Hs.355341	Hs.355341 Homo sapiens, clone IMAGE3536	2.20
	424512	XS3002	Hs.145846	NM_002213 Homo sapiens integrin, beta 5	2.20
	440883	BE614989	Hs.7503	Hs.7503 hypothetical protein FLJ14153	2.20
	411296	BE207307	Hs.10114	Hs.10114 growth suppressor 1	2.20
40	452288	NM_003512	Hs.20777	NM_003512 Homo sapiens KDA histone fami	2.20
	415810	AF038666	Hs.86019	NM_013232 Homo sapiens programmed cell d	2.19
	441415	H21497	Hs.7471	Hs.7471 BBP-like protein 1	2.19
	444212	AW503976	Hs.10649	NM_004848 Homo sapiens basement membrane	2.19
	428044	AA093322	Hs.301404	NM_006743 Homo sapiens R binding motif p	2.19
45	430017	AA263170	Hs.35	NM_002337 Homo sapiens protein tyrosine	2.19
	424490	AJ278016	Hs.55565	Hs.55565 ankyrin repeat domain 3	2.19
	431193	AW749505	Hs.296770	Hs.296770 KIAA1719 protein	2.19
	453686	AL110326	Hs.304679	Hs.304679 ESTs, Weakly similar to Z195_H	2.19
	446262	AB068330	Hs.198273	Hs.198273 ESTs	2.19
50	415665	BE267931	Hs.78596	NM_002692 Homo sapiens proliferating cel	2.19
	442045	C05768	Hs.8078	Hs.8078 Homo sapiens clone FBD3 Cn-de-c	2.19
	423804	AW403448	Hs.1705	NM_006084 Homo sapiens interferon-stimul	2.19
	428024	Z29067	Hs.2236	Hs.2236 NIMA (never in mitosis gene a) c	2.19
	424503	NM_002205	Hs.149609	NM_002205 Homo sapiens integrin, alpha 5	2.19
55	437696	Z83844	Hs.5790	Hs.5790 hypothetical protein d337E16.5	2.18
	405204				2.18
	426158	NM_001982	Hs.190087	NM_001982 Homo sapiens v-erb-b2 erythro	2.18
	417416	NM_002468	Hs.82116	NM_002468 Homo sapiens myriodin differet	2.18
	412773	H15785	Hs.74573	NM_012268 Homo sapiens similar to vaccin	2.18
60	409402	AF208234	Hs.695	NM_000100 Homo sapiens cystatin B (piti	2.18
	443791	N64458	Hs.143345	Hs.143345 ESTs	2.18
	435049	AL122067	Hs.4746	Hs.4746 hypothetical protein FLJ2132N	2.18
	413389	AA180613	Hs.28349	Hs.28349 ESTs	2.18
	450712	AJ732130	Hs.270496	Hs.270496 ESTs, Weakly similar to ALUB_H	2.18
65	422007	AJ739435	Hs.39168	Hs.39168 ESTs, Weakly similar to T17340	2.18
	453676	AW853745	Hs.286035	Hs.286035 hypothetical protein FLJ2656	2.18
	415718	F03631	Hs.200237	Hs.200237 ESTs	2.18
	452688	AA721140	Hs.49530	Hs.49530 ESTs, Weakly similar to B34087	2.18
	415988	BE407713	Hs.78943	NM_000386 Homo sapiens bleomycin hydroly	2.18
70	409453	AB055516	Hs.95612	Hs.95612 ESTs	2.17
	417512	X76534	Hs.82226	NM_002510 Homo sapiens glycoprotein (tra	2.17
	427202	BE272522	Hs.173936	NM_000628 Homo sapiens interleukin 10 re	2.17
	440983	M20681	Hs.7594	NM_006931 Homo sapiens solute carrier fa	2.17
	416084	L16991	Hs.79006	NM_012145 Homo sapiens deoxythymidylate	2.17
75	429642	X68264	Hs.211579	NM_006500 Homo sapiens melanoma adhesio	2.17
	427213	AW007211	Hs.346389	Hs.346389 hypothetical protein FLJ12876	2.17
	437763	AA469369	Hs.5831	NM_003524 Homo sapiens tissue lysine inhibi	2.17
	464000	AA040620	Hs.5672	Hs.5672 golgi membrane protein S8140	2.17
	424247	X14008	Hs.234734	NM_000239 Homo sapiens lysosome (rel amy	2.16
80	463857				2.16
	406648	AA563730	Hs.277477	Hs.277477 major histocompatibility compl	2.16
	402865				2.16
	442379	NM_004613	Hs.8265	NM_004613 Homo sapiens transglutinin 2	2.16
	441852	AA028981	Hs.8521	Hs.8521 KIAA0508 protein	2.16
	417446	AL118671	Hs.82163	NM_000858 Homo sapiens monoamine oxidase	2.16
	418386	AA361739	Hs.84549	NM_002454 Homo sapiens DH dehydrogenase (u	2.16
	414053	BE391635	Hs.75725	NM_003664 Homo sapiens transglut 2 (TAG	2.16

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5	440906	AW161556	Hs.240170	Hs.240170:hypothetical protein MGC2731	2.16
	447660	AW160386	Hs.163667	Hs.163667:ESTs, Weakly similar to CA1H_M	2.16
	408279	AF216965	Hs.44065	Hs.44065:cyclin M3	2.16
	426152	BE299130	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.15
	437352	D63209	Hs.5944	NM_004583:Home sapiens solute carrier fa	2.16
10	415661	AF057307	Hs.78575	Hs.78575:proapoptin (variant) Gaucher di	2.15
	425302	U79115	Hs.155666	NM_003805:Home sapiens CASP2 and RBP1 d	2.15
	425996	W67330	Hs.37451	Hs.37451:ESTs	2.15
	413745	AK247232	Hs.75514	NM_002770:Home sapiens nucleoside phosph	2.15
	422070	AF140785	Hs.111126	Hs.111126:pulmonary tumor-transforming 1	2.15
15	448424	AW009892	Hs.31924	Hs.31924:ESTs	2.15
	430035	NM_003463	Hs.227777	NM_003463:Home sapiens protein tyrosine	2.15
	438407	AJ657122	Hs.129773	Hs.129773:eukaryotic translation initiat	2.15
	435551	AF212365	Hs.5470	Hs.5470:Interferon 110 receptor	2.15
	437741	BE561610	Hs.5809	Hs.5809:putative transmembrane proteic	2.15
20	441192	AA526626	Hs.7736	NM_016504:Home sapiens mitochondrial rib	2.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.15
	411165	NM_001169	Hs.69089	NM_001169:Home sapiens glucosylase	2.14
	425252	AW081162	Hs.343306	Hs.343306:hypothetical protein FLJ31951	2.14
	427600	AW630918	Hs.179774	NM_002818:Home sapiens proteasome (proso	2.14
25	426818	AA554827	Hs.292996	Hs.292996:postmeiotic segregation increa	2.14
	442110	AF113008	Hs.8102	NM_001023:Home sapiens ribosomal protein	2.14
	407757	AK002524	Hs.39580	Hs.39580:uridine kinase like 1	2.14
	443044	N28522	Hs.8935	NM_014298:Home sapiens quinolite phospho	2.14
	437103	AW139408	Hs.152940	Hs.152940:ESTs	2.14
30	442069	AW664144	Hs.297007	Hs.297007:Home sapiens cbl FLJ32174 fa	2.14
	442494	NM_000546	Hs.1846	NM_000546:Home sapiens tumor protein p53	2.14
	458097	AW041135	Hs.58104	Hs.58104:Home sapiens, clone IMAGE:47309	2.14
	411925	AW014588	Hs.72925	NM_003475:Home sapiens chromosome 11 ope	2.14
	449644	AW960707	Hs.148324	Hs.148324:ESTs	2.14
35	422675	BE018517	Hs.119140	NM_001040:Home sapiens eukaryotic transl	2.14
	426586	M36712	Hs.2299	Hs.2299:CD8 antigen, beta polypeptide 1	2.14
	429379	NM_014640	Hs.200598	NM_014640:Home sapiens KIAA0537 gene pro	2.13
	410290	AA042307	Hs.322844	Hs.322844:hypothetical protein DKFZ55644	2.13
	443895	AW693048	Hs.232566	Hs.232566:YEAM protein	2.13
40	424145	BE243327	Hs.182626	NM_012264:Home sapiens chromosome 22 ope	2.13
	453518	AW503205	Hs.27268	Hs.27268:Home sapiens cDr FLJ21933 fa	2.13
	4456534	X31195	Hs.100623	Hs.100623:protein phosphatase 1, regulat	2.13
	419972	AL041465	Hs.182682	Hs.182682:pgin-67	2.13
	424960	AA402517	Hs.156974	Hs.156974:ESTs	2.13
45	427557	NM_002659	Hs.179567	NM_002659:Home sapiens plasminogen activ	2.13
	431449	M55994	Hs.256278	NM_001066:Home sapiens tumor necrosis fa	2.13
	418758	AW950311	Hs.172012	Hs.172012:hypothetical protein DKFZp434J	2.12
	434022	BE380411	Hs.3764	NM_003058:Home sapiens guanlylate kase 1	2.12
	433233	AB940927	Hs.307104	Hs.307104:KIAA1494 protein	2.12
50	452700	AB593090	Hs.288940	Hs.288940:transmembrane protein 8 (five	2.12
	438033	T26483	Hs.6059	NM_016938:Home sapiens EGF-containing li	2.12
	406847				2.12
	447547	NM_007229	Hs.18542	NM_007229:Home sapiens protein kase C an	2.12
	417052	NM_000712	Hs.81029	NM_000712:Home sapiens biliverdin reduct	2.12
55	413284	AU077055	Hs.289107	NM_001166:Home sapiens baculoviral IAP r	2.11
	434558	AW264102	Hs.39168	Hs.39168:ESTs, Weakly similar to T17340	2.11
	404030				2.11
	410801	BE275469	Hs.66493	Hs.66493:Down syndrome critical region g	2.11
	418613	AA744529	Hs.86575	Hs.86575:mitogen-activated protein kase	2.11
60	447087	AW403870	Hs.301872	Hs.301872:hypothetical protein MGC4940	2.11
	433026	AW180616	Hs.275921	NM_016127:Home sapiens hypothetical prot	2.11
	426433	L33869	Hs.168075	NM_007112:Home sapiens thrombospondin 3	2.11
	442439	U09759	Hs.246857	NM_002752:Home sapiens mitogen-activated	2.11
	437379	AI359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.11
65	402028				2.11
	457105	AW161061	Hs.356580	Hs.356580:ESTs, Weakly similar to zinc f	2.11
	417599	AA204688	Hs.62954	Hs.62954:keratin, heavy polypeptide 1	2.10
	416728	AB024597	Hs.79658	NM_001894:Home sapiens casein kase 1, ep	2.10
	439920	H05430	Hs.288433	Hs.288433:neurotrophin	2.10
70	422389	U79745	Hs.114624	NM_004694:Home sapiens solute carrier fa	2.10
	436114	AA778232	Hs.19515	Hs.19515:ESTs, Highly similar to NR3G_HU	2.10
	405517				2.10
	421872	AA359753	Hs.22824	Hs.22824:MYE binding protein (P160) 1a	2.10
	437172	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kase, rec	2.10
75	431214	AA294921	Hs.348024	NM_002881:Home sapiens v-rat simian leuk	2.10
	412856	BE386745	Hs.74631	NM_001728:Home sapiens badglin (ESG), mR	2.10
	442064	AI422867	Hs.88594	Hs.88594:Home sapiens, clone IMAGE:43329	2.10
	443445	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.09
	426728	NM_007118	Hs.307689	NM_007118:Home sapiens cryptic functio d	2.09
80	419596	BE373320	Hs.91448	NM_007026:Home sapiens disulf specifically	2.09
	448913	AA194422	Hs.22564	NM_004999:Home sapiens myosin VI (MYO6),	2.09
	414721	X30392	Hs.77091	NM_006730:Home sapiens deoxyribonuclease	2.09
	424658	NM_007406	Hs.151513	NM_007406:Home sapiens mannose (alpha-1	2.09
	428905	X94530	Hs.31407	Hs.31407:CD97 antigen	2.09
	447032	AA600310	Hs.17138	Hs.17138:hypothetical protein FLJ20303	2.09
	447484	AA454839	Hs.292546	Hs.292546:YEAM protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylglucosamine kase	2.09

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	445594	AF217518	Hs.8360	Hs.8360:PTD012 protein	2.09
	402559				2.09
	418043	AW377752	Hs.83341	Hs.83341:AXL receptor tyrosine kinase	2.09
5	448885	AW196663	Hs.200242	Hs.200242:cathepsin recruitment domain fam	2.09
	438910	AA528844	Hs.261587	Hs.261587:GCN2 est Znfha kinase	2.09
	422273	AW207985	Hs.295726	Hs.295726:integrin, alpha V (vitronectin)	2.08
	416448	L13210	Hs.79339	NM_005567: Homo sapiens lectin, galactoside	2.08
	428727	AF078847	Hs.191356	NM_001515: Homo sapiens general transcrip	2.08
10	410301	AW502535	Hs.740	Hs.740:PTK2 protein tyrosine kinase 2	2.08
	445538	AE59444	Hs.104679	Hs.104679: Homo sapiens, clone MGC:18216	2.08
	421205	AL137540	Hs.102541	Hs.102541: netrin 4	2.08
	411779	AA292811	Hs.72050	NM_003551: Homo sapiens non-metastatic ce	2.07
	427704	AW671063	Hs.292682	Hs.292682: ESTs	2.07
	413518	BE149455	Hs.75415	NM_004048: Homo sapiens beta-2-microglobu	2.07
15	447345	BE247767	Hs.18166	Hs.18166: KIAA0870 protein	2.07
	407143	C14076	Hs.332329	Hs.332329: EST	2.07
	446431	BE613061	Hs.337772	Hs.337772: hydropathical protein BC009331	2.07
	412760	AW379030	Hs.41324	Hs.41324: ESTs	2.07
	446029	AI494293	Hs.10297	NM_005694: Homo sapiens CCK17 homolog, cy	2.07
20	403966				2.07
	409155	AI223336	Hs.50651	NM_002227: Homo sapiens Janus kinase 1 (a p	2.07
	436823	AW748085	Hs.117077	Hs.117077: zinc finger protein 264	2.07
	414045	NM_002051	Hs.75722	NM_002051: Homo sapiens ribophylin II (RP	2.06
	413980	NM_002437	Hs.75659	NM_002437: Homo sapiens Mpv17 transgene,	2.06
25	439414	NM_001183	Hs.8551	NM_001183: Homo sapiens ATPase, H+-transp	2.06
	426059	BE252842	Hs.186120	NM_001572: Homo sapiens interferon regula	2.06
	429649	U33053	Hs.2499	NM_002741: Homo sapiens protein kinase C-4	2.06
	42424				2.06
	406626	X04626	Hs.215595	Hs.215595: guanine nucleotide binding pro	2.06
30	458911	AA371311	Hs.24322	Hs.24322: ATPase, H+-transporting, lysoso	2.05
	426086	T94967	Hs.188572	Hs.188572: ESTs	2.05
	419726	U50300	Hs.1274	NM_009122: Homo sapiens bone morphogenet	2.05
	452344	AI764357	Hs.55405	Hs.55405: hypothetical protein MGC16212	2.05
	424298	U54617	Hs.83364	NM_002612: Homo sapiens pyruvate dehydrog	2.05
35	422114	AW154851	Hs.111801	NM_013908: Homo sapiens aneuplo resistance	2.05
	413420	AW410225	Hs.75348	NM_002633: Homo sapiens proteasome (proso	2.05
	404330	R21945	Hs.346735	Hs.346735: Homo sapiens, clone IMAGE:3881	2.05
	409332	AI378750	Hs.57900	Hs.57900: adaptor-related protein complex	2.05
	434848	BE256304	Hs.32148	Hs.32148: AD-015 protein	2.04
40	453852	AW961818	Hs.374424	Hs.374424: ESTs	2.04
	427937	AK000815	Hs.175986	NM_005803: Homo sapiens flotillin 1 (FLOT	2.04
	400284				2.04
	430016	NM_004736	Hs.227656	NM_004736: Homo sapiens xenotropic and po	2.04
	410134	U68140	Hs.58527	Hs.58527: nuclear VCP-like	2.04
45	440975	AW499914	Hs.7579	Hs.7579: importin 9	2.04
	432280	BE440142	Hs.2943	NM_003133: Homo sapiens sig1 recognition	2.04
	409504	AA304961	Hs.659	NM_000942: Homo sapiens peptidylprolyl is	2.04
	412146	ME2444	Hs.73722	NM_001641: Homo sapiens APEX nuclease (mu	2.04
	434263	BE282677	Hs.283558	Hs.283558: hypothetical protein PRO1855	2.04
50	427254	AA316476	Hs.171811	Hs.171811: adenylate kinase 2	2.04
	405929	AA069711		AA069711: zmf52b11.1 Stratagene fibroblas	2.04
	413096	AA125641	Hs.183834	Hs.183834: ESTs	2.03
	424340	AA339036	Hs.7033	Hs.7033: ESTs	2.03
55	456440	AB044334	Hs.25901	NM_012079: Homo sapiens tyrosine 3-monoox	2.03
	424652	NM_002870	Hs.151536	NM_002870: Homo sapiens RAB13, member RAS	2.03
	415740	N80486	Hs.39911	Hs.39911: Homo sapiens mR for FLJ00089 pr	2.03
	412749	AA378417	Hs.74564	NM_003145: Homo sapiens sig1 sequence rec	2.03
	408323	AA1015318	Hs.221655	Hs.221655: ESTs	2.03
60	421295	AW081061	Hs.103180	Hs.103180: DC2 protein	2.03
	445417	AK001058	Hs.12680	Hs.12680: Homo sapiens cD FLJ10196 fls, c	2.03
	414683	AE296990	Hs.346689	NM_001826: Homo sapiens CDC28 protein kis	2.02
	447286	BE617537	Hs.23818	Hs.23818: phosphorotransferase-3-kinase, cytol	2.02
	459590	AA022848	Hs.170065	Hs.170065: ESTs	2.02
65	422785	AB241114	Hs.289088	Hs.289088: heat shock 90kD protein 1, alp	2.02
	452696	AB026645	Hs.211534	Hs.211534: Homo sapiens cD FLJ31055 fls,	2.02
	452056	AW955065	Hs.101150	Hs.101150: KIAA1949 protein	2.02
	456980	AA226696	Hs.353418	NM_014164: Homo sapiens FXRD domain-conta	2.01
	423527	AI206695	Hs.105661	Hs.105661: engulfment and cell motility 3	2.01
	429545	AB241164	Hs.356130	Hs.356130: ESTs	2.01
70	439180	AB393742	Hs.195057	Hs.195057: v-erb-b2 erythroblastic leukem	2.01
	437183	BE269100	Hs.269721	Hs.269721: growth arrest-specific 5	2.01
	436014	AF281134	Hs.283741	Hs.283741: axosome component, Rps46	2.01
	453329	T97205	Hs.153400	Hs.153400: interleukin 6 receptor	2.01
	407347	AA829647		T23514 seq325 -118 Homo sapiens cD clo	2.01
75	435370	AF94074	Hs.225838	Hs.225838: ESTs	2.01
	430617	AA462910	Hs.370502	Hs.370502: ESTs, Weakly similar to hypo	2.01
	427157	U51166	Hs.173824	NM_003211: Homo sapiens thymine D-glycosy	2.01
	424833	NM_003894	Hs.153405	NM_003894: Homo sapiens period homolog 2	2.01
80	440086	NM_004042	Hs.8906	NM_004042: Homo sapiens v-erbB simian leu	2.01
	438543	AA410141	Hs.192182	Hs.192182: ESTs	2.01
	417426	NM_002291	Hs.82124	NM_002291: Homo sapiens laminin, beta 1 (2.01
	412790	NM_014767	Hs.74583	NM_014767: Homo sapiens KIAA0275 gene pro	2.01
	445892	AB555500	Hs.93961	Hs.93961: Homo sapiens mR cD DKF Zp667009	2.01

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TABLE 38b:	
Play:	Unique Eos probe/seq identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers
1	
5	
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	419853	AF008283	DE24040	NM_002246:Homo sapiens potassium channel	4.11
	419858	AF009040	H039480	NM_004217:Homo sapiens tritor killer cell	4.11
	418751	BE309014	HL372548	NM_037248:phospholipaseC-3-like, recom	4.07
	414136	AB089894	HL75789	NM_005486:Homo sapiens N-acyl downstream	4.07
	414173	AB05653	HL75789	NM_037515:human C-X-C motif ligand	4.07
	416326	H03109	DE253395	NM_025395:Homo sapiens, transmembrane dom	3.92
	419175	AF027007	HL362996	NM_025996:KIA040779 protein	3.92
	424218	HL362996	HL143212	NM_036560:Homo sapiens transporter F (heko	3.91
	412640	KZ7788	HL362996	NM_036560:Homo sapiens transporter F (heko	3.91
	425023	KZ7522	HL362996	NM_000550:Homo sapiens cysteinylase 1, AT	3.87
	426482	KX0508	HL15362	NM_004154:Homo sapiens pyrimidinergic re	3.87
	449691	AF025344	HL133100	NM_013300:ESTs	3.87
	425157	AF554443	HL137447	NM_013747:Homo sapiens cys FLJ12169 fs	3.86
	420212	DL119	HL15418	NM_015418:ESTs	3.86
	443630	BE269042	HL9661	NM_028010:Homo sapiens desmosomes (proso	3.81
	448133	AA173157	HL7369	NM_038021:Homo sapiens folate receptor 1	3.79
	418030	BE363447	HL83321	NM_03321:neuroendocrine B	3.79
	421142	AW114491	HL7508	NM_005412:Homo sapiens serine threonine	3.79
	409162	H25530	HL5088	NM_002554:Homo sapiens solute carrier fa	3.79
	427115	AF525474	HL180428	NM_018042:KIA04181 protein	3.78
	412006	AW161518	HL790216	NM_019026:ESTs	3.78
	420419	AF540152	HL241359	NM_024135:Homo sapiens small inducible c	3.78
	422782	AF016225	HL114309	NM_014309:alpha2-macroglobulin 1, I	3.78
	420747	BE294407	HL9910	NM_09910:phospholipase, platelet	3.78
	414875	H26579	HL7522	NM_001020:Homo sapiens major histocomp	3.78
	418793	AF032287	HL80474	NM_00474:prostaglandin synthase, fibroblast	3.78
	418793	BE297145	HL14623	NM_003932:Homo sapiens integrin, gamma	3.78
	417289	DB8692	HL81815	NM_018185:growth factor receptor-bound p	3.78
	422872	X12784	HL119129	NM_011845:Homo sapiens collagen, type IV	3.78
	445695	BE362857	HL21406	NM_007315:Homo sapiens alpha1 transducin a	3.78
	418793	HL18081	HL32318	NM_032318:alpha2-macroglobulin 1, I	3.78
	408452	AA054683	HL192455	NM_019245:ESTs. Moderately similar to	3.78
	443996	AB181750	HL283437	NM_028347:H1 GNQ3 protein	3.78
	418689	AW516565	HL955636	AB565636:hOGG1, 1.8 kb, NHEC, C	3.78
	420998	HL765259	HL165590	NM_016590:Homo sapiens fibroblast	3.78
	418995	AW575522	HL190161	NM_014020:Homo sapiens Surcin protein (R18	3.6
	418199	AF297530	HL83668	NM_008211:Homo sapiens integrin, beta 2	3.6
	432595	AF297530	HL83668	NM_008211:Homo sapiens integrin, beta 2	3.6
	418765	NM_005424	HL51483	NM_005424:Homo sapiens, Similar to hREN	3.6
	418765	NM_005424	HL51483	NM_005424:Homo sapiens, Similar to hREN	3.6
	424263	BE521000	HL29444	NM_029444:protein small membrane	3.6
	424263	AW295112	HL153548	NM_015348:glutathione lysozyme phosphatase,	3.6
	420046	AA043655	HL206868	NM_020688:Homo sapiens cDN1A1056 fs,	3.6
	424415	NM_0010975	HL146530	NM_0010975:Homo sapiens epsilon2.2, (gamma	3.6
	420046	AF0200047	HL71113	NM_000077:Homo sapiens angiotensin I	3.6
	443834	AD145150	HL173548	NM_017354:ESTs	3.6
	431630	NM_002204	HL265829	NM_002204:Homo sapiens integrin, alpha 3	3.6
	418371	HL13560	HL84298	NM_004294:alpha1 integrin (variant) polypep	3.6
	418371	AV165180	HL208810	NM_020810:ESTs	3.6
	443834	AW564026	HL59952	NM_059525:ESTs. Weakly similar to alpha 5	3.6
	411393	AW19717437	HL69771	NM_019710:Homo sapiens B-factor, prop	3.6
	414311	HL085047	HL71746	NM_017146:alpha2-macroglobulin-1-like 1	3.5
	415143	X12451	HL76056	NM_001043:Homo sapiens protein, CTL	3.5
	415143	WT0448	HL179	NM_0179:human T65 myelocyte-specific protein	3.5
	414825	X03070	HL77432	NM_005228:Homo sapiens epidermal growth	3.5
	408194	AA501308	HL191797	NM_019179:ESTs	3.5
	416060	AW575472	HL351676	NM_035167:ESTs. Weakly similar to T0570	3.5
	416060	BE262545	HL80474	NM_003932:Homo sapiens small inducible c	3.5
	439656	AA169365	HL127310	NM_012730:hypothetical protein BC014915	3.4
	439656	BE260337	HL149693	NM_003932:Homo sapiens solute carrier fa	3.4
	413956	AF560441	HL28514	NM_028514:growth factor receptor-bound p	3.4
	413956	AW265197	HL240151	NM_024015:human Hmorgp 2 (Drosoph	3.4
	444488	AW192879	HL356660	NM_035660:peptide hydrolase transporter	3.4
	449475	AA340027	HL108557	NM_010857:hypothetical protein PI1057	3.4
	412276	BE262621	HL7398	NM_002415:Homo sapiens macrophage migra	3.4
	412276	AF0344	HL394	NM_001244:Homo sapiens calcium channel	3.4
	430301	AL127071	HL239927	NM_023927:Homo sapiens mRc cDN147544H1	3.4
	415388	AF018081	HL78409	Ilocus(NM_005682:Homo sapiens DNF22A	3.4
	432210	AF567421	HL273300	NM_027330:genf	3.4
	418717	AA4987	HL351554	NM_035154:Homo sapiens cDN1J32992 fs,	3.4
	425445	AL039185	HL774	NM_017758:Homo sapiens integrin receptor 1	3.4
	425445	AB002438	HL29596	NM_029596:Homo sapiens mRc from chromosome	3.4
	414803	X03100	HL914	NM_019149:histocompatibility complex,	3.4
	419001	M23234	HL1239	NM_001510:Homo sapiens apaf1 (nembrane	3.4
	430301	AF037848	HL127385	NM_012738:ESTs	3.4
	435021	AF021912	HL73962	NM_073962:ESTs	3.4
	417259	AW063838	HL81800	NM_018180:chondrin small lytic proteoglyc	3.4
	439373	AT5438	HL41271	NM_014127:Homo sapiens mRc full length	3.4
	419001	AA088171	HL12870	NM_012870:alpha19 protein	3.4
	431590	AF037789	HL263395	NM_026335:sema domain, transmembrane dom	3.4
	415000	AF025529	NL239812	NM_023982:serologically defined breast c	3.4
	416700	AA048958	HL34743	NM_001905:Homo sapiens caldesmon D4(50	3.4
	440516	S42303	HL161	NM_001792:Homo sapiens caldesmon D4(50	3.4
	440516	S42303	HL161	NM_001792:Homo sapiens caldesmon D4(50	3.4
	440516	S42303	HL161	NM_001792:Homo sapiens caldesmon D4(50	3.4

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421902	BE392717		BE392717/60130751F1 NIH_MGC_44 Homo sap	3.32
409220	BE243323	Hs.51233	Hs.51233 tumor necrosis factor receptor	3.32
421502	AF111856	Hs.105039	NM_005424:Homo sapiens solute carrier fa	3.32
416729	AA04165	Hs.1027	NM_004165:Homo sapiens Ras-related assoc	3.30
430302	AL137552	Hs.23867	Hs.23867Fg D protein	3.30
445084	H39914	Hs.250848	Hs.250848:Homo sapiens cD FLJ14761 fls,	3.29
406825	A982529	Hs.84298	Hs.84298:CD74 antigen [invariant polypep	3.28
446272	BE268912	Hs.14601	NM_005335:Homo sapiens hemagglutinin cel	3.28
437145	AF007216	Hs.5462	NM_003559:Homo sapiens solute carrier fa	3.27
444621	AE62808	Hs.110624	Hs.110624:ESTs	3.27
414652	AI036058	Hs.76807	Hs.76807:mapk heterocompatibility comple	3.27
436576	AA58213	Hs.77542	Hs.77542:ESTs, Weakly similar to S26650	3.26
424675	NM_005512	Hs.151641	NM_005512:Homo sapiens glycoprotein A re	3.25
437897	AA075561	Hs.146170	Hs.146170:hyposphthal protein FLJ20569	3.25
449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE3956	3.25
414788	X78342	Hs.77313	NM_003674:Homo sapiens cyclin-dependent	3.25
414249	AJ757994	Hs.273929	Hs.273929:gap25L2 protein	3.24
430396	D69742	Hs.241363	NM_004132:Homo sapiens cytochrome binding	3.23
424456	AA341017	Hs.25549	Hs.25549:hyposphthal protein FLJ20898	3.23
452303	R27257	Hs.57734	Hs.57734:G protein-coupled receptor like	3.22
425390	AJ092634	Hs.156114	NM_004548:Homo sapiens protein tyrosine	3.21
416033	NM_012201	Hs.76979	NM_012201:Homo sapiens gtp apparatus p	3.19
410531	N25156	Hs.25648	Hs.25648 tumor necrosis factor receptor	3.19
428065	AJ534046	Hs.157313	Hs.157313:ESTs	3.18
428216	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.18
429318	AW937046	Hs.6527	Hs.6527:G protein-coupled receptor 56	3.17
427640	AF058293	Hs.180515	NM_001355:Homo sapiens D-deoxycholate laul	3.17
409936	AK001691	Hs.57655	Hs.57655:dudulin 2	3.16
436001	AW903849	Hs.173840	Hs.173840:similar to endothelial cell-se	3.16
451154	AA015879	Hs.33536	Hs.33536:ESTs	3.16
422556	AW54722	Hs.76266	NM_001795:Homo sapiens cathepsin 5, type	3.16
407844	W25945	Hs.8173	Hs.8173:hyposphthal protein FLJ10803	3.15
428593	AW207440	Hs.185973	NM_003675:Homo sapiens degenerative sper	3.15
410026	AB12061	Hs.55016	Hs.55016:EP8B-related protein 2	3.15
445333	BE337941	Hs.44278	Hs.44278:RAB17, member RAS oncogene fami	3.14
448143	AF039704	Hs.20478	NM_003981:Homo sapiens ceroid-lipofuscin	3.14
423007	AA320134	Hs.196029	Hs.196029:Homo sapiens mR for KIAA1657 p	3.14
416511	NM_006762	Hs.79356	NM_005762:Homo sapiens Lysosomal-associ	3.13
429327	AAW08158	Hs.318893	Hs.318893:ESTs, Weakly similar to Z195_H	3.13
445699	NM_005397	Hs.16426	NM_005397:Homo sapiens podocytin-like	3.13
413916	N43613	Hs.75515	NM_000483:Homo sapiens apolipoprotein C-	3.13
434398	AA121098	Hs.3838	NM_006622:Homo sapiens serum-inducible k	3.12
441283	AA927670	Hs.131704	Hs.131704:ESTs	3.12
416945	BE246762	Hs.89499	NM_002698:Homo sapiens arachidonic 5-lipo	3.12
418458	AA332941	Hs.85226	NM_000235:Homo sapiens lipase A, lysosomal	3.11
409899	AW361656	Hs.49500	Hs.49500:KIAA0746 protein	3.11
436906	H95990	Hs.181244	Hs.181244 major histocompatibility compl	3.11
411089	AA455454	Hs.355702	Hs.355702:ESTs, Weakly similar to AC0048	3.11
423990	AL035071	Hs.279809	NM_005826:Homo sapiens tumor necrosis fa	3.11
425009	X58288	Hs.154151	NM_002845:Homo sapiens protein tyrosine	3.10
443601	AJ078554	Hs.42658	Hs.42658:Homo sapiens cD FLJ30167 fls, c	3.10
430603	AA148184	Hs.247280	Hs.247280:chromosome 20 open reading fra	3.10
413672	BE155536	Hs.32632	Hs.32632:ESTs, Moderately similar to hr	3.09
407786	AA687539	Hs.38922	NM_005727:Homo sapiens telraspin 1 (TSPA	3.09
414586	AA306160	Hs.16488	NM_002298:Homo sapiens lymphocyte cytoxo	3.08
423712	W46802	Hs.81988	Hs.81988:disabled homolog 2, mitogen-res	3.08
438652	AJ245820	Hs.6314	NM_012410:Homo sapiens type I transmembr	3.06
448364	T08558	Hs.292124	Hs.292124:ASPCH4 protein	3.06
426437	BE075537	Hs.165956	NM_004223:Homo sapiens ubiquitin-conjugat	3.06
437679	NM_014214	Hs.5753	NM_014214:Homo sapiens inositol(myo)-1p	3.06
422262	AJ022315	Hs.113387	NM_006498:Homo sapiens lectin, galactosid	3.05
410480	R57457	Hs.63884	NM_001257:Homo sapiens cathepsin 13, H-c	3.05
435818	AA700553	Hs.368614	Hs.368614:ESTs	3.05
418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	3.05
453613	F06838	Hs.374476	Hs.374476:ESTs	3.05
408051	AE623351	Hs.172146	Hs.172146:ESTs	3.05
432278	AL113205	Hs.274226	Hs.274226:hyposphthal protein FLJ23563	3.04
407949	W21874	Hs.247057	Hs.247057:ESTs, Weakly similar to 210926	3.04
418090	U57059	Hs.63429	NM_003810:Homo sapiens tumor necrosis fa	3.03
430165	AA578964	Hs.252437	Hs.252437:ESTs	3.03
429009	AA370362	Hs.573563	Hs.573563:EGF-TM7-ubiquitin-related pro	3.04
443864	N20617	Hs.194397	Hs.194397:ESTs, Moderately similar to 22	3.03
447831	AA433293	Hs.164115	Hs.164115:ESTs	3.02
413278	BE563085	Hs.833	NM_005101:Homo sapiens interferon-stimul	3.01
418870	AF147264	Hs.38914	Hs.38914:chemokine (C-X-C motif), recept	3.00
455376	AA653904	Hs.89862	Hs.89862:TNFRSF1A-associated via death d	3.00
439738	BE246502	Hs.9598	Hs.9598:sens domain, immunoglobulin doma	3.00
446416	AW288085	Hs.11156	NM_016454:Homo sapiens hyposphthal prot	3.00
406556	M16714	Hs.89643	Hs.89643:arabinoside kinase (Nucleoside Kinas	3.00
406826	AW516005	Hs.84298	Hs.84298:CD74 antigen [invariant polypep	2.99
418707	U97502	Hs.87497	Hs.87497:butyrophilin, subfamily 3, memb	2.99
421742	AW570004	Hs.107528	NM_016108:Homo sapiens androgen induced	2.99
406824	AW515961	Hs.84298	Hs.84298:CD74 antigen [invariant polypep	2.99

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435605	AF151815	Hs.4973	NM_015680	Homo sapiens hypothetical prot	2.98
410491	AA465131	Hs.64001	Hs.64001	Homo sapiens clone 25218 mRt seq	2.98
427648	AJ376722	Hs.180062	NM_004159	Homo sapiens proteasome (proso	2.98
411125	AA151547	Hs.68877	NM_000701	Homo sapiens cytochrome b-245,	2.98
435550	AJ244656	Hs.324507	Hs.324507	hypothetical protein FLJ02998	2.98
429373	NM_014694	Hs.200594	NM_014694	Homo sapiens KIAA0605 gene pro	2.98
444501	AF055581	Hs.13131	NM_005475	Homo sapiens lymphocyte adapto	2.97
416749	AH672727	Hs.16753	NM_000116	Homo sapiens endoglin (Osler-R	2.97
444207	AJ656064	Hs.374415	Hs.374415	ESTs	2.97
423325	AA652604	Hs.125359	NM_006286	Homo sapiens Thy-1 cell surfac	2.97
407792	AJ077715	Hs.39384	NM_014344	Homo sapiens four jointed box	2.97
445707	AA248720	Hs.114390	Hs.114390	ESTs	2.96
452688	AW954544	Hs.30942	NM_004053	Homo sapiens sphinx-92 (EFMB2)	2.96
418478	U93645	Hs.1174	Hs.1174	cyclin-dependent like inhibitor	2.95
411441	AL042355	Hs.70202	Hs.70202	WD repeat domain 10	2.95
443426	AF098158	Hs.9329	Hs.9329	chromosome 20 open reading fram	2.94
450876	AF189062	Hs.269576	Hs.269576	LAG1 longwey assurance homol	2.94
423539	AA374029	Hs.10902	Hs.10902	Homo sapiens cD FLJ23313	2.94
425421	L11669	Hs.157145	NM_001120	Homo sapiens tetraacycline tran	2.93
449879	HQ3573	Hs.267830	Hs.267830	Homo sapiens mR, cD DKFZp434E1	2.93
454075	R43826	Hs.16513	Hs.16513	Kruppel like zinc finger protei	2.93
421555	AB014520	Hs.301685	Hs.301685	KOXA020 protein	2.93
457949	W69171	Hs.334814	Hs.334814	hypothetical protein FLJ14868	2.92
443987	AW183128	Hs.10071	NM_016551	Homo sapiens seven transmembra	2.92
430259	BE550182	Hs.375142	Hs.375142	Raf/GEF-like protein 3, mouse h	2.91
415906	AF751387	Hs.26814	Hs.26814	Homo sapiens cD FLJ2256	2.91
429752	AJ344255	Hs.215354	NM_005913	Homo sapiens ring finger prote	2.91
451527	AF022813	Hs.26518	NM_003271	Homo sapiens transmembrane 4 s	2.91
425356	BE244879	Hs.155939	NM_005541	Homo sapiens inositol polyphos	2.91
427080	AW083287	Hs.301175	NM_002872	Homo sapiens ras-related C3 bo	2.91
425432	AF01501	Hs.189857	NM_003505	Homo sapiens paroxysm 2 (PON2	2.90
431476	BE612705	Hs.259697	Hs.259697	Nididine triad nucleotide bin	2.89
406659	AA663985	Hs.277477	Hs.277477	major histocompatibility compl	2.89
451144	AW956103	Hs.61712	Hs.61712	Homo sapiens cD FLJ1548	2.89
453062	AN973003	Hs.179959	Hs.179959	histamine receptor coactivator 1	2.88
426440	BE382756	Hs.169902	NM_005516	Homo sapiens solute carrier fa	2.88
456974	M12529	Hs.189401	NM_000041	Homo sapiens apolipoprotein E	2.88
418174	L20668	Hs.83656	Hs.83656	Rho GTP dissociation inhibitor	2.88
446055	AB15981	Hs.12909	Hs.12909	muclupin 1	2.88
423194	NM_004428	Hs.1624	NM_004428	Homo sapiens sphinx A1 (EF1)	2.87
427700	AA262294	Hs.180383	NM_001948	Homo sapiens dust specificity	2.87
410668	BE379794	Hs.159651	NM_016629	Homo sapiens hypothetical prot	2.87
444143	AW747996	Hs.160599	Hs.160599	ESTs, Weakly similar to I78865	2.87
407151	U25836	Hs.301527	Hs.301527	ESTs, Moderately similar to u	2.86
449549	AB25386	Hs.352579	Hs.352579	Homo sapiens, chromosome 20 p	2.85
439997	AA741151	Hs.137323	Hs.137323	ESTs	2.85
446143	BE245342	Hs.306079	NM_013338	Homo sapiens protein transport	2.85
417355	D13168	Hs.82202	Hs.82202	endothelin receptor type B	2.85
431985	AW298135	Hs.267659	NM_005113	Homo sapiens xav 3 oncogene IV	2.85
408877	AA479033	Hs.130315	Hs.130315	ESTs	2.85
429615	AF258827	Hs.211562	NM_005002	Homo sapiens ATP-binding casse	2.84
412014	AB20950	Hs.43761	Hs.43761	gap junction protein, alpha 7,	2.84
436749	AA584890	Hs.5302	NM_005140	Homo sapiens lectin, galactosi	2.84
419625	U91816	Hs.152885	NM_004556	Homo sapiens nuclear factor of	2.84
439941	AJ392640	Hs.18272	Hs.18272	solute carrier family 38, membe	2.84
436496	AA291959	Hs.5270	NM_004877	Homo sapiens gba maturation f	2.84
422100	AD95896	Hs.111554	NM_005373	Homo sapiens mR, cD DKFZp56O24	2.83
439730	AF035202	Hs.6654	Hs.6654	KIAA0667 protein	2.83
447217	BE465764	Hs.17778	NM_003872	Homo sapiens neurepin 2 (NRP	2.83
428343	AL043021	Hs.12705	Hs.12705	similar to HYPOTHETICAL 43.1 KD	2.82
440524	R71264	Hs.16798	Hs.16798	Homo sapiens mR, cD DKFZp56O24	2.82
415323	AL042003	Hs.296847	NM_003165	Homo sapiens specific paralog	2.81
439668	AB091277	Hs.302634	Hs.302634	krizled homolog 3 (Drosophila)	2.81
414570	Y00285	Hs.76473	NM_000876	Homo sapiens insulin-like grow	2.80
426535	AU077012	Hs.289582	NM_006287	Homo sapiens tissue factor pat	2.80
409849	AA159216	Hs.53505	Hs.53505	hypothetical protein FLJ20442	2.80
406655	M21533	Hs.277477	Hs.277477	major histocompatibility compl	2.79
415323	BE269352	Hs.949	NM_000433	Homo sapiens neutrophil cytosol	2.79
443195	BE148235	Hs.193063	Hs.193063	Homo sapiens cD FLJ14201	2.78
451356	AA748418	Hs.164577	Hs.164577	ESTs	2.78
420708	AA376654	Hs.350065	Hs.350065	Homo sapiens FLJ130634	2.78
433681	A004377	Hs.200360	Hs.200360	Homo sapiens cD FLJ13027	2.77
442559	AF078037	Hs.324051	NM_006663	Homo sapiens RNA-associated i	2.76
414509	AW161311	Hs.76294	NM_001780	Homo sapiens CD63 antigen (mel	2.76
431394	A0006092	Hs.252351	Hs.252351	HEVRI LTR-associating 7	2.76
417331	AA411297	Hs.61972	Hs.61972	SHC (Src homology 2 domain cont	2.76
415995	NM_004573	Hs.358888	NM_004573	Homo sapiens phospholipase C,	2.75
414811	NM_000707	Hs.77602	NM_000707	Homo sapiens damage-specific D	2.75
425076	C79594	Hs.334514	Hs.334514	chromosome 5 open reading fram	2.75
407893	BE408359	Hs.43621	Hs.43621	hypothetical protein MRC3205	2.75
407903	AJ287341	Hs.154029	Hs.154029	bHLH factor Hes4	2.75
416062	AA724811	Hs.334791	Hs.334791	similar to neural tetraspanin	2.75
428494	AA233439	Hs.184634	Hs.184634	hypothetical protein FLJ20005	2.75

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421506	BE302796	Hs.135297	NM_003258.Homo sapiens thymidine kiaz.	2.74
427581	NM_014788	Hs.179703	NM_014788.Homo sapiens tripartite motif.	2.74
424527	AW138558	Hs.334873	Hs.334873.carboxypeptidase M	2.74
439578	AW261234	Hs.355547	Hs.355547.nuclear receptor co-repressor	2.73
425188	AK020552	Hs.155271	Hs.155271.chromosome 20 open reading fra	2.74
428013	AF151020	Hs.181444	NM_016456.Homo sapiens hypothetical prot	2.73
430333	AW384710	Hs.132986	Hs.132986.Homo sapiens cD FLJ13588 fs,	2.73
450935	BE514743	Hs.355753	NM_009851.Homo sapiens tumor suppressor	2.73
421532	AW138207	Hs.146170	Hs.146170.hypothetical protein FLJ22995	2.73
445032	AB024113	Hs.78281	Hs.78281.regulator of G-protein siglin	2.73
444981	AW655398	Hs.12210	Hs.12210.tumor endothelial marker 6	2.72
439219	NJ3883	Hs.41322	Hs.41322-ESTs	2.72
410847	L3821	Hs.80281	NM_006403.Homo sapiens enhancer of filam	2.72
431319	AW262945	Hs.162459	Hs.162459-ESTs	2.72
424528	AW073971	Hs.238954	Hs.238954-ESTs. Weakly similar to putati	2.71
411213	AA676939	Hs.69285	NM_003873.Homo sapiens neuropilin 1 (NRP	2.70
433012	NM_004045	Hs.278910	NM_004045.Homo sapiens ATX1 antioxican	2.69
425345	AU077297	Hs.155994	NM_002877.Homo sapiens protein tyrosine	2.69
428923	BE047698	Hs.188785	Hs.188785-ESTs	2.69
427923	AW274357	Hs.301406	Hs.301406.hypothetical protein PP3501	2.69
446644	NM_003272	Hs.15791	NM_003272.Homo sapiens transmembrane 7 s	2.68
421143	T39528	Hs.107614	Hs.107614.hKFPZP5641171 protein	2.68
415207	NM_014745	Hs.75977	NM_014745.Homo sapiens KIAA0233 gene pro	2.68
420372	AW960049	Hs.293660	Hs.293660.gene overexpressed in astrocyt	2.68
420562	NM_000505	Hs.1321	NM_000505.Homo sapiens coagulation facto	2.67
425069	AA687465	Hs.299184	Hs.299184.potassium voltage-gated charme	2.67
416556	AW022266	Hs.61131	NM_003234.Homo sapiens F-act (TWRF3) ass	2.67
426251	M24263	Hs.168383	NM_000201.Homo sapiens intercellular adh	2.66
406701	AA780613	Hs.62954	Hs.62954.ferritin, heavy polypeptide 1	2.66
431681	AK000378	Hs.267566	Hs.267566.hypothetical protein FLJ20371	2.66
412833	AW955547	Hs.258632	Hs.258632.tubosomal protein S19	2.66
433011	AW672217	Hs.12082	Hs.12082-TRGA1	2.66
414774	X02419	Hs.77724	NM_002558.Homo sapiens plasminogen activ	2.66
427666	AC60119.comp	Hs.181013	NM_002529.Homo sapiens phosphoglycerate	2.66
413929	BE501089	Hs.75017	Hs.75017.collagen, type IV, alpha 2	2.66
424762	AL119442	Hs.183984	Hs.183984.eukaryotic translation initiat	2.65
422046	NM_012445	Hs.288126	NM_012445.Homo sapiens spondin 2, extrac	2.65
431350	AI192528	Hs.164537	Hs.164537-ESTs	2.65
450184	VG1096	Hs.237617	Hs.237617.vitellogenin/peptidase 9	2.65
419285	CG1887	Hs.89898	Hs.89898.HMAA002 protein	2.65
412157	AC059268	Hs.279898	Hs.279898.Homo sapiens cD FLJ23165 fs,	2.64
451253	H48299	Hs.26126	NM_006984.Homo sapiens claudin 10 (CLDN1	2.64
453905	AW997484	Hs.5003	Hs.5003.SUIT-RCBO Rho GTPase-activating	2.64
432581	AU076485	Hs.278441	NM_014634.Homo sapiens KIAA0016 gene pro	2.63
415702	AA169345	Hs.123177	Hs.123177.hypothetical protein EC011405	2.63
430223	NM_002514	Hs.235935	NM_002514.Homo sapiens nephroblastoma ov	2.63
417526	AA568906	Hs.82240	NM_004177.Homo sapiens syntaxin 3A (STX3	2.63
409956	AW103394	Hs.727	NM_002192.Homo sapiens inhibin, beta 1 (2.62
449843	RE5337	Hs.24030	NM_001860.Homo sapiens solute carrier fa	2.62
417389	BE260564	Hs.82045	NM_002391.Homo sapiens milkline (neutrit	2.62
446312	BE387853	Hs.171802	Hs.171802.Homo sapiens, clone IMAGE:3956	2.62
435099	AC034770	Hs.4756	Hs.4756.fap structure-specific endonuc	2.62
417920	SA7833	Hs.82827	NM_004037.Homo sapiens adenosine monoph	2.62
435102	AK033847	Hs.152001	Hs.152001.Homo sapiens, clone MGC:45521	2.62
422959	AV647015	Hs.349256	Hs.349256.paired immunoglobulin-like rec	2.62
419938	AU076772	Hs.1279	NM_001733.Homo sapiens complement compo	2.61
409584	AB047440	Hs.23691	NM_005856.Homo sapiens receptor (olactot	2.61
421552	BE314828	Hs.107911	Hs.107911-LATP-binding cassette, sub-fam	2.61
443577	AU078033	Hs.177170	Hs.177170-ESTs. Weakly similar to ALLU_H	2.61
453886	R66282	Hs.20247	Hs.20247-ESTs	2.61
421883	XS5079	Hs.1437	NM_000152.Homo sapiens glucosylidase, alph	2.60
440457	BE387593	Hs.21321	Hs.21321-granule cell differentiation pr	2.60
410295	AA741357	Hs.356624	Hs.356624-ESTs	2.59
420679	XS7152	Hs.99853	NM_001436.Homo sapiens fibrinogen (FBL)	2.59
451558	NM_001089	Hs.26630	NM_001089.Homo sapiens A-TD-binding casse	2.59
444672	259536	Hs.11669	Hs.11669.tumor necrosis factor, alpha 5	2.59
408669	HA425931	Hs.78146	Hs.78146.plaetel-derived endothelial cell adhes	2.59
426194	T50872	Hs.2001	Hs.2001.thrombospondin A synthase 1 (ptate	2.59
421814	L12350	Hs.108623	NM_003247.Homo sapiens thrombospondin 2	2.59
456371	S7625	Hs.89695	Hs.89695.insulin receptor	2.59
429098	AF030249	Hs.196176	NM_001358.Homo sapiens enoyl Coenzyme A	2.59
414443	AU077258	Hs.76144	NM_002605.Homo sapiens platelet derived	2.59
428484	AF104032	Hs.184601	NM_003486.Homo sapiens solute carrier lo	2.59
453309	A751809	Hs.32949	NM_005218.Homo sapiens desferrioxamine, beta 1	2.59
412867	AU076861	Hs.714637	NM_003217.Homo sapiens testis enhancin g	2.59
432827	208128	Hs.3109	Hs.3109-Rho GTPase activating protein 4	2.58
412669	AW880841	Hs.96908	NM_006034.Homo sapiens p53-induced prot	2.58
412115	AK001763	Hs.73239	Hs.73239.hypothetical protein FLJ10901	2.58
452860	T02069	Hs.258016	Hs.258016.Homo sapiens cD FLJ12143 fs,	2.58
435129	A338169	Hs.267096	Hs.267096-ESTs	2.57
424282	BE268621	Hs.149155	NM_003374.Homo sapiens voltage-dependent	2.57
410494	M36564	Hs.64016	NM_000313.Homo sapiens protein S (alpha)	2.56
433995	A1287912	Hs.3628	NM_004834.Homo sapiens mitogen-activated	2.56

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442666	R37337	Hs.12111	Hs.12111-ESTs	2.56
417640	D30857	Hs.82353	NM_006404.Homo sapiens protein C receptor	2.56
442622	NM_000435	Hs.8546	NM_000435.Homo sapiens Notch homolog 3 (2.56
430346	AJ000331	Hs.293441	Hs.293441.retinoblastoma-associated fact	2.55
415844	U94905	Hs.277445	Hs.277445.fatty acyl-CoA synthetase 10A	2.55
426500	NM_014638	Hs.170156	NM_014638.Homo sapiens KIAA0450 gene pro	2.55
408048	NM_007203	Hs.42322	NM_007203.Homo sapiens A kinase (PRKA) anc	2.54
450700	AW732799	Hs.25348	NM_005969.Homo sapiens foliastatin-like	2.54
417019	M16036	Hs.80867	NM_002350.Homo sapiens w-yes-1 Yamauchi	2.54
419378	R24922	Hs.90078	Hs.90078.nucleotide-sugar transporter si	2.54
422451	AA310753	Hs.42491	Hs.42491-ESTs, Moderately similar to hyp	2.53
435906	A186379	Hs.110796	Hs.110796.SAR1 protein	2.53
400231				2.53
417849	AW291587	Hs.82733	NM_007361.Homo sapiens nidogen 2 (NID2),	2.53
427380	NM_005534	Hs.177559	NM_005534.Homo sapiens interferon gamma	2.52
428385	AF112213	Hs.184062	Hs.184062.chromosome 20 open reading fra	2.52
438000	A182380	Hs.5385	Hs.5385.non-kise Cdc42 effector protein	2.52
446719	AA033627	Hs.21858	Hs.21858.serine (or cysteine) protease I	2.52
422396	W21872	Hs.7907	Hs.7907-3.Apoase kase	2.52
420787	AA564248	Hs.351292	Hs.351292.Homo sapiens cD FLJ32605 fs,	2.51
430590	AW363947	Hs.246381	NM_001251.Homo sapiens CD98 antigen (CD6	2.51
447026	BE313144	Hs.324644	Hs.324644.hypothetical protein IMAGE3455	2.51
439223	AW238299	Hs.256618	Hs.256618.U1L1 binding protein 2	2.50
435151	AA348482	Hs.4788	Hs.4788.nicotin	2.50
448202	AB002292	Hs.20695	NM_014629.Homo sapiens Rho guanine nucle	2.50
449943	AF104266	Hs.24212	Hs.24212.21arophin	2.50
425743	BE394495	Hs.159428	Hs.159428.H2L2-associated X protein	2.50
444681	AJ243337	Hs.288316	Hs.288316.chromosome 6 open reading fram	2.50
421643	BE281170	Hs.100357	NM_007126.Homo sapiens valosin-containin	2.50
425865	DE3476	Hs.172813	NM_003699.Homo sapiens Rho guanine nucle	2.49
423206	Y16207	Hs.300200	NM_005295.Homo sapiens protein phosphat	2.49
421846	AA017707	Hs.1432	NM_002743.Homo sapiens protein kase C su	2.49
421905	AI600247	Hs.32693	Hs.32693.Homo sapiens, Similar to RIKEN	2.49
419493	AF001212	Hs.30144	NM_002615.Homo sapiens proteasome (proso	2.49
422530	AW972300	Hs.116110	NM_004335.Homo sapiens bone marrow stem	2.48
444821	BE391629	Hs.8752	NM_014255.Homo sapiens transmembrane pro	2.48
416919	T97839	Hs.80454	NM_006402.Homo sapiens hepatitis B virus	2.48
443010	X97673	Hs.9004	NM_001697.Homo sapiens chondroin sulfa	2.48
403046	AW500115	Hs.227622	NM_014267.Homo sapiens p45 protein (P45)	2.48
426028	US2112	Hs.182018	NM_001562.Homo sapiens interleukin-1 rec	2.47
424307	AW293399	Hs.356377	Hs.356377.Homo sapiens, clone IMAGE3633	2.46
434511	R26982	Hs.18106	Hs.18106-ESTs, Weakly similar to T06291	2.46
454390	AB020713	Hs.56595	Hs.56595.KIAA0906 protein	2.46
417785	X59812	Hs.62568	NM_000784.Homo sapiens cytochrome P450,	2.46
424673	AA345051	Hs.294022	Hs.294022.Homo sapiens nrl full length in	2.46
422003	AA361760	Hs.296326	Hs.296326-ESTs, Weakly similar to A33633	2.46
432126	AA865239	Hs.37196	Hs.37196.putative G protein coupled rece	2.46
444937	AA542943	Hs.321231	NM_003779.Homo sapiens UDP-Galactose 4-ep	2.46
403534	N98188	Hs.158472	Hs.158472.Homo sapiens cD FLJ2224 fs,	2.46
401179				2.46
418151	AA864238.comp	Hs.83883	NM_005731.Homo sapiens actin related pro	2.45
422648	D66963	Hs.118693	Hs.118693.Melanoma associated gene	2.45
427789	BE243578	Hs.2200	NM_005041.Homo sapiens perlecan 1 (perle	2.45
431222	X56777	Hs.273730	NM_007155.Homo sapiens zo pellucida glyco	2.45
411529	AA430348	Hs.317596	Hs.317596.Homo sapiens cD FLJ12927 fs,	2.45
426825	AL132415	Hs.297753	NM_003380.Homo sapiens vimentin (VIM), m	2.45
422442	AJ251760	Hs.273365	NM_018652.Homo sapiens GS complex locus	2.44
409105	AY152207	Hs.270977	Hs.270977-ESTs	2.44
426410	BE298446	Hs.305890	Hs.305890.BCL2-like 1	2.44
421064	A245432	Hs.101382	NM_006291.Homo sapiens tumor necrosis fa	2.44
428157	AF1789719	Hs.198427	NM_000183.Homo sapiens hemokinin 2 (HK2),	2.44
424308	BE338787	Hs.146163	NM_014883.Homo sapiens homocysteine-indu	2.44
424825	AF207069	Hs.153357	NM_001084.Homo sapiens procollagen-lysin	2.44
426031	AA295251	Hs.166066	Hs.166066.cisplatin resistance associa	2.43
409817	BE296464	Hs.56607	Hs.56607.Williams-Beuren syndrome chromo	2.43
423559	AF00462	Hs.22039	NM_004955.Homo sapiens matrix metallopro	2.43
426761	A015700	Hs.172089	Hs.172089.pro-oncotic receptor inducin	2.43
429332	AF030403	Hs.199263	NM_013233.Homo sapiens serine threonine	2.43
425923	NM_005026	Hs.162908	NM_005026.Homo sapiens phosphatidylste-	2.43
432211	BE245350	Hs.273333	Hs.273333.hypothetical protein FLJ10385	2.43
433330	AF019226	Hs.80136	Hs.80136.FAHS3, member RAS oncogene famil	2.42
420539	AA282735	Hs.44004	Hs.44004.A0031 protein	2.42
413243	AA769266	Hs.193657	Hs.193657-ESTs	2.42
435029	AF167706	Hs.15280	Hs.15280.cysteine-rich motor neuron 1	2.42
422374	AF173269	Hs.1519	Hs.1519.protein kase, cAMP-dependent, re	2.42
444501	AW247624	Hs.11342	NM_001448.Homo sapiens nupurine 1 (PINU1	2.42
414919	AW087337	Hs.194461	Hs.194461-ESTs	2.42
419555	AA428520	Hs.30001	NM_006667.Homo sapiens progesterone rece	2.42
430642	AF264422	Hs.119178	Hs.119178.cation-chloride cotranspor	2.42
418245	AA086767	Hs.83883	Hs.83883.transmembrane, prostate androge	2.42
444215	AB033075	Hs.10669	Hs.10669.development and differentiation	2.41
408683	S18665	Hs.46647	NM_016614.Homo sapiens TRAF and TNF rece	2.41
423701	AA329856	Hs.143022	Hs.143022-ESTs	2.41

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5	441783	BE13412	He 7961	He 7961:1 Homo sapiens clone 25012 mR seq	2.41
	428072	BE298602	He 182366	NM_016252:Homo sapiens heat shock protel	2.41
	434599	AB002313	He 3989	He 3889:plexin B2	2.40
	442351	W52642	He 8261	He 8261:SPRY domain-containing SOCS box	2.40
	407894	AJ278133	He 41143	He 41143:phospholipase C, beta 1 (phosph	2.40
10	454499	W16752	He 32961	He 32961:1:sem domain, immunoglobulin dom	2.40
	408688	AI634522	He 152926	He 152926:KIAA1268 protein	2.40
	422448	AW372922	He 116774	He 116774:4:nintegrin, alpha 1	2.39
	416269	AA177138	He 101671	He 101671:ESTs	2.39
	435679	AJ23607	He 435663	He 435663:transmembrane, prostate and/or	2.38
15	429281	NM_002733	He 3136	NM_002733:Homo sapiens protein kinase, AMP	2.38
	419846	NM_015977	He 285681	He 285681:Williams Beuren syndrome chrom	2.38
	422110	AJ26736	He 111179	He 111179:5:scroled protein, acidic, cyst	2.38
	413992	AA128656	He 118665	He 118665:ESTs	2.38
	433969	AW207279	He 271786	He 271786:ESTs, Weakly similar to PCA395	2.37
20	451267	AJ033894	He 117865	He 117865:solute carrier family 17 (anio	2.37
	447526	AI048753	He 303649	NM_002982:Homo sapiens small inducible c	2.37
	441623	AA315805	He 348710	He 348710:Homo sapiens, clone IMAGE-4242	2.37
	421255	NM_007289	He 1299	NM_007289:Homo sapiens membrane metallo	2.37
	409274	NM_003930	He 52644	NM_003930:Homo sapiens src family associ	2.36
25	422801	AF125672	He 287994	He 287994:nuclear receptor co-repressor	2.36
	407387	AA575668	He 41072	He 41072:2:amine (or cysteine) protein 1	2.36
	405212	AA297567	He 43728	NM_015569:Homo sapiens weakly similar to	2.36
	430478	NM_014349	He 241535	NM_014349:Homo sapiens apolipoprotein L	2.36
	405102				2.35
30	425953	AL122055	He 129836	He 129836:KIAA1028 protein	2.35
	426125	XJ7241	He 166494	NM_003451:Homo sapiens FAT tumor suppres	2.35
	422024	NM_002436	He 1861	NM_002436:Homo sapiens membrane protein,	2.35
	420676	AJ434780	He 4248	He 4248:Homo sapiens PP3751 mR, complete	2.35
	421079	AW404994	He 101695	He 101695:WCK adaptor protein 2	2.35
35	480309	AF207989	He 58014	He 58014:G protein-coupled receptor, fam	2.34
	412658	BE391679	He 75087	NM_005112:Homo sapiens FAST kinase (FASTK)	2.34
	430363	M28713	He 274464	NM_000398:Homo sapiens diaphorase (DH) (2.34
	425297	JO4088	He 155346	NM_001067:Homo sapiens topoisomerase (D)	2.34
	451035	AL678785	He 430	NM_002670:Homo sapiens plasmin 1 (I) iso	2.34
40	445027	AJ271216	He 22380	He 22380:diaphorase II	2.34
	429457	BE243065	He 202955	He 202955:hypothetical protein FLJ20507	2.34
	417709	DE7434	He 82426	NM_014734:Homo sapiens KIAA0247 gene pro	2.34
	412826	AW954569	He 278875	He 278875:bromodomain-containing 4	2.34
	425147	W19744	He 180059	He 180059:Homo sapiens c-Fos 13.90 fts	2.34
45	430702	U56979	He 278558	NM_000186:Homo sapiens H factor 1 (comp	2.33
	456804	AA21645	He 139651	NM_001233:Homo sapiens caveolin 2 (CAV2)	2.33
	453648	W12493	He 28329	He 28329:cytosolic phosphatase 1, regulato	2.33
	450812	AB002380	He 25515	He 25515:MCF-2 cell line derived transfo	2.33
	422575				2.33
50	424670	W61215	He 116651	NM_005797:Homo sapiens epithelial V-like	2.32
	452960	AK001336	He 31137	NM_006504:Homo sapiens protein tyrosine	2.32
	442988	AK000606	He 8988	NM_004871:Homo sapiens golgi SP receptor	2.32
	410639	BE260447	He 55234	He 55234:DEAD(H) Asp-Glu-Ala-Asp(His) bo	2.32
	416169	W42913	He 79389	NM_004231:Homo sapiens ATPase, H+ transp	2.32
55	450160	BE048099	He 163788	He 183738:FERM, RhoGEF (ARHGEF) and p1ec	2.32
	407223	H96850		H96850:rw03b12.s1 Soares melanocyte 2Noh	2.32
	426780	BE242284	He 172199	NM_001114:Homo sapiens adenylate cyclase	2.32
	434987	AW975114	He 371677	He 371677:ESTs	2.32
	416354	NM_000633	He 79241	NM_000533:Homo sapiens B-cell CLL/lympho	2.31
60	453107	NM_016113	He 279746	NM_016113:Homo sapiens transient recepto	2.31
	422953	M79141	He 13234	He 13234:ESTs, Weakly similar to hypoph	2.31
	433618	AA602639	He 345494	He 345494:ESTs, Moderately similar to ZN	2.31
	435854	AA811347		AA811347:wb01n06.s1 NC1_CGAP_GCB1 Homo s	2.31
	446125	AW085909	He 356618	He 356618:ESTs, Weakly similar to PC259	2.31
65	408716	AW57639	He 151714	He 151714:peroxisomal proliferator-activ	2.30
	433250	AW156134	He 220277	He 220277:ESTs, Weakly similar to expres	2.30
	410168	AW834050	He 351432	He 351432:tensin	2.30
	446342	BE298665	He 14846	He 14846:Homo sapiens mR, cD DKFZp564D01	2.30
	418452	BE379749	He 85201	NM_005127:Homo sapiens C-type (calcium d	2.30
70	453175	NM_006534	He 32217	NM_006534:Homo sapiens RAB32, member RAS	2.29
	409012	AL117435	He 497426	He 497426:DKFZP434C216 protein	2.29
	452848	AA171193	He 288912	He 288912:BBP-like protein 2	2.29
	418838	AW385224	He 351598	He 351598:actinucleotide pyrophosphatase/	2.29
	422562	A962063	He 118397	NM_001129:Homo sapiens AE binding protei	2.28
75	432628	AA042326	He 287402	He 287402:chromitin H-sulfotransferase	2.28
	412948	BE243313	He 334851	NM_005149:Homo sapiens LIM and SH3 prote	2.28
	426068	AF029778	He 166154	NM_002226:Homo sapiens jagged 2 (JAG2),	2.28
	456919	NM_003900	He 182248	NM_003900:Homo sapiens sequestosome 1 (S	2.28
	452886	AW045449	He 58373	He 58373:ESTs	2.28
80	453963	H94987	He 164450	He 164450:ESTs	2.28
	407736	NI4714	He 349326	He 349326:Homo sapiens cD FLJ30677 fs,	2.28
	413211	AW967107	He 109274	He 109274:hypothetical protein MGCA85	2.28
	422051	AW327546	He 111024	He 111024:solute carrier family 25 proto	2.27
	428438	AA267992	He 505951	He 505951:Juncus kinase 1 (a protein tyrosi	2.27
	436278	BE395290	He 5097	NM_004710:Homo sapiens syngaprin 1 (SYN	2.27
	454080	AI199711	He 576	NM_000147:Homo sapiens luciferase, alpha	2.27
	426542	AF190746	He 170310	NM_017424:Homo sapiens cat eye syndrome	2.27

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	417115	AW952792	Hs.334612	NM_003094 Homo sapiens small nuclear nb	2.21
	420291				2.25
	412898	A129903	Hs.74669	NM_006534 Homo sapiens vesicle-associate	2.25
	413020	R98736		R98736.y11609.1 Soares fetal liver cpl	2.25
5	413939	AL07051	Hs.199961	Hs.199961-ESTs, Weakly similar to hypoth	2.25
	408681	AW553853	Hs.281462	Hs.281462 hypothetical protein FLJ14251	2.25
	412330	NM_005100	Hs.788	NM_005100 Homo sapiens A kinase (PRKA) anc	2.25
	442083	R50192	Hs.162062	Hs.162062-ESTs	2.25
	412171	NM_000519	Hs.43523	NM_000519 Homo sapiens peptidylglycine a	2.25
10	433376	A219361	Hs.74122	NM_001225 Homo sapiens caspase 4, apopto	2.25
	438562	A1566826	Hs.25890	Hs.25890-ESTs, Weakly similar to transdu	2.25
	443883	AA114212	Hs.9530	NM_001235 Homo sapiens serine (or cystei	2.25
	416976	BE423895	Hs.80800	Hs.80800-major vault protein	2.24
	416944	AA344481	Hs.80426	Hs.80426-brain and reproductive organ-ex	2.24
15	400288	X06256	Hs.149609	NM_002205 Homo sapiens integrin, alpha 5	2.24
	407504	W44735	Hs.107260	Hs.107260-putative UDP-Galac polypeptide	2.24
	429690	AW956329	Hs.23721	Hs.23721-ESTs	2.24
	443813	AA878372	Hs.93961	Hs.93961 Homo sapiens mR, cd DKF Zp67009	2.24
	427458	BE208364	Hs.29283	Hs.29283-ESTs, Weakly similar to LKHU pr	2.24
20	454294	AB000734	Hs.50640	NM_003745 Homo sapiens JAK binding prote	2.24
	407192	AA609200	Hs.366318	Hs.366318-ESTs	2.23
	425751	T10239	Hs.1940	NM_001816 Homo sapiens crystallin, alpha	2.23
	456437	A1924228	Hs.115185	Hs.115185-ESTs	2.23
25	413019	BE281604	Hs.75140	NM_002337 Homo sapiens low density lipop	2.23
	418862	BE550964	Hs.85939	Hs.85939-ATP synthase, H+ transporing,	2.23
	433284	AA879470	Hs.56849	Hs.56849-Homo sapiens cd FLJ11492 fl, c	2.23
	429530	M85289	Hs.211573	NM_005529 Homo sapiens heparan sulfatase p	2.23
	427699	AK000436	Hs.179791	Hs.179791-RAB20, member RAS oncogene fam	2.23
30	421917	AB028943	Hs.109445	Hs.109445-hypermethylated in cancer 2	2.23
	446616	BE5964	Hs.334873	Hs.334873-carboxypeptidase M	2.23
	407232	X04526		X04526-human liver mR for beta-subunit 5	2.23
	427398	AF047033	Hs.132904	Hs.132904-sodium carrier family 4, sodiu	2.23
	446755	AW451473	Hs.16134	NM_005990 Homo sapiens serine/threonine	2.22
35	452665	A1924046	Hs.119567	Hs.119567-ESTs, Weakly similar to ALU1_H	2.22
	431393	AW971493	Hs.134269	Hs.134269-ESTs, Weakly similar to 20040	2.22
	431890	X17033	Hs.271996	NM_002203 Homo sapiens integrin, alpha 2	2.22
	428782	X12830	Hs.193400	NM_000565 Homo sapiens interleukin 6 rec	2.22
	466006	NM_004403	Hs.135330	NM_004403 Homo sapiens deafness, autosom	2.22
40	436418	AL261874	Hs.4245	Hs.4245-chromosome 11 hypothetical prote	2.22
	423869	BE493301	Hs.134012	NM_005868 Homo sapiens C1q-related fact	2.21
	437730	AW071087	Hs.239176	Hs.239176-insulin-like growth factor 1 r	2.21
	444020	R92962	Hs.35052	Hs.35052-ESTs	2.21
	413882	AA132973	Hs.184492	Hs.184492-Homo sapiens mR, cd DKF Zp66780	2.21
45	412654	AB034980	Hs.374319	Hs.374319-ESTs	2.21
	446988	Y09763	Hs.22785	NM_004951 Homo sapiens gamma-aminobutyri	2.21
	426841	A052358	Hs.131741	Hs.131741-ESTs	2.21
	408196	AL034548	Hs.43627	NM_009493 Homo sapiens SRY (sex determin	2.21
	451711	AK000461	Hs.26890	Hs.26890-cat eye syndrome chromosome 10q	2.20
50	414325	AA251929	Hs.353341	Hs.353341 Homo sapiens, clone IMAGE 3533	2.20
	424512	X53002	Hs.149846	NM_002213 Homo sapiens integrin, beta 5	2.20
	448883	BE614989	Hs.7503	Hs.7503-hypothetical protein FLJ14153	2.20
	411296	BE207307	Hs.10114	Hs.10114-growth suppressor 1	2.20
	452268	NM_003512	Hs.28777	NM_003512 Homo sapiens H2A histone famil	2.20
55	416810	AF035606	Hs.80019	NM_011232 Homo sapiens programmed cell d	2.20
	441415	H21497	Hs.7471	Hs.7471-BBP-like protein 1	2.20
	444212	AW503976	Hs.10649	NM_004848 Homo sapiens basement membrane	2.19
	428644	AA953322	Hs.301404	NM_006743 Homo sapiens R-binding motif p	2.19
	430017	AA263172	Hs.35	NM_002832 Homo sapiens protein tyrosine	2.19
	424490	AJ278016	Hs.55565	Hs.55565-ankyrin repeat domain 3	2.19
60	431193	AW748505	Hs.296770	Hs.296770-XGA1719 protein	2.19
	453686	AL110326	Hs.334679	Hs.334679-ESTs, Weakly similar to Z195_H	2.19
	444822	AW180830	Hs.186273	Hs.186273-ESTs	2.19
	416065	BE207931	Hs.78996	NM_002952 Homo sapiens proliferating cel	2.19
	442045	C05768	Hs.8078	Hs.8078-Homo sapiens clone FB03 Cri-de-c	2.19
65	423604	AW463448	Hs.17706	NM_006084 Homo sapiens interferon-stimul	2.19
	426024	Z29067	Hs.22236	Hs.22236-NMAA (never in mitosis gene abn	2.19
	424503	NM_002205	Hs.149509	NM_002205-Homo sapiens integrin, alpha 5	2.19
	437696	Z83844	Hs.5790	Hs.5790-hypothetical protein dJ37E16.5	2.18
	405204				2.18
70	426168	NM_001982	Hs.199067	NM_001982-Homo sapiens v-erb-b2 erythro	2.18
	417418	NM_002468	Hs.82116	NM_002468-Homo sapiens myoid different	2.18
	412773	H15785	Hs.74573	NM_012598 Homo sapiens similar to vaccin	2.18
	409402	AF208234	Hs.695	NM_000100 Homo sapiens cystatin B (ptef	2.18
	443791	WE4458	Hs.143345	Hs.143345-ESTs	2.18
75	435349	AL122648	Hs.4746	Hs.4746-hypothetical protein FLJ21324	2.18
	418399	AA830613	Hs.293849	Hs.293849-ESTs	2.18
	460712	AJ732130	Hs.270496	Hs.270496-ESTs, Weakly similar to ALUB_H	2.18
	422007	AJ739435	Hs.39168	Hs.39168-ESTs, Weakly similar to T17340	2.18
	453676	AW853745	Hs.286035	Hs.286035-hypothetical protein FLJ22686	2.18
80	415718	F30631	Hs.200237	Hs.200237-ESTs	2.18
	452688	AA721140	Hs.49930	Hs.49930-ESTs, Weakly similar to B34087	2.18
	415888	BE407713	Hs.78943	NM_000396 Homo sapiens bleomycin hydrola	2.17
	409453	A885516	Hs.95612	Hs.95612-ESTs	2.17

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417512	X76534	Hs.82226	NM_002510 Homo sapiens glycoprotein (tra	2.17
427202	BE272922	Hs.173936	NM_000628 Homo sapiens interleukin 10 m	2.17
440983	M20681	Hs.7594	NM_006931 Homo sapiens solute carrier fa	2.17
416084	116991	Hs.79006	NM_012145 Homo sapiens deoxythymidylate	2.17
429942	X6264	Hs.211579	NM_006500 Homo sapiens melanoma adhesio	2.17
427213	AW007211	Hs.348389	Hs.348389 hypothetical protein FLJ12876	2.17
337763	AA469369	Hs.5831	NM_003254 Homo sapiens tissue inhibitor	2.17
454000	AA040620	Hs.5672	Hs.5672 gcj2 membrane protein S8140	2.17
424267	X14008	Hs.234734	NM_000233 Homo sapiens tyrosine (ret amy	2.16
403857				2.16
406648	AA563730	Hs.277477	Hs.277477 major histocompatibility compl	2.16
400265				2.16
442379	NM_004613	Hs.6265	NM_004613 Homo sapiens transferrin 2	2.16
441892	AB028981	Hs.8021	Hs.8021 KIAA1065 protein	2.16
417446	AL118671	Hs.82163	NM_000836 Homo sapiens monomine oxidase	2.16
418386	AA361739	Hs.84549	NM_002494 Homo sapiens DH dehydrogese (u	2.16
414053	BE391635	Hs.75725	NM_003564 Homo sapiens transgene 2 (TAG	2.16
440906	AW161556	Hs.240170	Hs.240170 hypothetical protein MGC2731	2.16
447690	AW160386	Hs.163667	Hs.163667 ESTs, Weakly similar to CAT1_H	2.16
408279	AF216955	Hs.44095	Hs.44095 cyp19c1 (cytochrome) onkofuncta	2.16
426152	BE299190	Hs.167246	Hs.167246 P450 (cytochrome) onkofuncta	2.16
437952	DE3209	Hs.5347	NM_014585 Homo sapiens solute carrier fa	2.15
415661	AF057307	Hs.76575	Hs.76575 procaspase (variant) Gaudier die	2.15
425302	U79115	Hs.155566	NM_003805 Homo sapiens CASP2 and RIPK1 d	2.15
425996	W67330	Hs.374451	Hs.374451 ESTs	2.15
413745	AW247262	Hs.75514	NM_000270 Homo sapiens nucleoside phosph	2.15
422070	AF149765	Hs.111126	Hs.111126 putative tumor-transforming 1	2.15
448424	AW008982	Hs.31924	Hs.31924 ESTs	2.15
430035	NM_003463	Hs.227777	NM_003463 Homo sapiens protein tyrosine	2.15
430407	AA57122	Hs.129673	Hs.129673 eukaryotic translation initiat	2.15
435551	AF212365	Hs.5479	Hs.5479 nucleoside 17B recepto	2.15
437741	BE561610	Hs.5809	Hs.5809 putative transmembrane protein;	2.15
441192	AA526626	Hs.7736	NM_016504 Homo sapiens mitochondrial rib	2.15
435780	AB029012	Hs.4990	Hs.4990 KIAA1089 protein	2.15
411155	NM_000169	Hs.63989	NM_000169 Homo sapiens galactosidase, at	2.14
425692	AW381162	Hs.343806	Hs.343806 hypothetical protein FLJ13951	2.14
427600	AW630518	Hs.179774	NM_002618 Homo sapiens proteasome (proso	2.14
426818	AA554827	Hs.292996	Hs.292996 postmeiotic segregation increa	2.14
442110	AF113006	Hs.8102	NM_001023 Homo sapiens ribosomal protein	2.14
407797	AW005254	Hs.39850	Hs.39850 kinase-like 1	2.14
443044	N28522	Hs.8935	NM_014298 Homo sapiens quinoline phospho	2.14
437103	AW136408	Hs.152940	Hs.152940 ESTs	2.14
442069	AW664144	Hs.297007	Hs.297007 Homo sapiens cdc FLJ32174, fcs	2.14
424984	NA_000546	Hs.1840	NM_000546 Homo sapiens tumor protein p53	2.14
455007	AW341135	Hs.58104	Hs.58104 Homo sapiens, clone IMAGE 47309	2.14
411926	AW014588	Hs.72925	NM_003475 Homo sapiens chromosome 11 ope	2.14
449644	AW960707	Hs.148324	Hs.148324 ESTs	2.14
422675	BE0116517	Hs.115140	NM_001970 Homo sapiens eukaryotic transl	2.14
426566	N56712	Hs.2229	Hs.2229 CD9 antigen, beta polypeptide 1	2.14
493979	NM_014840	Hs.200598	NM_014840 Homo sapiens KIA0537 gene pro	2.13
410290	AA402307	Hs.322844	Hs.322844 hypothetical protein DKFZ564A	2.13
443895	AW979048	Hs.292566	Hs.292566 YEAM protein	2.13
428145	BE243327	Hs.162626	NM_012264 Homo sapiens chromosome 22 ope	2.13
453518	AW503205	Hs.27268	Hs.27268 Homo sapiens cdc FLJ21933, fcs	2.13
456534	X91195	Hs.100623	Hs.100623 protein phosphatase 1, regulat	2.13
419972	AL041465	Hs.162562	Hs.162562 p21ip1-67	2.13
424950	AA602917	Hs.156974	Hs.156974 ESTs	2.13
427557	NM_002659	Hs.179657	NM_002659 Homo sapiens plasminogen activ	2.13
431449	MS5964	Hs.256278	NM_001066 Homo sapiens tumor necrosis fa	2.13
418758	AW959311	Hs.172012	Hs.172012 hypothetical protein DKFZp434J	2.13
434202	BE362411	Hs.31764	NM_000856 Homo sapiens gamma-tubule kise 1	2.13
433233	AB040207	Hs.301804	Hs.301804 KIAA1104 protein	2.12
452700	AA859390	Hs.288940	Hs.288940 transmembrane protein 8 (five	2.12
438033	T26483	Hs.6059	NM_016938 Homo sapiens EGF-containing fi	2.12
400847				2.12
447547	NA_007229	Hs.18842	NM_007229 Homo sapiens protein kise C an	2.12
417052	NM_000712	Hs.81029	NM_000712 Homo sapiens biliverdin reduct	2.12
413284	AW077055	Hs.289107	NM_001166 Homo sapiens becalovirus IAP r	2.11
434558	AW264102	Hs.39168	Hs.39168 ESTs, Weakly similar to 117340	2.11
404030				2.11
410801	BE275469	Hs.66493	Hs.66493 Down syndrome critical region 9	2.11
418613	AA744529	Hs.86575	Hs.86575 mitogen-activated protein kise	2.11
447087	AW603870	Hs.301872	Hs.301872 hypothetical protein MGC4640	2.11
433026	AW160616	Hs.273921	NM_016127 Homo sapiens hypothetical prot	2.11
426433	L138619	Hs.163875	NM_001714 Homo sapiens fibronectin 3	2.11
424239	U09759	Hs.256857	NM_002752 Homo sapiens mitogen-activated	2.11
437279	AL359575	Hs.23765	Hs.23765 membrane metallo-endopeptidase-	2.11
400708				2.11
455705	AW161061	Hs.356580	Hs.356580 ESTs, Weakly similar to zinc f	2.11
417599	AB023468	Hs.62954	Hs.62954 dentin, heavy polypeptide 1	2.10
416728	AB024597	Hs.79658	NM_001894 Homo sapiens casain kise 1, ep	2.10
429520	H05430	Hs.288433	Hs.288433 neurotrophin	2.10
422209	U79745	Hs.114924	NM_004694 Homo sapiens solute carrier fa	2.10

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5	436114	AA778232	Hs.19515	Hs.19515:ESTs. Highly similar to NR63_HU	2.10
	405517				2.10
	421872	AA359753	Hs.22824	Hs.22824:MYB binding protein (P160) 1a	2.10
	437172	X04558	Hs.45544	Hs.45544:neurotrophic tyrosine kinase, rec	2.10
	431214	AA294921	Hs.348024	NM_002811:Human sapiens vnf similar like	2.10
	412856	BE386745	Hs.74631	NM_001728:Human sapiens basigin (BSG), mR	2.10
	442064	AA223667	Hs.88594	Hs.88594:Human sapiens, clone IMAGE:43329	2.10
	434845	BE670507	Hs.325321	Hs.325321:WD repeat domain 18	2.10
10	426728	NM_007118	Hs.367889	NM_007118:Human sapiens triple function 4	2.09
	415696	BE370320	Hs.51444	NM_002705:Human sapiens dual specificity	2.09
	448913	AA194422	Hs.22564	NM_004599:Human sapiens myosin VI (MYO6)	2.09
	414721	X90392	Hs.77091	NM_006730:Human sapiens deoxythionuclease	2.09
	446588	NM_002406	Hs.15153	NM_002406:Human sapiens mannoseyl (alpha 1	2.09
	432095	X94630	Hs.3107	Hs.3107:CD97 antigen	2.09
15	447032	AK000310	Hs.17138	Hs.17138:hypothetical protein FLJ20303	2.09
	447484	AA464839	Hs.292566	Hs.292566:YEA4 protein	2.09
	440188	AK001812	Hs.7036	Hs.7036:N-acetylglucosamine kinase	2.09
	445584	AF217518	Hs.8360	Hs.8360:PDZD12 protein	2.09
	402559				2.09
20	418943	AW377752	Hs.83341	Hs.83341:AXL receptor tyrosine kinase	2.09
	448888	AW166663	Hs.200242	Hs.200242:caspase 9 recruitment domain fam	2.09
	4391010	AA026844	Hs.261587	Hs.261587:GCH2 eff2Alpha kinase	2.09
	422573	AW027985	Hs.295726	Hs.295726:integrin, alpha V (vitronectin	2.08
	416448	L13210	Hs.79339	NM_005567:Human sapiens lectin, galactosi	2.08
25	428727	AF078847	Hs.191356	NM_005151:Human sapiens general transcrip	2.08
	410301	AW302935	Hs.740	Hs.740:PTK2 protein tyrosine kinase 2	2.08
	446538	AB594444	Hs.104679	Hs.104679:Human sapiens, clone MGC:13216	2.08
	421205	AA137540	Hs.102541	Hs.102541:nuclein 4	2.08
	411779	AA202811	Hs.72050	NM_003551:Human sapiens non-metastatic ce	2.08
30	427704	AW3971063	Hs.292882	Hs.292882:ESTs	2.07
	413510	BE149455	Hs.7541	NM_004043:Human sapiens beta-2-microglobu	2.07
	447345	BE247787	Hs.18166	Hs.18166:KIAA0870 protein	2.07
	407143	C14076	Hs.332329	Hs.332329:EST	2.07
	448431	BE613061	Hs.337772	Hs.337772:hypothetical protein BC009331	2.07
35	412760	AW379630	Hs.41324	Hs.41324:ESTs	2.07
	446859	AA94299	Hs.16297	NM_005694:Human sapiens COX17 homolog, cy	2.07
	403966				2.07
40	409115	AA223335	Hs.50651	NM_002227:Human sapiens Janus kinase 1 (a p	2.07
	436823	AW149665	Hs.117077	Hs.117077:zinc finger protein 264	2.07
	414045	NM_002551	Hs.75727	NM_002551:Human sapiens riboprotein II (pP	2.06
	413980	NM_002437	Hs.75659	NM_002437:Human sapiens Mpv17 transgene,	2.06
	439414	NM_001183	Hs.6551	NM_001183:Human sapiens ATPase, H+ transp	2.06
	426059	BE252842	Hs.166120	NM_001572:Human sapiens interferon regula	2.06
45	429849	U33063	Hs.2499	NM_002741:Human sapiens protein kinase C-4	2.06
	402424				2.06
	406626	X04526	Hs.215595	Hs.215595:guanine nucleotide binding pro	2.06
	458911	AA373131	Hs.24322	Hs.24322:ATPase, H+ transporting, lysoso	2.05
	426086	T94307	Hs.188572	Hs.188572:ESTs	2.05
50	419726	U03330	Hs.1274	NM_000129:Human sapiens bone morphogenesi	2.05
	452344	AA064357	Hs.55405	Hs.55405:hypothetical protein MGC16212	2.05
	442498	U54617	Hs.8364	NM_002512:Human sapiens pyruvate dehydrog	2.05
	422114	AW194851	Hs.111901	NM_015908:Human sapiens arsenite resistance	2.05
	413420	AA410235	Hs.75348	NM_006263:Human sapiens proteasome (lipo	2.05
55	409430	R21945	Hs.346735	Hs.346735:Human sapiens, clone IMAGE:3951	2.05
	409932	AA376750	Hs.57600	Hs.57600:adaptor-related protein complex	2.05
	434848	BE256304	Hs.321448	Hs.321448:AD-015 protein	2.04
	453852	AW65818	Hs.374424	Hs.374424:ESTs	2.04
	427637	AK200816	Hs.179596	NM_005693:Human sapiens flotillin 1 (FLOT	2.04
60	400264				2.04
	430016	NM_004736	Hs.227556	NM_004736:Human sapiens xenotropic and po	2.04
	410134	U69140	Hs.53827	Hs.53827:nuclear VCP-like	2.04
	440975	AA495914	Hs.75979	Hs.75979:inhibitor 9	2.04
	432280	BE440142	Hs.2943	NM_003135:Human sapiens sig1 recognition	2.04
	409504	AA304951	Hs.699	NM_000942:Human sapiens peptidylprolyl is	2.04
65	412146	M62444	Hs.73722	NM_001641:Human sapiens APEX nucleosom	2.04
	434203	BE262677	Hs.283558	Hs.283558:hypothetical protein PRO1855	2.04
	422754	AA316476	Hs.171811	Hs.171811:acetylcholine kinase 2	2.04
	406729	AA069711	AA069711:zm52b11.1 Stratagene fibroblas		2.04
	413086	AA126841	Hs.183834	Hs.183834:ESTs	2.03
70	424340	AA339036	Hs.7033	Hs.7033:ESTs	2.03
	455440	AB024334	Hs.259001	NM_010479:Human sapiens tyrosine 3-monoox	2.03
	424652	NM_002870	Hs.151536	NM_002870:Human sapiens RAB13, member RAS	2.03
	415740	N80486	Hs.39911	Hs.39911:Human sapiens mR for FLJ00899 pr	2.03
	412749	AA379417	Hs.74564	NM_003145:Human sapiens sig1 sequence rec	2.03
75	408383	AA015318	Hs.23165	Hs.23165:ESTs	2.03
	421235	AW081051	Hs.103180	Hs.103180:DC2 protein	2.03
	445417	AK001058	Hs.12680	Hs.12680:Human sapiens cD FLJ10196 fts, c	2.03
	414883	AA926960	Hs.348669	NM_001826:Human sapiens CDC28 protein kin	2.02
80	447298	BE017527	Hs.239818	Hs.239818:phosphonotidase-3 kinase, catal	2.02
	459980	AA022888	Hs.176055	Hs.176055:ESTs	2.02
	422785	AA824114	Hs.289088	Hs.289088:heat shock 90kD protein 1, alp	2.02
	452696	AA92645	Hs.211534	Hs.211534:Human sapiens cD FLJ13665 fts,	2.02
	452056	AW955065	Hs.101150	Hs.101150:KIAA1949 protein	2.02

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5	450690	AA296696	Hs.333418	NM_014154: Homo sapiens FXYD domain conta	2.02
	432527	A20965	Hs.105961	Hs.105961 engulfment and cell motility 3	2.01
	429545	A824164	Hs.356130	Hs.356130.ESTs	2.01
	439180	LA393742	Hs.195067	Hs.195067 v-erb-b2 erythroblastic leukemia	2.01
	437139	BE259190	Hs.269721	Hs.269721 growth arrest-specific 5	2.01
10	436014	AF28134	Hs.283741	Hs.283741 taxosome component Ptp46	2.01
	453329	197205	Hs.193400	Hs.193400 interleukin 6 receptor	2.01
	407347	AA299847		TZ3514 seq325 1 N80 Homo sapiens cdo	2.01
	435370	A954074	Hs.225838	Hs.225838.ESTs	2.01
	430657	AA402510	Hs.370922	Hs.370925.ESTs, Weakly similar to hyotho	2.01
15	427157	U51166	NM_003211	Homo sapiens Thymine-D glycosyl	2.01
	424833	NM_003894	Hs.153405	NM_003894: Homo sapiens period homolog 2	2.01
	440605	NM_005402	Hs.8306	NM_005402: Homo sapiens v-ral simian leuk	2.01
	435543	JA610141	Hs.192182	Hs.192182.ESTs	2.01
	417426	NM_002291	Hs.82124	NM_002291: Homo sapiens laminin, beta 1 (2.01
20	417290	NM_014767	Hs.74583	NM_014767: Homo sapiens KIAA0275 gene pr	2.01
	445892	AV65500	Hs.93951	Hs.93951: Homo sapiens mRc cdo DKF2p667D09	2.01
TABLE 39B:					
25	Pkey:	Unique Eric probe/seq identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
30	Pkey	CAT	Accession		
	409745	MI194_5			
35	418669	12789_1			
	421902	276321_1			
	40231	MI194_5			
40	438584	1241536_1			
	413020	1485985_1			
	402525	1145_1			
45	4199143	U51166			
	4199143	U51166			
	4199143	U51166			
50	4199143	U51166			
	4199143	U51166			
	4199143	U51166			
55	4199143	U51166			
	4199143	U51166			
	4199143	U51166			
60	4199143	U51166			
	4199143	U51166			
	4199143	U51166			
70	4199143	U51166			
	4199143	U51166			
	4199143	U51166			
75	4199143	U51166			
	4199143	U51166			
	4199143	U51166			
80	4199143	U51166			
	4199143	U51166			
	4199143	U51166			

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5	401179	9436647	Plus	1134771-113893
	405102	8076881	Minus	120922-121296
	402575	9884830	Minus	109742-109883
	402901	8894222	Minus	175426-175667
	405204	7230116	Plus	125659-126754
10	403657	7709101	Minus	2524-3406
	403847	9188605	Plus	44543-44835
	404030	7671252	Plus	119362-151749
	405517	9454624	Plus	114757-114857
	402559	9864273	Plus	33539-33715
	403956	8568881	Plus	158193-158277,160116-160290
	402424	9796344	Minus	64925-65073

15	TABLE 40A: ABOUT 977 GENES UP-REGULATED IN STOMACH CANCER			
	Table 40A lists about 977 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probe sets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.0. The "average" stomach cancer level was set to the 90th percentile amongst various stomach cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.			
20	Phy:	Unique Eos probe set identifier number		
	ExAccn:	Exon accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
25	RT:	Ratio of tumor to normal adult tissues		

Phy:	ExAccn	UnigeneID	Unigene Title	RT
30	411243	AB039886	Hs.65919	CAT1
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial)
	444325	AW152618	Hs.16757	ESTs
	445891	AW031342	Hs.199460	ESTs
	446811	AS050771	Hs.174759	ESTs
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZP564B0262 f
	409757	NM_001898	Hs.123114	cystatin SN
35	421100	AJ250717	Hs.1355	cathespain E
	423368	BE440342	Hs.83326	matrix metalloproteinase 3 (stromelysin
	445918	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZP564B0262 f
	406687	M01126	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	428551	AF196478	Hs.188401	annexin A10
40	425211	M16867	Hs.1857	progastrin (pepsinogen C)
	423670	BE030054	Hs.8695	matrix metalloproteinase 12 (macrophage
	409583	U33317	Hs.711	defensin, alpha 5, Paneth cell-specific
	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITB
	426654	AK001666	Hs.189095	similar to SALL1 (rat) (Drosophila-like
45	405041	AB033025	Hs.50081	KIAA1159 protein
	408380	AF123050	Hs.44532	ducriguan
	428953	AA300610	Hs.194676	DKFZP434C013 protein
	450685	L15530	Hs.423	pancreatitis-associated protein
	409187	AF184830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch
50	434206	AW119573	Hs.288516	ESTs, Weakly similar to S65990 mlogen i
	421346	Z34277	Hs.103707	apomucin
	427585	D31152	Hs.173729	collagen, type X, alpha 1 (Schmid metaph
	425679	X05997	Hs.159177	lysozyme, gastric
	421582	AS910276	Hs.1405	tetral factor 1 (breast cancer, estrogen
55	434414	AF198376	Hs.122579	gpr34b07.x1 NCX_CGAP_Ov23 Homo sapiens
	422956	BE545072	Hs.122579	hypocholesterolemia protein FLJ10461
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN TRANS
	423575	C11863	Hs.163443	Homo sapiens cDNA FLJ11576 fs, clone HE
60	113385	M34655	Hs.840	indoleamine-pyrole 2,3-dioxygenase
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	448693	AW064854	Hs.228320	Homo sapiens cDNA; FLJ23537 fs, clone L
	441377	BE216239	Hs.228556	ESTs
	415278	AJ076799	Hs.1247	apoptosis factor A.IV
65	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon
	403422			
	403776			
	418478	U38545	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholestergic
	421341	AJ243212	Hs.2795611	deleted in malignant brain tumors 1
70	451181	AJ796330	Hs.207461	ESTs
	432168	AK006563	Hs.272805	hypocholesterolemia protein FLJ20596
	454454	AW811606	Hs.271819	Homo sapiens cDNA; FLJ22751 fs, clone K
	448844	AS81519	Hs.177164	ESTs
	428434	AW363990	Hs.655551	ESTs, Weakly similar to AF127993 1 PLUNC
75	452461	N78223	Hs.108106	transcription factor
	409420	Z15098	Hs.54451	laminin, gamma 2 (piscin (100kD), latini
	431611	U58766	Hs.264428	tissue specific transplantation antigen
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy
	430044	AA444510	Hs.152812	ESTs
80	409956	AW133564	Hs.1727	inhibin, beta A (piscin A, activin AB a
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam
	420159	AS172490	Hs.99785	Homo sapiens cDNA; FLJ21245 fs, clone C
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy

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5	422168	AAS96894	Hs.112408	S100 calcium-binding protein A7 (psoriasis)	3.87
	452304	AA023396	Hs.61311	ESTs, Weakly similar to S10590 cysteine	3.84
	412140	AA219691	Hs.73625	RA86 interacting, kinesin-like (rakibins)	3.82
	414812	XZ7255	Hs.77367	monokine induced by gamma interferon	3.81
	419833	AA251131	Hs.720697	ESTs	3.81
10	446232	AG281848	Hs.165547	ESTs	3.74
	432398	AA307808	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	3.70
	451105	AU761324	Hs.34396	gb w65b01.1 NC1_OGAP_Co16 Homo sapiens	3.67
	413281	AA661271	Hs.13396	ESTs	3.66
	432867	AW016036	Hs.233364	ESTs	3.65
15	424046	AF027966	Hs.138202	serine (or cysteine) proteinase inhibitor	3.65
	457465	AW301344	Hs.195969	ESTs	3.65
	414918	AJ219207	Hs.72222	Homo sapiens cDNA FLJ13459 fs, clone PL	3.61
	418738	AW388633	Hs.6562	ESTs	3.60
	427778	AA412323	Hs.105323	ESTs	3.60
20	454293	HA9739	Hs.134013	ESTs, Moderately similar to NK homeobox	3.59
	452194	AU684413	Hs.298262	ESTs, Weakly similar to dJ8B8.1 [Hsapi]	3.57
	442577	AA252998	Hs.163900	ESTs	3.57
	426174	AA547959	Hs.115838	ESTs	3.53
	452862	AW378065	Hs.8687	ESTs	3.51
25	418869	AW516565	Hs.256279	ESTs	3.49
	430178	AW448612	Hs.152475	ESTs	3.48
	430367	AB24533	Hs.105607	ESTs	3.46
	419054	NM_002318	Hs.83354	lysyl oxidase-like 2	3.45
	442295	AJ827248	Hs.224398	Homo sapiens cDNA FLJ11469 fs, clone HE	3.44
30	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter)	3.44
	421764	AA512122	Hs.271819	Homo sapiens cDNA: FLJ22751 fs, clone K	3.43
	421948	LC2553	Hs.111758	keratin 6A	3.43
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CAS4_HUMAN COLLA	3.41
	442896	R37725	Hs.261108	ESTs	3.41
35	452261	TS3506	Hs.26792	Homo sapiens cDNA FLJ11041 fs, clone PL	3.39
	444783	AK001468	Hs.62180	anilin (Drosophila Scraps homolog), act	3.39
	408832	AW085690	Hs.63428	ESTs	3.39
	406685	M18728	Hs.14564	gb-human nonspecific crossreacting antig	3.37
	437527	AJ241019	Hs.14564	ESTs	3.37
40	433884	MH1079	Hs.282265	fatty acid binding protein 2, intestinal	3.37
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.36
	441316	AJ078234	Hs.176130	ESTs	3.35
	453897	U85642	Hs.138508	ESTs	3.33
	413903	JO2877	Hs.183163	caldesmon 1	3.33
45	411274	NM_002776	Hs.69423	kallikrein 10	3.32
	418406	X73501	Hs.84905	cytokeratin 20	3.32
	419559	Y07828	Hs.91096	ring finger protein	3.32
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.31
	423271	W42725	Hs.126256	interleukin 1, beta	3.31
50	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.30
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	3.30
	422310	AA316622	Hs.98370	cytochrome P540 family member predicted	3.30
	430704	AW813091	Hs.69360	gb:FC1195-240403.111-607 S10186 Homo	3.29
	411263	BE297602	Hs.69360	kinesin-like 6 (mitotic centromere-associ	3.29
55	443211	AJ128388	Hs.143655	ESTs	3.29
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.28
	441085	AA133651	Hs.181245	Homo sapiens cDNA FLJ12532 fs, clone NT	3.28
	452121	NM_004081	Hs.70306	deleted in ataxoparasia	3.27
	438633	AW963372	Hs.46677	PRO2000 protein	3.27
60	447342	AJ199268	Hs.19322	ESTs	3.25
	419529	A627237	Hs.282884	ESTs	3.24
	443957	AA521649	Hs.34487	hypothetical protein FLJ23412	3.23
	452699	AW295390	Hs.213062	ESTs	3.23
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.23
65	430289	XJ7820	Hs.2258	mutic methylproteohase 10 (pilocarpin	3.21
	438524	D87942	Hs.46328	hecyltransferase 2 (acessor status in	3.20
	437897	AA773561	Hs.146170	hypothetical protein FLJ22969	3.20
	453922	AF053306	Hs.36708	building uninhibited by benzimidazoles 1	3.19
	453160	AE263307	Hs.146228	ESTs	3.19
70	406890	N25540	Hs.225529	carcinembryonic antigen-related cell ad	3.19
	430187	AF795909	Hs.158889	ESTs	3.18
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast), h	3.16
	447048	AW393090	Hs.228320	Homo sapiens cDNA: FLJ23537 fs, clone L	3.14
	408113	TS2427	Hs.194101	Homo sapiens cDNA: FLJ20669 fs, clone A	3.14
75	425465	LI18964	Hs.1904	protein kinase C, beta	3.13
	425826	U97698	Hs.159593	mucin 6, gastric	3.13
	431662	AA513406	Hs.152307	ESTs	3.13
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	3.13
	415823	AS4942	Hs.833758	CD228 protein kinase 2	3.12
80	417315	AG080042	Hs.180450	ribosomal protein S24	3.11
	433001	AF217513	Hs.279905	clone H00310 PRO0310p1	3.11
	459587	AA031956	Hs.200771	gb:zh15c04.s1 Soares_pregnant uterus_NMH	3.11
	450159	AJ020416	Hs.58346	ESTs, Weakly similar to CAK2_HUMAN CALPA	3.11
	434370	AF130938	Hs.58346	downless (mouse) homolog	3.10
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	3.10
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.10
	420380	AA640891	Hs.102406	ESTs	3.10

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414774	XQ2419	Hs.72774	plasminogen activator, urokinase	3.10
415889	A1267700	Hs.111128	ESTs	3.09
407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	3.09
407289	AA135159	Hs.203249	Homo sapiens cDNA FLJ12149 fs, clone MA	3.09
402097	A0262772	Hs.68823	ESTs	3.08
447519	JA6258	Hs.23448	ESTs	3.08
448045	AJ297436	Hs.20166	prostate stem cell antigen	3.07
431956	AK002637	Hs.272245	Homo sapiens cDNA FLJ11170 fs, clone PL	3.06
413285	AJ739159	Hs.61888	DKFZP566N24 protein	3.05
402532	W74201	Hs.55279	serine (or cysteine) proteinase inhibitor	3.05
454034	NM_000691	Hs.575	aldehyde dehydrogenase 3	3.05
436481	AA379597	Hs.5199	HSPC191 protein similar to ubiquitin-con	3.05
403573	AA744590	Hs.136345	ESTs	3.05
429987	NM_004761	Hs.194710	glucosaminyl (N-acetyl) transferase 1	3.04
424252	AK000520	Hs.143811	hypothetical protein FLJ20513	3.04
436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.03
415992	C05637	Hs.145007	Homo sapiens cDNA FLJ13593 fs, clone PL	3.03
411789	AF245505	Hs.72157	Homo sapiens adiccan mRNA, complete cds	3.02
417956	AA217074	Hs.150465	ESTs	3.02
408908	BE296727	Hs.48915	serine/threonine kinase 15	3.01
422330	D00763	Hs.115263	epinephrin	3.01
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.00
425781	AN064214	Hs.196728	ESTs	2.99
432978	AF126743	Hs.279684	DNAJ domain-containing	2.99
418546	AA224827		gbrnc3Qp0.4s1 NIC1_CGAP_P2 Homo sapiens	2.99
425371	D49441	Hs.155981	mesothelin	2.99
422440	NM_024012	Hs.115724	aldo-keto reductase family 1, member B11	2.98
439453	BE254974	Hs.5556	thyroid hormone receptor interactor 13	2.98
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	2.97
428450	NM_014791	Hs.184339	KIAA0175 gene product	2.95
424345	AC001380	Hs.146479	Homo sapiens cDNA FLJ110518 fs, clone NT	2.95
431333	AB007249	Hs.104741	PDZ-binding kinase, T-cell originator pr	2.94
432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (p-met	2.94
432917	NM_014125	Hs.279812	PROG327 protein	2.94
433384	AC021992	Hs.124244	ESTs	2.93
432311	R31178	Hs.287620	flavonoid 1	2.93
425552	AK000492	Hs.59806	hypothetical protein	2.92
428303	AW974475	Hs.183501	regulator of G-protein signalling 15	2.92
409687	TS1125	Hs.8493	ESTs	2.91
434377	AW137148	Hs.193448	oncostatin specific factor 2 (fascic	2.89
417751	AW965339	Hs.111471	ESTs	2.89
457288	AA521458	Hs.192738	ESTs	2.89
456181	L34463	Hs.1030	ras inhibitor	2.89
461530	TS1387		glycylglycyl18 Stratagene fetal spleen (9	2.88
411573	AB029000	Hs.70823	KIAA1077 protein	2.88
430204	AA618335	Hs.146137	ESTs, weakly similar to putative [C. eleg	2.87
434808	AF155108	Hs.265150	ESTs, highly similar to NY-REN 41 antigen	2.87
450983	AA303584	Hs.25740	ERD1 (S. cerevisiae)-like	2.87
416870	AA601036	Hs.285063	ESTs	2.87
415951	AA634543	Hs.79440	IGF-1 mRNA-binding protein 3	2.87
409723	AW885757	Hs.257852	ESTs	2.87
435099	AC094770	Hs.4756	flap structure-specific endonuclease 1	2.86
468850	AA555775	Hs.250523	ESTs	2.85
434032	AW026651	Hs.206852	ESTs	2.85
418216	AA662240	Hs.263099	AF15q14 protein	2.85
453331	AT240655	Hs.8495	ESTs	2.85
460221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.84
460975				2.84
410145	AW886300		gbr-RC-OT0078-100400-023-C11 OT0078 Homo	2.83
410681	AW246890	Hs.55425	cathepsin B, (23kD)	2.83
439867	AA847510	Hs.151292	ESTs	2.83
443715	AA583187	Hs.97000	cyclin E1	2.83
420005	AW271106	Hs.133294	ESTs	2.83
417360	BE185289	Hs.1075	small proline-rich protein 16 (comelin)	2.83
422283	AW411307	Hs.114311	CD45 (cell division cycle 45, S.cerevis	2.82
404567				2.82
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.82
449224	AW959511	Hs.299683	hypothetical protein FLJ23399	2.81
407584	YK26945	Hs.18745	ESTs	2.81
450384	AA355925	Hs.36232	KIAA0166 gene product	2.81
449332	AA045513	Hs.27930	nuclear factor (myeloid-derived 2)-lik	2.80
428209	AK001379	Hs.121028	hypothetical protein FLJ10549	2.79
449722	BE280074	Hs.23960	cyclin B1	2.79
445676	AJ247763	Hs.16928	ESTs	2.78
424338	AW973531	Hs.154443	minichromosome maintenance deficient (S.	2.78
453028	AB006532	Hs.31442	RecD protein-like 4	2.77
421777	BE562088	Hs.108196	HSPD037 protein	2.78
452571	W31518	Hs.34665	ESTs	2.77
420759	T11832	Hs.127797	ESTs	2.77
422875	BE018517	Hs.119140	eukaryotic translation initiation factor	2.77
412723	AA648459	Hs.179912	ESTs	2.76
439670	AF088076	Hs.55907	ESTs, weakly similar to AC004858 3 U1 sm	2.76
400298	AA032279	Hs.61535	six transmembrane epithelial antigen of	2.76

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	414569	AF109298	Hs.118258	prostate cancer associated protein 1	2.76
	445378	AW664026	Hs.59892	ESTs	2.75
	423903	M57765	Hs.1721	interleukin 11	2.75
5	412059	AA317962	Hs.249721	ESTs	2.75
	431104	AF070859	Hs.269109	ESTs	2.75
	439759	AL359655	Hs.67709	Homo sapiens mRNA full length insert cDN	2.75
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fs, clone MA	2.75
	452940	AA029722	Hs.20279	ESTs	2.74
	408690	AF086452	Hs.20279	gn.F144-SN0016-120500-003-b07 SN0016 Homo	2.74
10	407777	AA161071	Hs.71465	squalene epoxidase	2.73
	432201	AE38613	Hs.136657	ESTs	2.73
	414416	AV405958	Hs.76004	lamin B2	2.73
	414617	AC39520	Hs.20524	ESTs, Moderately similar to hexokinase 1	2.73
	432007	AA221038	Hs.265206	HER4/H-1.171 associating 1	2.73
15	444301	AK001136	Hs.10760	hypothetical protein FLJ20129	2.72
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	2.72
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E.coli Re	2.72
	400298	AF143235	Hs.271933	Homo sapiens cDNA FLJ27785 fs, clone K	2.72
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	2.71
20	429432	AI678059	Hs.202675	synaptonemal complex protein 2	2.71
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71
	427528	AL077143	Hs.175655	mini-chromosome maintenance deficient (S.	2.71
	418801	AA228366	Hs.115122	ESTs	2.71
	440283	AI732892	Hs.150489	ESTs	2.71
25	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	2.70
	408366	AW511255	Hs.758082	ESTs	2.71
	400399				2.69
	434217	AW014795	Hs.23349	ESTs	2.68
	449785	AI275235	Hs.285300	Homo sapiens cDNA: FLJ23231 fs, clone C	2.68
30	446269	AW263155	Hs.14659	hypothetical protein FLJ10540	2.68
	443349	AI522172	Hs.265864	ESTs	2.68
	426514	BE516633	Hs.301122	bone morphogenetic protein 7 (osteogenic	2.67
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.67
	444754	T33911	Hs.11851	transmembrane 4 superfamily member 4	2.67
35	424637	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.66
	432019	AW402091	Hs.6803	hypothetical protein FLJ10430	2.65
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.65
	430832	AI073913	Hs.100696	ESTs, Weakly similar to secreted cement	2.65
40	427217	AA399272	Hs.144341	ESTs	2.65
	429170	NM_001384	Hs.2369	dual-specificity phosphatase 4	2.64
	450400	AI694722	Hs.279744	ESTs	2.64
	435380	AA679001	Hs.192221	ESTs	2.64
	432375	BE536069	Hs.2967	S100 calcium-binding protein P	2.63
	453700	AB209426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	2.63
45	422938	NM_001809	Hs.1594	centromere protein A (CTP)	2.63
	453134	AA032211	Hs.118493	ESTs	2.63
	420727	IT5701	Hs.59986	complement component 4-binding protein,	2.62
	408868	AW292286	Hs.255058	ESTs	2.62
50	414977	BE263742	Hs.77095	KIAA008 gene product	2.62
	440255	AI532285	Hs.160569	ESTs	2.62
	403055				2.62
	443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	2.62
	447600	AK000322	Hs.18457	hypothetical protein FLJ20015	2.61
55	413753	U17760	Hs.301103	Human DNA sequence from clone 27ZL16 on	2.61
	445114	AW691959	Hs.254664	ESTs	2.61
	427297	AJ232366	Hs.115051	myeloma overexpressed gene(in a subset o	2.60
	407366	AF028942		gbl homo sapiens c-g33 mRNA, partial seq	2.60
	432009	AL137424		gbl Homo sapiens mRNA: cDNA DNF Zp71G2123	2.60
60	440249	A246590	Hs.125325	ESTs	2.60
	433220	AI076192	Hs.131933	ESTs	2.60
	438533	AA402065	Hs.170673	ESTs, Weakly similar to AF126780 1 resin	2.60
	436251	BE515265	Hs.5092	nuclear protein (pNED) repeat	2.60
	474717	H03754	Hs.152213	wingless-type MMTV integration site fami	2.60
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	2.60
65	425463	AK000740	Hs.157986	hypothetical protein FLJ20733	2.60
	435370	AF064074	Hs.225638	ESTs	2.59
	432215	AI076609	Hs.2534	ribonucleotide reductase M1 polypeptide	2.59
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	2.59
	443919	AI091284	Hs.135224	ESTs	2.58
70	413268	AL039079	Hs.75256	regulator of G-protein signalling 1	2.58
	404519				2.58
	414998	NM_002543	Hs.77729	oxidized low density lipoprotein (lectin	2.57
	479597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.57
	428941	AI052308	Hs.193725	ESTs	2.57
75	416768	AA363723	Hs.1032	regenerating islet-derived 1 alpha (panc	2.57
	417933	X02308	Hs.87962	thymidylate synthetase	2.56
	433675	AW977653	Hs.110771	Homo sapiens cDNA: FLJ21904 fs, clone H	2.56
	441384	AA447849	Hs.288660	protease, serine, 23	2.56
	451939	U80456	Hs.73311	single-minded (Drosophila) homolog 2	2.56
80	418867	D31771	Hs.68044	msk (Drosophila) homeo box homolog 2	2.55
	449042	AW234985	Hs.301148	potassium voltage-gated channel, b-kel	2.55
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.55
	414132	AI801335	Hs.48480	ESTs	2.55

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431890	X17033	Hs 271586	integrin, alpha 2 (CD45b), alpha 2 subunit	2.55
407830	NM_001086	Hs 587	arylamide deacetylase (esterase)	2.55
434815	AF155582	Hs 46744	core1 UDP-glucosyl-N-acetylglucosamin	2.54
415250	P02614	Hs 27319	ESTs	2.54
435447	AK533040	Hs 49823	ESTs	2.54
459306	AW578452	Hs 232588	ESTs, Weakly similar to mucin [H sapiens	2.54
414361	AJ086138	Hs 204044	ESTs	2.54
427872	U64648	Hs 155625	cell growth regulatory with EF-hand doma	2.53
416884	H38765	Hs 80706	diaphorase (NADH:NADPH) cytochrome b-5	2.53
431183	NM_006855	Hs 250695	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.53
436043	AW593638	Hs 168830	Homo sapiens cDNA FLJ12135 fs, clone MA	2.53
456743	AK301124	Hs 7434	ESTs	2.53
410268	AA315181	Hs 61635	six transmembrane epithelial antigen of	2.52
424955	NM_002457	Hs 153704	rRNA (never in mitosis: gene d-related k	2.52
411734	AW374954	Hs 71779	Homo sapiens DNA from chromosome 19, cos	2.52
432657	AA831815	Hs 270940	ESTs	2.51
434080	AB207119	Hs 154662	hypothetical protein PR01472	2.51
438190	AA760200	Hs 136798	ESTs	2.51
418969	W33191	Hs 28907	hypothetical protein FLJ20258	2.51
446405	AW451259	Hs 57851	ESTs	2.51
450002	AI679524	Hs 201629	ESTs, Moderately similar to ALUR_HUMAN A	2.51
431868	AK0703	Hs 270833	amphiregulin (Schwannoma-derived growth	2.51
429053	NM_000253	Hs 193789	microsomal triglyceride transfer protein	2.50
447634	AW967902	Hs 5152	Homo sapiens cDNA: FLJ22618 fs, clone H	2.50
436383	AW022213	Hs 143617	ESTs	2.50
453751	R35762	Hs 101262	Homo sapiens mRNA; cDNA DKFZp434B102 (p	2.49
446669	AI570830	Hs 174870	ESTs	2.49
445865	AI252594	Hs 145575	ESTs	2.49
448437	AI470125		gbw50c04.x1 NCI_OGAP_Pant Homo sapiens	2.48
414883	AA526590	Hs 77550	CDC28 protein kinase 1	2.48
437477	AE52153	Hs 217453	annexin A2	2.48
449521	AB012113	Hs 105330	small inducible cytokine subfamily A (Cy	2.48
425322	J05068	Hs 2012	transcobalamin 1 (vitamin B12 binding pr	2.48
412903	BE007567	Hs 155795	ESTs	2.48
422515	AW506470	Hs 117930	multifunctional polypeptide similar to S	2.48
441030	AW444655	Hs 232184	ESTs	2.48
448454	NM_005879	Hs 21254	TRAF interacting protein	2.48
415092	J05581	Hs 89603	mucin 1, transmembrane	2.48
406671	AA128547	Hs 283754	met proto-oncogene (hepatocyte growth fa	2.48
405640	U07122	Hs 55481	zinc finger protein 165	2.48
424639	AI517494	Hs 131329	ESTs	2.48
404171				2.47
414747	U30872	Hs 77204	centromere protein F (350/400kD, mitosi	2.47
407839	AJ045144	Hs 151566	ESTs	2.47
410405	AI955703	Hs 301842	ESTs	2.47
452220	BE158006	Hs 212296	ESTs	2.46
427591	AW154476	Hs 20726	ESTs	2.46
421463	BE300341	Hs 104625	ectodermal-neural cortex (with ETB-like	2.46
444838	AI551680	Hs 209556	ESTs	2.46
413816	AW58181	Hs 189998	ESTs	2.46
408295	AI117452	Hs 44155	DKFZP586G1517 protein	2.46
436613	AA972691	Hs 192974	Homo sapiens cDNA FLJ12735 fs, clone NT	2.45
445417	AK201058	Hs 12680	Homo sapiens cDNA FLJ10196 fs, clone HE	2.45
422674	W54322	Hs 279551	melanoma inhibitory activity	2.45
452668	AI807883	Hs 156932	ESTs	2.45
425397	J04088	Hs 156346	topoisomerase (DNA) II alpha (170kD)	2.45
468308	AI033377	Hs 44167	hypothetical protein DKFZp564D0462	2.45
427961	AW238155	Hs 140134	ESTs	2.45
422363	T55979	Hs 115474	replication factor C (activator 1) 3 (38	2.45
433083	AI042759	Hs 151752	ESTs	2.45
435848	AW575248		gbtE129135f MAGE resequences, MAGP Homo	2.44
411924	AK006859	Hs 272203	Homo sapiens cDNA FLJ20843 fs, clone AD	2.44
411457	NM_012211	Hs 256297	integrin, alpha 11	2.44
443949	AW827419	Hs 235070	ESTs	2.44
416498	U33632	Hs 79351	potassium channel, subfamily K, member 1	2.44
426484	AF104632	Hs 184601	solute carrier family 7 (cationic amino	2.43
431558	X63629	Hs 2877	cadherin 3, type 1, P-cadherin (placenta	2.43
413833	Z15005	Hs 75573	centromere protein E (32kD)	2.43
407243	AA058357	Hs 74466	carcinoembryonic antigen-related cell ad	2.43
410044	BE586742	Hs 58165	highly expressed in cancer, rich in leuc	2.43
424273	W00460	Hs 144442	phospholipase A2, group X	2.42
409533	AW959543	Hs 21291	mitogen-activated protein kinase kinase	2.42
453966	BE148734	Hs 252833	ESTs	2.42
427043	AA397679	Hs 290490	ESTs	2.42
415141	NM_007019	Hs 93002	ubiquitin carrier protein E3-C	2.42
449887	AW075749	Hs 184719	ESTs, Weakly similar to AF116721 112 PRO	2.42
433159	AB035898	Hs 150587	kinesin-like protein 2	2.42
439396	BE562958	Hs 74346	ESTs, Weakly similar to prediction	2.42
426427	M86899	Hs 165840	TYK protein kinase	2.41
434725	AK000796	Hs 4104	hypothetical protein	2.41
427719	AI393122	Hs 134726	ESTs	2.41
433312	AI241331	Hs 131765	ESTs	2.41
432615	AA557191	Hs 55028	ESTs	2.41

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	407047	X55965	gh.H.sapiens SOD-2 gene for manganese su	2.41
	419220	AA811938	Hs.291759 ESTs	2.40
	416530	U52801	Hs.79361 kalikrein 6 (neurosin, zyme)	2.40
5	435219	AA676349	Hs.190331 ESTs	2.40
	447164	AF026941	Hs.17516 Homo sapiens cigs mRNA, partial sequence	2.40
	416713	U70174	gb:cy18603 s1 Stratagene lung (937210) H	2.40
	418322	AA284166	Hs.84113 cyclin-dependent kinase inhibitor 3 (CDK	2.40
	409902	AC337658	Hs.150351 ESTs	2.40
	413597	AA078418	gb:u05603 x1 Soares liver_spleen_	2.40
10	424253			2.40
	428970	BE276891	Hs.194691 retinoic acid induced 3	2.40
	434362	AI064690	Hs.171176 ESTs	2.39
	418693	AI750878	Hs.87409 thrombospondin 1	2.39
	451237	AW600293	gb:EST00049 pGEM-T library Homo sapiens	2.39
15	407756	AA116021	Hs.38260 ubiquitin specific protease 18	2.39
	437935	AW936591	Hs.5540 hypothetical protein FLJ20063	2.39
	414675	BE246743	Hs.268529 Homo sapiens cDNA: FLJ22635 fs, clone H	2.39
	435937	AA833893	Hs.119169 ESTs	2.39
	438993	AA828995	gb:u07708 s1 NCI_CGAP_Ov2 Homo sapiens	2.38
20	422082	AA015188	Hs.111244 hypothetical protein	2.38
	435649	BE305242	Hs.112442 ESTs, Weakly similar to CLDE_HUMAN CLAUD	2.38
	407282	M18726	gb:human neurotrophic cytoskeleton antig	2.38
	460395	AKU77002	Hs.24950 regulator of G-protein signalling 5	2.38
	430354	AA554810	Hs.239784 human homolog of Drosophila Scribble	2.38
25	422578	AF723666	Hs.1545 caudal type homeo box transcription fact	2.38
	446312	BE239665	Hs.14846 Homo sapiens mRNA: cDNA DHF7z9540016 (H	2.38
	450737	AW007152	Hs.203530 ESTs	2.38
	428070	T63918	Hs.182313 retinol-binding protein 2, cellular	2.38
	416111	AA033813	Hs.79018 chromatin assembly factor 1, subunit A (2.37
30	433345	AI981545	Hs.152582 Homo sapiens cDNA FLJ13117 fs, clone NT	2.37
	427557	NM_002659	Hs.179557 plasminogen activator, urokinase receptor	2.37
	423554	MS0516	Hs.1674 glutamine-fructose-5-phosphate transamin	2.37
	452304	R10799	Hs.191990 ESTs	2.37
	453876	AW021748	Hs.110406 ESTs	2.36
35	425081	X74794	Hs.154443 minichromosome maintenance deficient (S	2.36
	434682	AA821155	Hs.191958 ESTs	2.36
	439737	AT051438	Hs.41271 Homo sapiens mRNA full length insert cDN	2.36
	414108	AI267592	Hs.75761 SFPS serine kinase 1	2.36
40	417900	BE250127	Hs.82906 CDC20 (cell division cycle 20, S. cerevi	2.36
	428045	AW612765	Hs.155361 ESTs, Moderately similar to UBR022 hypot	2.36
	448826	AI580252	Hs.293246 ESTs, Weakly similar to putative p150 (H	2.36
	441020	W79283	Hs.35962 ESTs	2.36
	448019	AW947154	Hs.195641 ESTs	2.36
	411753	XT6029	Hs.2841 neuromedin U	2.36
45	441703	AW390054	Hs.192843 ESTs	2.36
	410361	BE391804	Hs.52651 guanylate binding protein 1, interferon-	2.36
	418526	BE019020	Hs.85838 solute carrier family 15 (monocarboxylic	2.36
	444478	W07318	Hs.240 M-phase phosphoprotein 1	2.36
50	421676	AA295652	Hs.111495 Homo sapiens cDNA FLJ11643 fs, clone HE	2.36
	428388	AA728827	Hs.101265 Homo sapiens cDNA: FLJ22593 fs, clone H	2.36
	436961	AW375974	Hs.156704 ESTs	2.35
	408194	AA801038	Hs.191797 ESTs	2.35
	438578	AA811244	Hs.164168 ESTs	2.35
55	429183	AB014604	Hs.197955 KIAA0704 protein	2.35
	435653	AI023707	Hs.134273 ESTs	2.35
	430290	AT134110	Hs.135355 ESTs	2.34
	423441	R88649	Hs.278359 absent in melanoma 1 like	2.34
	453900	AW003582	Hs.226414 ESTs, Weakly similar to ALUR_HUMAN ALU S	2.33
	450378	AW249181	Hs.19954 ESTs, Weakly similar to cDNA EST yk3861	2.33
60	432877	AW974111	Hs.292477 ESTs	2.33
	451928	AB273801	Hs.30315 ESTs	2.33
	426227	U87068	Hs.158102 Human proteinase activated receptor 2 mR	2.33
	418245	AA068767	Hs.83883 transmembrane, prostate androgen induced	2.33
65	415083	AI632683	Hs.271719 Homo sapiens cDNA FLJ12933 fs, clone NT	2.33
	453106	AA100847	Hs.193380 ESTs, Highly similar to AF174690 1 F-box	2.33
	432153	AA372264	Hs.273193 hypothetical protein FLJ10706	2.33
	458531	AA367718	Hs.159083 ESTs	2.33
	449532	W74653	Hs.271593 ESTs	2.33
	446354	AW449650	Hs.207249 ESTs	2.33
70	409703	NM_006187	Hs.58009 Z-S-oligodendrocyte synthetase 3	2.33
	419373	NM_003244	Hs.90077 TG-mitochondrial factor (TALE family homoo	2.32
	435607	W73428	Hs.8750 uncharacterized bone marrow protein BM04	2.32
	405818			2.32
	423132	AF070647	Hs.124126 Homo sapiens clone 24438 mRNA sequence	2.32
75	444311	BE540274	Hs.259 forkhead box M1	2.32
	432675	AI091855	Hs.105884 ESTs	2.32
	411773	NM_006799	Hs.72026 protease, sorin, 21 (testisin)	2.31
	448569	BE382657	Hs.21486 signal transducer and activator of trans	2.31
	434775	AA548983	Hs.212911 ESTs	2.31
80	407378	AA292964	gb:EST11152 Uturus Homo sapiens cDNA S	2.31
	442353	BE379594	Hs.49136 ESTs	2.31
	422611	AA158177	Hs.118722 fucosyltransferase 8 (alpha 1-6) fucosy	2.31
	409965	AA079279	gb:zmf5504.r1 Stratagene colon HT29 (837	2.31

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	421677	HE4092	HE.36282	ESTs	2.31
	419493	AF001212	HE.90744	proleasome (prosome, macropain) 26S subu	2.31
	424435	AB011167	HE.146557	KIAA0555 protein	2.30
5	446880	AB11807	HE.109646	Homo sapiens cDNA FLJ12531 fs, clone NT	2.30
	452795	AK392555	HE.18876	hypothetical protein FLJ21680	2.30
	425934	AG386527	HE.105685	ESTs	2.30
	409262	AK000631	HE.52256	hypothetical protein FLJ20524	2.30
	428125	AA393071	HE.182579	leucine aminopeptidase	2.30
10	417655	AA789091	HE.14014	ESTs, Weakly similar to KIAA09973 protein	2.29
	407291	AB178112	HE.201450	ESTs, Weakly similar to ALU4_HUMAN/ALU S	2.29
	428923	BE047698	HE.186785	ESTs	2.29
	452203	XF5722	HE.158164	ATP-binding cassette, sub-family B (ABC/	2.29
	409402	AF208234	HE.605	cystatin B (stefin B)	2.29
15	415559	AL043002	HE.90073	chromosome segregation 1 (yeast homolog)	2.29
	451999	AW176401	HE.27424	DEADH (Asp-Glu-Ala-Asp) box polypr	2.29
	400811	AF219139	HE.87726	KIAA0154 protein; ADP-ribosylation facto	2.29
	436396	AB63487	HE.299112	Homo sapiens cDNA FLJ11441 fs, clone HE	2.28
	442152	R35246	HE.239656	Homo sapiens cDNA FLJ13455 fs, clone PL	2.28
20	429311	AF344157	HE.109431	small inducible cytokine B subfamily (Cy	2.28
	410174	AA308007	HE.59461	DKFZP434C245 protein	2.28
	425247	NM_005940	HE.155324	matrix metalloproteinase 11 (stromelysin	2.28
	438170	AB916685	HE.194601	ESTs	2.28
	445378	AV533564	HE.226946	ESTs	2.28
25	428048	AA705745	HE.185070	ESTs	2.28
	414696	AF002020	HE.76518	Niemann-Pick disease, type C1	2.27
	444665	BE613126	HE.47783	ESTs, Weakly similar to T12640 hypoth	2.27
	421660	AJ141320	HE.114121	Homo sapiens cDNA FLJ22228 fs, clone C	2.27
	421228	AW381145	HE.33382	gb:OV0-OT0033-010406-182-af01 OT0033 Homo	2.27
	433536	AF111106	HE.33382	protein phosphatase 4, regulatory subun	2.27
30	415857	AA865115	HE.301645	Homo sapiens cDNA FLJ11381 fs, clone HE	2.27
	421155	HB7879	HE.102267	lysyl oxidase	2.27
	405645				2.27
	449467	AW205006	HE.197042	ESTs	2.27
35	445537	AJ245671	HE.12844	EGF-like domain, multiple 5	2.27
	450580	AF131784	HE.25318	Homo sapiens clone Z5194 mRNA sequence	2.26
	422634	AB959928	HE.1690	heparin-binding growth factor binding pr	2.26
	443063	W89483	HE.253650	ESTs	2.26
40	407742	AF186252	HE.38084	sulfotransferase family, cytosolic, 1C,	2.26
	428330	L22624	HE.2256	matrix metalloproteinase 7 (matrilysin,	2.26
	432655	AA832155	HE.252266	ESTs	2.26
	429231	AK001552	HE.212172	beta,beta-carotene 15,15'-dioxygenase ho	2.26
	400514				2.26
	431846	BE019524	HE.211590	uroplakin 1B	2.26
45	435521	AB809555	HE.58349	ESTs	2.26
	425010	AA136583	HE.1975	Homo sapiens cDNA: FLJ21007 fs, clone C	2.26
	437641	AA811452	HE.291911	ESTs	2.26
	418592	A348838	HE.13073	ESTs	2.26
	411393	AW797437	HE.69771	B factor, propionid	2.26
50	414805	AJ344599	HE.77356	transferrin receptor (p90, CD71)	2.26
	419488	AA316241	HE.50591	nucleosiphosmin/nucleosiphosmin 3	2.25
	434540	NM_016045	HE.5184	TH1 drosophila homolog	2.25
	445952	AA004879	HE.187820	ESTs	2.25
	410156	AG36442	HE.59338	hypothetical protein FLJ10808	2.25
55	458444	AJ264155	HE.152081	CDP-diacylglycerol synthase (phosphatid	2.25
	414368	W70171	HE.75399	uridine monophosphate kinase	2.25
	408353	BE439838	HE.44258	hypothetical protein	2.25
	439223	AY238209	HE.23945	ESTs	2.25
	448753	AL040868	HE.224355	ESTs, Weakly similar to A39650 protein k	2.25
60	428479	Y00272	HE.184572	cell division cycle 2, G1 to S and G2 to	2.24
	432403	AA550815	HE.124840	ESTs	2.24
	424971	AA473005	HE.154036	tumor suppressing subunit/nucleolar candid	2.24
	432673	AB028859	HE.278605	ER-associated DNAB; ER-associated Hsp40	2.24
	446887	AJ346656	HE.156652	Homo sapiens cDNA: FLJ22800 fs, clone K	2.24
65	452833	BE559581	HE.30736	KIAA0124 protein	2.24
	409432	DM5372	HE.54450	small inducible cytokine subfamily A (Cy	2.24
	422039	BE367632	HE.62148	hypothetical protein	2.24
	429526	NM_000796	HE.226213	cyclohexin P450, S1 (lanosterol 14-alpha	2.24
	445413	AA151342	HE.12677	CG-147 protein	2.24
70	423645	AJ215632	HE.147487	ESTs	2.23
	447532	AK000614	HE.18751	hypothetical protein FLJ20607	2.23
	423515	AA370107	HE.162204	ESTs	2.23
	444743	AA045648	HE.15817	nucleic (nucleoside diphosphate linked moi	2.23
	434518	HS6955	HE.37372	Homo sapiens DNA binding peptide mRNA, p	2.23
75	435602	AF217515	HE.283532	unchar-acterized bone marrow protein BM03	2.23
	449574	AB910946	HE.269103	ESTs	2.23
	424527	AW573856	HE.153550	hypothetical protein C3D212.4	2.23
	457982	AW856093	HE.183617	ESTs	2.23
	414420	AA043424	HE.76095	immediate early response 3	2.23
80	449319	AB940935	HE.67776	ESTs, Weakly similar to ALU7_HUMAN/ALU S	2.23
	411840	AA534966	HE.2960	POU domain, class 5, transcription facto	2.23
	452930	AA1195285	HE.194097	ESTs	2.23
	436351	AJ227852	HE.145274	ESTs	2.23
	439186	AB972274	HE.6487	Xq28, 2000bp sequence contig, ORF	2.23

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	427254	AL121523	Hs 97774	ESTs	2.22
	424517	AIS39443	Hs 137447	Homo sapiens cDNA FLJ12169 fs, clone MA	2.22
	414732	AW410976	Hs 77152	minichromosome maintenance deficient (S	2.22
	411835	U28343	Hs 72550	hyaluronate-mediated mobility receptor (R	2.22
5	427547	W19744	Hs 180259	Homo sapiens cDNA FLJ20853 fs, clone KA	2.22
	438223	AA781171	Hs 24505	gb:aj24505.s1 Scoring_testis_NHT Homo sap	2.22
	434504	AIB37341	Hs 121590	Homo sapiens cDNA FLJ12827 fs, clone NT	2.22
	450149	AW959781	Hs 253440	ESTs, Moderately similar to ZIC2 protein	2.22
	439211	AIB90347	Hs 271923	Homo sapiens cDNA: FLJ22785 fs, clone K	2.22
10	401519			ESTs	2.22
	441794	AW197794	Hs 253336	ESTs	2.22
	412108	AA100293	Hs 185043	ESTs	2.22
	431849	AIB70823	Hs 85573	Homo sapiens mRNA: cDNA DKFZp556N034 (fr	2.22
	444969	AQ033394	Hs 169528	ESTs	2.21
15	408901	AK001330	Hs 48855	hypothetical protein FLJ10468	2.21
	434423	NM_006769	Hs 3844	LIM domain only 4	2.21
	439328	W07411	Hs 118212	ESTs, Moderately similar to ALU3_HUMAN A	2.21
	100221			APFX control: STAT1	2.21
	432140	AK000404	Hs 272668	hypothetical protein FLJ20397	2.21
20	434170	AA626509	Hs 122332	ESTs	2.21
	434353	AW450737	Hs 128791	CGI-09 protein	2.21
	426438	NM_001955	Hs 22711	endothelin 1	2.21
	433102	AJ343066	Hs 158625	ESTs	2.21
	421470	R27496	Hs 1378	annexin A3	2.21
25	426499	T62489		gb:yc0309.s1 Stratagene lung (S37210) H	2.21
	438280	AW015534	Hs 217493	annexin A2	2.21
	440381	AA517308	Hs 190495	ESTs	2.20
	435779	NC5187	Hs 43388	ESTs	2.20
	433627	AF078866	Hs 284296	Homo sapiens cDNA: FLJ22993 fs, clone K	2.20
30	417944	ALU07196	Hs 82885	collagen, type V, alpha 2	2.20
	452299	AA206533	Hs 73239	hypothetical protein FLJ10961	2.20
	422689	AW885665		gb:RCC-CT0297-290100-013-003 CT0297 Homo	2.20
	448457	H65629	Hs 245997	ESTs	2.20
	416221	BE513171	Hs 79086	mitochondrial ribosomal protein L3	2.20
35	428125	XB7241	Hs 106594	FAT tumor suppressor (Drosophila) homolog	2.20
	430603	AA148164	Hs 247280	HIV associated factor	2.20
	425274	BE281191	Hs 155462	minichromosome maintenance deficient (mi	2.20
	452679	Z42387	Hs 4299	Homo sapiens cDNA: FLJ20965 fs, clone A	2.20
40	410619	BE512730	Hs 65114	keratin 18	2.20
	424332	AA338919	Hs 101615	ESTs	2.20
	442490	AW968978	Hs 30212	thyroid receptor interacting protein 15	2.20
	418661	NM_001949	Hs 1189	Human mRNA for KIAA2075 gene, partial of	2.20
	419341	N71463	Hs 119589	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.20
	427920	Z11502	Hs 181107	annexin A13	2.19
45	413819	AA152961	Hs 212523	Homo sapiens cDNA: FLJ22572 fs, clone H	2.19
	419752	AA243673	Hs 152618	ESTs	2.19
	441436	AW137772	Hs 185980	ESTs	2.19
	413095	AA494359	Hs 30715	ESTs	2.19
50	423208			ESTs	2.19
	422596	AF063611	Hs 118633	Z'-5'-oligoadenylate synthetase-like	2.19
	444261	AA289858	Hs 10724	MDG023 protein	2.19
	419474	AY988619	Hs 155849	ESTs	2.19
	453853	AK583516	Hs 77448	aldehyde dehydrogenase 4 (glutamate gamma	2.18
55	423401	NM_001962	Hs 128087	coagulation factor II (thrombin) receptor	2.18
	453450	AW797627	Hs 89474	ADP-ribosylation factor 6	2.18
	440250	AA876179	Hs 134650	ESTs	2.18
	443334	BE296785	Hs 10818	KIAA0187 gene product	2.18
	427616	AF971153	Hs 207854	ESTs	2.18
	451807	W52854	Hs 27099	DKFZP564J0663 protein	2.18
	430441	BE398091	Hs 6880	DKFZP54J0156 protein	2.18
	414602	AW650088	Hs 76550	Homo sapiens mRNA: cDNA DKFZp564B1264 (f	2.18
	411678	AS07114	Hs 71465	squellone epoxidase	2.18
	453735	AA066929	Hs 125073	ESTs	2.18
	450499	AA235207	Hs 250456	hypothetical protein DKFZp76JF2011	2.18
65	452291	AF015592	Hs 28553	CDC7 (cell division cycle 7, S. cerevisi	2.18
	421532	AW136237	Hs 146170	hypothetical protein FLJ22969	2.18
	444342	NM_014598	Hs 10687	similar to lysosome associated membrane	2.18
	451099	RS2795	Hs 22954	interleukin 13 receptor, alpha 2	2.18
	444207	AK565004	Hs 79572	cathepsin D (lysosomal aspartyl protease	2.18
70	426873	NM_013390	Hs 160417	transmembrane protein 2	2.17
	417494	NM_007350	Hs 82101	pleckstrin homology-like domain, family	2.17
	449437	ALU70308	Hs 100057	Homo sapiens cDNA: FLJ22902 fs, clone K	2.17
	446995	AK355012		gb:ql16d10.s1 NCI_CGAP_Ov23 Homo sapiens	2.17
75	431548	AIB34273	Hs 9711	Homo sapiens cDNA FLJ13018 fs, clone NT	2.17
	411127	AA688995	Hs 218329	hypothetical protein	2.17
	439961	AA857451	Hs 86996	ESTs	2.17
	429125	AA446854	Hs 271004	ESTs	2.17
	407103	AA424881	Hs 256301	ESTs	2.17
	439990	AK015862	Hs 131793	ESTs	2.17
80	415116	AA160383	Hs 269966	ESTs	2.17
	440052	AIB33744	Hs 195648	ESTs	2.17
	423961	D13666	Hs 136348	osteoblast specific factor 2 (twinclin	2.17
	431070	AW408164	Hs 249184	transcription factor 19 (SC1)	2.16

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43598	AI075559	Hs.134125	ESTs	2.18
43623	AB011117	Hs.129943	KIAA0545 protein	2.16
427258	AA400091	Hs.39421	ESTs	2.16
418113	A1272141	Hs.83484	SRF (sex determining region Y)-box 4	2.16
450385	BE267773	Hs.25594	hypothetical protein FLJ10703	2.16
428698	AA852773	Hs.297939	ESTs, Weakly similar to T17344 hypothetical	2.16
421408	AB882223	Hs.104114	H.sapiens HCG mRNA	2.16
490507	AB037784	Hs.22941	KIAA1363 protein	2.16
408947	AL380393	Hs.49117	Hs.sapiens mRNA; cDNA DKF-Zp56N1662 (l)	2.16
443552	NR6902	Hs.109434	ESTs	2.16
448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevisiae)	2.16
424653	AW975534	Hs.151469	calcium/calmodulin-dependent serine prot	2.16
431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	2.16
433865	AJ524046	Hs.115567	ESTs	2.16
432789	D26361	Hs.3104	KIAA0042 gene product	2.16
438580	AA811262	Hs.299202	ESTs	2.16
422192	AA305159	Hs.113019	ts485	2.15
425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	2.15
447269	AW247017	Hs.36978	melanoma antigen, family A, 3	2.15
447674	BE270640	Hs.19192	cyclin-dependent kinase 2	2.15
441021	AW578716	Hs.7644	H1 histone family, member 2	2.15
442432	BE035589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.15
425471	M22440	Hs.170029	transforming growth factor, alpha	2.15
431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	2.15
414761	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.15
447033	AJ357412	Hs.157601	ESTs	2.15
410407	XG5839	Hs.63267	carbonic anhydrase IX	2.15
446077	BE251048	Hs.22579	Homo sapiens clone CDABP0036 mRNA sapien	2.15
420800	ALJ45633	Hs.44269	ESTs	2.15
411975	AJ910508	Hs.144353	ESTs, Weakly similar to gag (H.sapiens)	2.15
415238	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	2.15
446671	AW016812	Hs.200266	ESTs	2.15
452721	AJ265628	Hs.30377	Homo sapiens EST from clone 470080, full	2.15
410491	AA465131	Hs.64301	Homo sapiens clone 25218 mRNA sequence	2.14
410954	NM_005033	Hs.65370	lyase, endothelial	2.14
435730	AB200636	Hs.4984	KIAA028 protein	2.14
452835	AK001269	Hs.30738	hypothetical protein FLJ10407	2.14
452082	BE245374	Hs.27842	hypothetical protein FLJ11210	2.14
401708				2.14
411420	AA311919	Hs.69851	GARI protein	2.14
448526	AB028946	Hs.21361	KIAA1023 protein	2.14
421175	AB79099	Hs.102397	G10T-3 for gonadotropin inducible transc	2.14
412336	AA151507	Hs.69485	Homo sapiens cDNA FLJ12436 fis, clone NT	2.14
420894	AA744697	Hs.88854	ESTs	2.14
429235	AA188827	Hs.7998	ESTs, Weakly similar to endo-alpha D-man	2.14
412870	N22788	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	2.14
447760	AI431328	Hs.291179	ESTs, Weakly similar to topoisomerase I	2.14
413511	AB271778	Hs.75412	Arginine-rich protein	2.13
423945	AL343043	Hs.271357	ESTs, Weakly similar to unnamed protein	2.13
418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.13
441790	AW254909	Hs.132208	ESTs	2.13
425928	AK000209	Hs.155556	hypothetical protein FLJ20002	2.13
453956	AW153531	Hs.205647	ESTs, Moderately similar to ALU1_HUMAN A	2.13
419609	AF761561	Hs.91143	pigged 1 (Piglike syndrome)	2.13
421508	NM_004833	Hs.105115	absent in melanoma 2	2.13
453975	AK008908	Hs.270829	ESTs	2.13
413670	AB000115	Hs.75410	hypothetical protein, expressed in octeo	2.13
422783	AA599856	Hs.120439	ethanolamine kinase	2.13
444542	AI161293	Hs.146882	ESTs, Weakly similar to KIAA0525 protein	2.13
410418	C31382	Hs.63325	transmembrane protease, serine 4	2.13
419791	AB79909	Hs.105104	ESTs	2.13
414800	BE255593	Hs.77302	methionine adenosyltransferase II, alpha	2.13
425860	L29339	Hs.1904	solute carrier family 5 (sodium)/glucose	2.13
414839	X63692	Hs.77462	DNA (cytosine 5)-methyltransferase 1	2.13
437040	AB766420	Hs.291600	ESTs	2.13
433217	NA7863	Hs.180450	ribosomal protein S24	2.12
420923	AF097021	Hs.273221	differentially expressed in hematopoiesi	2.12
409012	AL117435	Hs.49725	DKFZP434I216 protein	2.12
450645	AL117441	Hs.25264	DKFZP434I216 protein	2.12
431322	AW970672		gib-EST1382704 MAGE: repeat sequences, MAGK Homo	2.12
451356	AA748418	Hs.164577	ESTs	2.12
429534	AW976987	Hs.163227	ESTs	2.12
428365	AA255331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	2.12
441485	AW294603	Hs.127039	ESTs	2.12
443564	AB21681	Hs.199713	ESTs	2.12
410839	NM_005849	Hs.656581	protein disulfide isomerase	2.12
433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ25338 fis, clone L	2.12
442947	R60800	Hs.21303	ESTs	2.12
414987	AA524384	Hs.165544	ESTs	2.12
450510	AA010056	Hs.242998	ESTs	2.12
427475	AA403151	Hs.191605	ESTs	2.12
444670	H58373	Hs.37494	ESTs	2.12
452099	BE612592	Hs.27931	hypothetical protein FLJ10507 similar to	2.12

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	433748	R12244	gb.y33c12.r1 Scores fetal liver spleen	2.12
	415138	C18356	Hs.78045 tissue factor pathway inhibitor 2	2.11
	438138	R98299	Hs.177502 ESTs	2.11
5	414788	X78342	Hs.77313 cyclin-dependent kinase (CDC2-like) 10	2.11
	415474	NM_014252	Hs.78957 soluble carrier family 25 (mitochondrial)	2.11
	416472	AA180756	Hs.193294 ESTs, Weakly similar to ALU1_HUMAN	2.11
	412490	AW803564	Hs.288850 Homo sapiens cDNA: FLJ22526 fs, clone H	2.11
	410718	A1502083	Hs.191435 ESTs	2.11
10	422811	ALD39104	Hs.159557 karyopherin alpha 2 (RAG cohort 1, import)	2.11
	413344	A111596	Hs.188753 ESTs, Weakly similar to ALU1_HUMAN	2.11
	417197	R36075	gb.y68601.1 Scores placenta Nb2HP Homo	2.11
	431621	AW292329	Hs.163481 ESTs	2.11
	418529	AA659036	Hs.7148 Homo sapiens cDNA: FLJ21950 fs, clone H	2.11
15	433649	BE465884	Hs.280728 ESTs	2.11
	438338	A1732629	Hs.194161 ESTs, Weakly similar to TA2R_HUMAN	2.11
	422032	AA476966	Hs.110857 polymerase (RNA) III (DNA directed) poly	2.11
	409717	AW452871	Hs.56043 OGI-115 protein	2.11
	415366	AA373210	Hs.43047 Homo sapiens cDNA FLJ13585 fs, clone PL	2.11
20	445837	A261700	Hs.145544 ESTs	2.11
	414334	AA824268	Hs.21331 hypothetical protein FLJ110036	2.11
	436326	BE085236	Hs.181244 major histocompatibility complex, class	2.10
	422890	BE278111	Hs.134200 DKFZP564C186 protein	2.10
	421574	AJ000152	Hs.105924 defensin, beta 2	2.10
25	437103	AW139408	Hs.152940 ESTs	2.10
	436550	A224456	Hs.4934 H.sapiens polyA site DNA	2.10
	405474	A094821	Hs.48306 ESTs, Highly similar to EWS_HUMAN	2.10
	430333	AW243364	Hs.5409 RNA polymerase I subunit	2.10
	417540	D39857	Hs.82363 protein C receptor, endothelial (EPCR)	2.10
	431120	AA492588	gb.ng9308.1 NCL_GCAP_Thy1 Homo sapiens	2.10
30	430510	AW162916	Hs.241576 hypothetical protein PRO2577	2.10
	429669	BE185499	Hs.2471 KIAA0200 gene product	2.10
	427651	AW072203	Hs.40268 heparan sulfate (glucosamine) 3-O-sulfat	2.10
	436124	AA705012	Hs.269584 ESTs	2.10
35	436415	BE265254	Hs.5181 proliferation-associated 24, 39kD	2.10
	415121	AW973795	Hs.128927 Homo sapiens cDNA FLJ11903 fs, clone TH	2.10
	435668	AA841443	Hs.62711 ESTs	2.10
	437549	AA759149	gb.bah70603.1 Scores testis NHT Homo sapiens	2.10
	407887	AA579668	Hs.41072 serine (or cysteine) proteinase inhibito	2.10
	447720	AA138765	Hs.161304 ESTs	2.09
40	434765	AA648884	Hs.134278 Homo sapiens cDNA FLJ112676 fs, clone NT	2.09
	429743	AA804308	Hs.268695 hypothetical protein FLJ20613	2.09
	447815	A1432199	Hs.247084 ESTs	2.09
	441675	A914329	Hs.5461 ESTs	2.09
45	434274	AA628539	Hs.118252 ESTs, Moderately similar to ALU1_HUMAN	2.09
	411571	AA122393	Hs.70811 hypothetical protein FLJ25516	2.09
	442525	AF150282	Hs.145945 ESTs	2.09
	423750	AF165883	Hs.132415 pretdln 2	2.09
	449199	AF990122	Hs.196988 ESTs	2.09
50	415363	A1673947	Hs.78406 phosphatidylinositol-4-phosphate 5-kinase	2.09
	412543	AA552650	Hs.152423 Homo sapiens cDNA: FLJ21274 fs, clone C	2.09
	418462	BE001596	Hs.85266 integrin, beta 4	2.09
	432093	H28383	gb.y52c03.r1 Scores breast 3NBH61 Homo	2.09
	407862	BE542867	Hs.50724 Homo sapiens cDNA FLJ110934 fs, clone OV	2.09
55	434442	AA737415	Hs.132626 ESTs	2.09
	442671	A1005668	Hs.134719 EST	2.09
	428771	AB028902	Hs.193143 KIAA1069 protein	2.09
	430335	DB0007	Hs.239499 KIAA0185 protein	2.08
	425087	RB2424	Hs.120059 ESTs	2.08
60	412530	AA766268	Hs.266273 Homo sapiens cDNA FLJ13346 fs, clone OV	2.08
	443450	N66045	Hs.133629 ESTs	2.08
	418753	BE217818	Hs.87016 Homo sapiens cDNA: FLJ22538 fs, clone K	2.08
	432204	AS916132	Hs.121553 Homo sapiens cDNA FLJ13123 fs, clone NT	2.08
	429018	AW300867	Hs.265828 ESTs, Weakly similar to uncraned protein	2.08
65	416300	A1433074	Hs.86682 Homo sapiens cDNA: FLJ21578 fs, clone C	2.08
	431628	AF146277	Hs.265561 CD2-associated protein	2.08
	446528	AU075640	Hs.15243 nuclear protein 1 (120kD)	2.08
	432284	AA532607	Hs.105822 ESTs	2.08
	411372	A1147661	Hs.213289 low density lipoprotein receptor (fam11)	2.08
	450319	NM_000059	gb.h30m.sapiens breast cancer 2, early o	2.08
70	428730	AV660717	Hs.47144 DKFZP568N0819 protein	2.08
	443607	AA452612	Hs.134069 ESTs	2.08
	422058	AA862251	Hs.51253 gbse13g03.1 NCL_GCAP_Ov2 Homo sapiens	2.08
	409220	BE243323	Hs.51253 tumor necrosis factor receptor superfam	2.08
75	429504	X99133	Hs.204238 lipocatin 2 (pncogene 24p3)	2.08
	429686	AK003002	Hs.55875 Homo sapiens mRNA for FLJ00036 protein,	2.08
	438394	BE379623	Hs.27693 CD4 protein	2.08
	413092	AA126856	Hs.118665 ESTs	2.08
	413715	AW851121	Hs.75497 Homo sapiens cDNA: FLJ22139 fs, clone H	2.08
80	423020	AA353092	Hs.1608 replication protein A3 (14kD)	2.07
	438378	AW970529	Hs.86434 Homo sapiens cDNA: FLJ21816 fs, clone H	2.07
	463379	AA035261	Hs.61753 ESTs	2.07
	432125	AW972667	Hs.287510 Homo sapiens cDNA FLJ12300 fs, clone MA	2.07
	449370	AK002114	Hs.23455 hypothetical protein FLJ11252	2.07

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440318	AI235021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog]	2.07
450096	AI682088	Hs.223368	ESTs	2.07
454011	M31008	Hs.37009	alkaline phosphatase, intestinal	2.07
427876	AI494291	Hs.111577	ESTs	2.07
422901	R51636	Hs.121576	aspartate beta-hydroxylase	2.07
419235	AI470411	Hs.268433	neurofilin	2.07
445207	AI444222	Hs.23255	nucleoporin 159kD	2.07
408243	Y00787	Hs.624	interleukin 8	2.07
415652	T79213	Hs.272073	ESTs	2.07
445446	BE167887	Hs.156528	ESTs	2.07
411765	HA3346	gb:395a04.1	Soares breast 3Nbh8st Homo	2.07
423421	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.07
434711	AK001581	Hs.80961	polymerase (DNA directed), gamma	2.07
456157	AI0979153	Hs.357523	53 MAGe resequences, MAGP Homo	2.06
407143	C14076	Hs.248968	EST	2.06
454269	AI961050	Hs.295411	ESTs, Moderately similar to KF1A_HUMAN K	2.06
432440	X63597	Hs.2936	sucrase-isomaltase	2.06
419665	BE375794	Hs.65403	hypothetical protein	2.06
422765	AI430701	Hs.1519	bicellular LAP-repeat-containing 5 [sur	2.06
450434	AA166950	Hs.18645	ESTs, Weakly similar to parier CDS [Ca	2.06
439832	T81829	Hs.14870	ESTs	2.06
456284	AI0974175	Hs.105251	ESTs	2.06
431201	AA679405	Hs.8854	Human transcription unit PVT gene, exons	2.06
445021	AK002925	Hs.12251	Homo sapiens cDNA FLJ11163 fs, clone PL	2.06
438714	AA814855	Hs.294112	ESTs	2.06
443518	AI090652	Hs.200985	ESTs	2.06
433951	AC347267	Hs.124538	ESTs	2.06
433651	AB044372	Hs.200350	Homo sapiens cDNA FLJ131027 fs, clone NT	2.06
428307	W27333	Hs.183548	protein tyrosine phosphatase, receptor I	2.06
426874	N67325	Hs.247132	ESTs	2.06
451255	AF557212	Hs.17132	ESTs	2.06
432684	AA328329	Hs.47099	Homo sapiens cDNA: FLJ121212 fs, clone C	2.06
433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.06
433716	AA608808	Hs.225118	ESTs	2.06
429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	2.06
428235	AS61194	Hs.34407	ESTs	2.06
449026	BE500945	Hs.200105	ESTs	2.05
437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.06
400019	AI045017	Hs.23247	AFFX control: STAT1	2.06
408873	AA306997	Hs.268362	ESTs	2.05
425447	BE088746	Hs.6817	ESTs, Weakly similar to hypothetical pro	2.06
439975	AW328081	Hs.6817	Homo sapiens putative oncogene protein m	2.06
430037	NM_014158	Hs.279538	HSPC087 protein	2.06
440086	NM_005402	Hs.289757	v-rf simian leukemia viral oncogene hom	2.06
435414	BE254633	Hs.143638	WD repeat domain 4	2.05
411770	NM_014278	Hs.17952	heat shock protein (hsp110 family)	2.05
407253	AA602234	Hs.270551	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
429459	D85407	Hs.54481	low density lipoprotein receptor-related	2.05
436238	AK002163	Hs.301724	ESTs, Highly similar to unnamed protein	2.05
400517	AF242388	Hs.145885	lengsin	2.05
439943	AI083789	Hs.124620	ESTs	2.05
421934	BE135333	Hs.109309	hypothetical protein FLJ20535	2.05
417850	AA215724	Hs.82741	primase, polypoidase 1 (PRN2)	2.05
417491	AW376842	Hs.1085	guanylate cyclase 2C (heat stable entaro	2.05
453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.05
436625	AB31797	Hs.123310	ESTs	2.05
412637	BE391895	Hs.74276	chloride intracellular channel 1	2.05
436702	AI008525	Hs.134182	ESTs	2.05
440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.05
432979	AA573263	Hs.120860	ESTs	2.05
417308	H60720	Hs.81852	KIA0101 gene product	2.05
432925	AA578324	Hs.152234	ESTs	2.05
446311	AI007294	Hs.145795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.05
427871	AI0902405	Hs.55622	ESTs, Weakly similar to unknown H.sapie	2.05
453504	AA306204	Hs.35276	KIA0052 protein	2.05
449339	T86420	Hs.272139	ESTs	2.05
455666	BE065813	gb:RC2 BT0318.110100.012 a09 BT0318 Homo		2.05
417819	AJ253112	Hs.133540	ESTs	2.04
427747	AI0411425	Hs.180655	serine/threonine kinase 12	2.04
415009	CJ5253	Hs.220950	ESTs	2.04
437829	AI358522	Hs.270188	ESTs	2.04
435381	AW136397	Hs.247572	ESTs	2.04
438778	AI106729	Hs.18948	ESTs, Highly similar to HPS1_HUMAN PROTE	2.04
426753	AI0539252	Hs.152527	hypothetical protein FLJ20251	2.04
446475	AK008188	Hs.295245	ESTs	2.04
431384	AK000692	Hs.252351	HERV4H LTR associating 2	2.04
423701	AA328586	Hs.143022	ESTs	2.04
430680	AI0138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.04
422389	AI005216	Hs.115541	Janus kinase 2 (a protein tyrosine kinas	2.04
423481	AI0451645	Hs.151594	Homo sapiens cDNA FLJ11973 fs, clone HE	2.04
443746	AI0861375	Hs.160602	ESTs	2.04
400782	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434C0515 (f	2.04

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5	432933	AW205863	Hs.133888	ESTs, Weakly similar to US2B25 gene MAC2	2.04
	430785	Z30201		gb MHEA22G Atmum cDNA library Human hea	2.04
	426343	AL043021	Hs.12705	ESTs, Weakly similar to plectrophilin 2b [2.04
	415329	AY007220	Hs.288998	S100-type calcium binding protein A14	2.04
	425488	N74921	Hs.184399	ESTs	2.04
10	430485				2.04
	413313	NM_002047	Hs.75280	glycyl-tRNA synthetase	2.04
	407634	AW016569	Hs.301280	ESTs, Highly similar to AF241831.1 intra	2.04
	433266	AD39486	Hs.159430	ESTs	2.03
	451129	BE072881		gb:R02.ET054B-200300-012.e09 ET054B Homo	2.03
15	429165	AW009886	Hs.118258	prostate cancer associated protein 1	2.03
	422963	M79141	Hs.13234	ESTs	2.03
	418884	U82987	Hs.87246	Ic12 binding component 3	2.03
	407674	AA147884	Hs.9812	ESTs	2.03
	434551	BE387162	Hs.286858	ESTs, Highly similar to XPB_HUMAN DNA-RE	2.03
20	440246	W52010	Hs.191379	ESTs	2.03
	444006	BE350855	Hs.10086	type 1 transmembrane protein Fn14	2.03
	431301	AA02384	Hs.151529	ESTs	2.03
	452705	H49805	Hs.246005	ESTs	2.03
	421724	AB037832	Hs.107287	KUAA1411 protein	2.03
25	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	2.03
	450200	AW975625	Hs.173088	ESTs	2.03
	447474	AW614220	Hs.189402	ESTs	2.03
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	2.03
	445019	AI205540	Hs.281295	ESTs	2.03
30	433602	AB711313	Hs.176204	KIA06551 protein	2.03
	431042	NM_005764	Hs.271473	epithelial protein up-regulated in carci	2.03
	436198	AK001125	Hs.300522	Homo sapiens cDNA FLJ10263 fs, clone HE	2.03
	440773	AA352702	Hs.37747	hypothetical protein FLJ2484	2.03
	442425	AI065775	Hs.133397	ESTs	2.03
35	454166	AW963556	Hs.2055	ubiquitin-activating enzyme E1 (p159) an	2.03
	407835	X89426	Hs.41715	endothelial cell-specific molecule 1 (EO	2.03
	428299	AL038004	Hs.29419	ESTs	2.03
	418735	N48769	Hs.44609	ESTs	2.03
	442053	R35343	Hs.24988	Human DNA sequence from clone RP1-233G16	2.03
40	415757	AA439854	Hs.181818	ESTs	2.03
	432559	AW452948	Hs.257631	ESTs	2.03
	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl	2.02
	419395	BE268326	Hs.50280	S-aminimidazole-4-carboxamide ribonucle	2.02
	417576	AA338448	Hs.32205	phosphotyrosyl-tyrosinamide formyltransfer	2.02
45	418559	AA225048	Hs.104207	ESTs	2.02
	410855	X97795	Hs.65718	RAD54 (S.cerevisiae)-like	2.02
	433906	AI167816	Hs.43335	ESTs	2.02
	422072	AB018255	Hs.111138	KIAA0712 gene product	2.02
	419546	AA244199		giac0605.s1 NCL_GCAP_Pr1 Homo sapiens	2.02
50	446229	AI744964	Hs.14449	KIAA1605 protein	2.02
	450516	AA902656	Hs.21943	NF3 (Ngg1 interacting factor 3, S.pombe	2.02
	431721	AB032995	Hs.258044	KIAA1170 protein	2.02
	415807	R77402		glycyl-tRNA11 s1 Scarus placenta Nu2HP Homo	2.02
	438192	AI855065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.02
55	443129	R15075	Hs.21558	ESTs	2.02
	426991	AK001536	Hs.265823	Homo sapiens cDNA FLJ12852 fs, clone HT	2.01
	414731	AB80434	Hs.77135	Homo sapiens mRNA; cDNA DKFZp688A191 (p	2.01
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associa	2.01
	413293	AL047483	Hs.75270	GTP-binding protein homologous to Saccha	2.01
60	435787	AW162767	Hs.100914	hypothetical protein FLJ10352	2.01
	422599	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	2.01
	442660	AW138174	Hs.130651	ESTs	2.01
	456553	AA721325	Hs.189058	ESTs, Weakly similar to cAMP-regulated g	2.01
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD45C, alpha	2.01
65	431300	AA502346		gb:nt20b03.s1 NCL_GCAP_Co3 Homo sapiens	2.01
	443180	R15875	Hs.70945	ESTs	2.01
	450914	AI743761	Hs.142528	ESTs	2.01
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	2.01
	455484				2.01
70	436489	AK001455	Hs.5198	Down syndrome critical region gene 2	2.01
	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.01
	439696	W95298	Hs.171882	ESTs	2.01
	432378	AI493046	Hs.146133	ESTs	2.01
	4117915	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fs, clone L	2.01
75	453665	AA626290	Hs.181165	eukaryotic translation elongation factor	2.01
	419981	AA897581	Hs.128773	ESTs	2.01
	444508	AV655234	Hs.298083	ESTs	2.01
	435767	H73525	Hs.117874	ESTs	2.01
	430466	AF032573	Hs.241517	polymyrase (DNA directed), beta	2.01
80	452747	BE153855	Hs.61460	ESTs	2.01
	422790	AA809875	Hs.25933	ESTs	2.01
	443303	U67319	Hs.9276	casepase 7, apoptosis-related cysteine pr	2.01
	453929	AI79469	Hs.27379	ESTs	2.01
	410008	AA079552		gb:zm2012.s1 Stratagene pancreas (S3720	2.01
	448854	AB014564	Hs.22616	KIAA0664 protein	2.00
	440774	AI420611	Hs.127832	ESTs	2.00

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451351	AW058261	Hs 168213	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.00
424261	BE114474	Hs 289074	Homo sapiens cDNA FLJ13966 fs, clone Y7	2.00
424420	BE114743	Hs 146688	prostaglandin E synthase	2.00
407154	H79677		gdyr7g10.5.1 Soares fetal liver spleen	2.00
410240	AL157424	Hs 61289	synaptotagmin 2	2.00
426830	AA385751	Hs 160392	ESTs	2.00
435014	BE506896	Hs 10026	ribosomal protein L17 isoform	2.00
406620	AF18693	Hs 81848	RAD21 (c. pombe) homolog	2.00
432629	W60377	Hs 57772	ESTs	2.00
406752	A286598	Hs 217453	annexin A2	2.00

TABLE 40A:

15	Phy:	Unique Eos probest identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
20	Phy:	Accession
	CAT number	
	Accession	
25	Phy:	Accession
	CAT number	
	Accession	
30	Phy:	Accession
	CAT number	
	Accession	
35	Phy:	Accession
	CAT number	
	Accession	
40	Phy:	Accession
	CAT number	
	Accession	

45	Phy:	Accession
	CAT number	
	Accession	
50	Phy:	Accession
	CAT number	
	Accession	
55	Phy:	Accession
	CAT number	
	Accession	
60	Phy:	Accession
	CAT number	
	Accession	

TABLE 40C:

65	Phy:	Unique number corresponding to an Eos probest
	Ref:	Sequence source: The 7 digit numbers in the column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosomes 22" Dunham, et al. (1990) Nature 402:469-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NI_position	Indicates nucleotide positions of predicted exons.

70	Phy:	Ref	Strand	NI_position
75				
80				

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	404519	8152000	Plus	12817-13000
	404587	7249169	Minus	101320-101501
	405484	5922025	Plus	199214-199579,199572-199920,200262-200495
	405545	1054740	Plus	118677-118697,119091-119296,121526-121823
5	405818	4071056	Plus	29355-29195
	406399	9256298	Minus	63448-63554

TABLE 41A: ABOUT 534 SEQUENCES UP-REGULATED IN STOMACH CANCER
Table 41A includes 534 genes up-regulated in stomach cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as being predicted to be extracellular or cell-surface proteins (e.g. by Ig, In3, egl, 7m domains). Predicted protein domains are noted.

	Key	Exon	UnigeneID	Unigene Title	PSDomain	R1
	UnigeneID	Unigene number	Unigene title	Protein Structural Domain	Ratio of tumor to normal adult tissues	
15	411243	AB039886	Hs.69319	CA11	SS	30.66
	418007	M13509	Hs.83159	matrix metallo	hemopexin,Peptidase_M10,SS	16.94
	448611	A192071	Hs.174759	ESTs	TM	11.08
	409757	NM_001858	Hs.123114	cystatin SN	cystatin,SS	10.38
	421110	AJ250717	Hs.1355	cathepsin E	asp,SS	9.11
20	428369	BE440042	Hs.83325	matrix metallo	hemopexin,Peptidase_M10,SS	8.66
	405687	M11225	Hs.272529	pregnancy speci	hemopexin,TM	7.11
	428653	U33317	Hs.158401	anexin A10	anexin,TM	6.86
	425211	M18657	Hs.1857	progastricin (asp,TM,SS	5.51
	423673	BE003054	Hs.1595	matrix metallo	hemopexin,Peptidase_M10,SS	5.49
	428653	U33317	Hs.711	defensin, alpha	defensin,prop,SS	5.39
	428654	A002166	Hs.163905	similar to SALL	zf-C2H2,TM,SS	5.25
	408300	AF120350	Hs.44532	dibiquitin	ubiquitin,7m,3,ANF_receptor,sushi,7m,1,TM	5.20
	428953	AA306610	Hs.194576	DKFZP434C013 pr	art,TNFR,c5_DEAD,Stathmin,TM,SS	5.46
30	405685	L15533	Hs.423	pancreatitis-as	lectin_c,TM,SS	5.40
	409187	AF154303	Hs.509367	carbamoyl-phosp	CATase,CPase,L_chain,CPase_sm_chain,MOS,TM	5.34
	434205	AW133973	Hs.288515	ESTs, Weakly si	PH,TM	5.16
	421346	Z34277	Hs.103707	apomucin	Cys_knot,vwd,	5.14
	427585	D31152	Hs.178729	collagen, type	C1q,Collagen,TM,SS	5.06
40	425679	YS5587	Hs.158177	lysoz, gastric	aliphatic,SS	4.94
	421582	A1910275	Hs.1465	trefoil factor	trefoil,lysoz,TM,SS	4.93
	422956	BE545072	Hs.122579	hycothetical pr	TM	4.89
	448105	AW591433	Hs.170675	ESTs, Weakly si	lysoz,TM	4.84
	413385	M31455	Hs.840	indoleamine-pyr	IO3,TM	4.72
45	417855	AW527003	Hs.82772	collagen, type	TSPN,Collagen,COLFI,SS	4.68
	419278	AU075799	Hs.1247	apc/coproline	Apoc/coproline,SS	4.46
	407811	AW195092	Hs.40098	cysteine knot s	SS	4.47
	403422				SS	4.36
	403776				IL8,TM,SS	4.32
50	418479	U38945	Hs.1174	cyclin-dependen	ank,TM,SS	4.32
	428242	H55709	Hs.2250	leukemia inhibi	LIF_OSM,SS	4.30
	421341	AJ243212	Hs.279611	deleted in mal	SS	4.30
	428434	AW383590	Hs.05551	ESTs, Weakly si	SS	4.13
55	429420	Z15908	Hs.54451	laminin, gamma	laminin_EGF,Jamain,B,SS	4.04
	431511	U50795	Hs.264428	issue specific	Epimerase,TM,SS	4.04
	413719	BE436580	Hs.75498	small inducible	IL8,SS	4.03
	409556	AW103384	Hs.727	inhibin, beta A	TGF-beta,TGFB_propeptide,SS	4.01
	424240	U03398	Hs.1524	tumor necrosis	TNF,TM	4.00
60	428227	AA321549	Hs.2248	small inducible	IL8,TM,SS	3.97
	422158	AA586894	Hs.112408	S100 calcium-bi	ethand,TM	3.81
	412140	AA218691	Hs.73525	RAB6 interacti	kinetin,TM,SS	3.82
	414812	X77355	Hs.77367	monokine induce	8.3,SS	3.81
	419853	AA251131	Hs.220687	ESTs	WHEP-TR5,TM	3.74
	445232	AJ281845	Hs.185547	ESTs	7m,3,TM	3.74
65	432388	AA307806	Hs.2979	trefoil factor	trefoil,TM,SS	3.70
	432867	AW016936	Hs.233364	ESTs	GSHpH,TM,SS	3.65
	424046	AF027866	Hs.136202	actine (or cyst	sepin,TM	3.65
	414918	AJ129207	Hs.77222	Homo sapiens cD	TM	3.61
	454293	H49739	Hs.134013	ESTs, Moderate	TM	3.59
70	442577	AA292988	Hs.163900	ESTs	TM	3.57
	426174	AA547859	Hs.115838	ESTs	SS	3.53
	418869	AW515565	Hs.258279	ESTs	Soma,TM	3.45
	418054	NM_002318	Hs.83354	lysyl oxidase-I	Lysyl_oxidase,SROR,SS	3.48
	442295	AB82748	Hs.224398	Homo sapiens cD	Collagen,COLFI,vwc,TM,SS	3.44
75	425821	NM_007231	Hs.162711	sickle carrier	SNF,TM	3.44
	421948	L42583	Hs.111758	keratin 6A	Blamnet,TM	3.43
	444783	AA001468	Hs.67180	anilin (Drosop	PH,TM	3.39
	437527	AJ241019	Hs.145644	ESTs	PIPSK,TM,SS	3.37
	433084	M18079	Hs.262705	lipoic acid bind	Ipoicoin,SS	3.37
80	453401	NM_007115	Hs.29352	tumor necrosis	20kD,CLUB,TM,SS	3.36
	458897	U85642	Hs.138056	ESTs	TM	3.33
	413808	J00287	Hs.181283	caldesmon 1	asp,TM,SS	3.33
	411274	NM_002776	Hs.69423	kallikrein 10	trypsin,TM	3.32

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418496	X73501	Hs.84905	cytokeratin 20	3.32
419559	UY7828	Hs.91096	ring finger pro	3.32
423217	NM_000094	Hs.1640	collagen, type	3.31
411558	AA102670	Hs.70725	gamma-aminobuty	3.30
427722	AA000123	Hs.150479	hypothetical pr	3.30
422319	AA516622	Hs.88370	cyclochrome P540	3.30
411263	BE297802	Hs.69360	kinesin-like 6	3.29
443426	AF098158	Hs.9329	chromosome 20 o	3.28
452121	NM_004081	Hs.70936	deleted in azoo	3.27
441742	AI199268	Hs.15322	ESTs	3.25
452699	AW295390	Hs.213062	ESTs	3.23
425188	AA002052	Hs.155071	hypothetical pr	3.23
400289	XO7800	Hs.2228	matrix metallopr	3.21
429534	D87542	Hs.46328	luciferin transfer	3.20
437897	AA770561	Hs.146170	hypothetical pr	3.20
453922	AF053306	Hs.36708	budding uninhib	3.19
406690	M29540	Hs.220529	carcinoembryoni	3.19
416209	AA236776	Hs.79678	MAO2 (mitotic a	3.16
408113	T80427	Hs.194101	Homo sapiens cD	3.14
425465	L18964	Hs.1904	protein kinase	3.13
419216	AU076718	Hs.164021	small inducible	3.13
416803	X54942	Hs.83758	CDC28 protein k	3.12
417315	A099042	Hs.109450	ribosomal prote	3.11
433001	AF217513	Hs.279905	clone HQ0310 PR	3.11
459887	AA031956	Hs.150451	gbr2k150451 S	3.11
421379	Y15221	Hs.103982	small inducible	3.10
414774	X02419	Hs.72724	plasmaogen act	3.10
407289	AA135159	Hs.203349	Homo sapiens cD	3.09
447519	U46258	Hs.23448	ESTs	3.08
448045	AI297436	Hs.20166	prostate stem c	3.07
431956	AA020232	Hs.272245	Homo sapiens cD	3.06
409632	WY4001	Hs.55276	sevine (or cyt	3.05
454034	NM_000691	Hs.575	aldehyde dehydr	3.05
436481	AA379597	Hs.5199	HSPC150 protein	3.05
428987	NM_004751	Hs.194710	glucosaminyl (N	3.04
424352	AB00520	Hs.143811	hypothetical pr	3.04
436291	BE569452	Hs.5101	protein regulat	3.03
411789	AF245905	Hs.72157	Homo sapiens ad	3.02
417956	AA210704	Hs.159465	ESTs	3.02
408986	BE298227	Hs.49015	serine/threonine	3.01
422330	D30783	Hs.115263	epinephrine	3.01
425971	NM_013989	Hs.154424	deiodinase, iod	3.00
425761	AW664214	Hs.196729	ESTs	2.99
432978	AF126743	Hs.273984	DNAX domain-con	2.99
418546	AA224927	Hs.203204	gbr2k3204 s1 H	2.99
425371	D49441	Hs.155991	mesothelin	2.99
422440	NM_004812	Hs.116724	aldo-keto reduct	2.98
439453	BE264974	Hs.6566	thyroid hormone	2.98
413278	BE363085	Hs.833	interferon-gam	2.97
428450	NM_014791	Hs.184339	KIAA0175 gene p	2.95
424345	AK001380	Hs.145479	Homo sapiens cD	2.95
431313	AB027249	Hs.104741	PDZ-binding kin	2.94
432289	NM_002447	Hs.2942	macrophage slim	2.94
432917	NM_014125	Hs.273912	PROX27 protein	2.93
432731	R31178	Hs.287620	Bromocriptin 1	2.93
420552	AK000492	Hs.98806	hypothetical pr	2.92
428303	AW974476	Hs.183501	regulator of G-	2.92
420587	T51125	Hs.8463	ESTs	2.91
457288	AA521458	Hs.192738	ESTs	2.89
456181	L36463	Hs.1030	ras inhibitor	2.89
450190	T51387	Hs.161292	gbr2k08r1 s1 S	2.88
430324	AA618335	Hs.146137	ESTs, Hsally si	2.88
434608	AF155108	Hs.256150	ESTs, Highly a	2.87
450963	AA305384	Hs.25740	ERO1 (S. cerevi	2.87
418670	AA601036	Hs.285083	ESTs	2.87
416661	AA634543	Hs.79440	KIF-II mRNA-bin	2.87
435899	AC004770	Hs.4756	flap structure	2.86
420075			serpin, TM	2.84
410681	AW246890	Hs.65425	cathodion 1, (2	2.83
439667	AA847510	Hs.161292	ESTs	2.83
443715	AB631167	Hs.9700	cyclin E1	2.83
417266	BE185289	Hs.1076	small profilin o	2.83
422283	AW411307	Hs.114311	CDC45 (cell div	2.82
404567			HECT, zt-UBRI, TM	2.82
427158	L10343	Hs.112341	protease inhibi	2.82
448204	AW995911	Hs.259883	hypothetical pr	2.81
407594	W25945	Hs.18745	ESTs	2.81
453884	AA355925	Hs.36232	KIAA0186 gene p	2.81
449324	AA045573	Hs.22390	nuclear factor	2.80
422809	AB011379	Hs.121008	hypothetical pr	2.79
427027	BE280074	Hs.233690	cyclin B1	2.79
453028	AB065632	Hs.31442	RecQ protein-f	2.78
421777	BE562088	Hs.108196	HSPC237 protein	2.77

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	452571	W31518	Hs.34665	ESTs	TM	2.77
	422675	BE01817	Hs.115140	eukaryotic tran	eIF-5a, TM,	2.77
	400298	AA032279	Hs.61635	six transmembra	TM	2.76
	414569	AF.109298	Hs.118258	prostate cancer	TM	2.76
5	445378	AW654026	Hs.59892	ESTs	TM	2.75
	422803	M57765	Hs.1721	interleukin 11	TM,SS	2.75
	431104	AW970859	Hs.269109	ESTs	Sema, TM,SS	2.75
	452940	AA029722	Hs.20279	ESTs	7m, 1, TM, SS	2.74
	432201	A1536813	Hs.135657	ESTs	lysozin, TM,	2.73
10	414617	A133520	Hs.20524	ESTs, Moderat	hemolitic, TM,	2.72
	444301	AK000135	Hs.10760	hypothetical pr	LRR, TM,	2.72
	428711	AA383471	Hs.180699	conserved gene	TM	2.71
	429432	A1678059	Hs.202676	synaptonemal co	TM	2.71
	450505	NM_004450	Hs.418	fibroblast acti	Popliteal_S9, DPPN, H_1em, SS	2.71
15	427528	AU077143	Hs.175555	minichromosome	TM,SS	2.71
	418801	AA228366	Hs.115122	ESTs	integrin_AFG-GAP, TM, SS	2.71
	429486	AF155827	Hs.203963	hypothetical pr	SNF2_N, helicase_C, TM,	2.71
	406365	AW511255	Hs.258082	ESTs	SS	2.70
	406399				karat, TM, SS	2.68
20	446269	AW263155	Hs.14559	hypothetical pr	TM	2.68
	426514	BE16633	Hs.301122	bone morphogene	TGF_beta, TGFb_proppeptide, TM, SS	2.67
	410709	U65590	Hs.81134	interleukin 1 r	IL1, SS	2.67
	444754	T83911	Hs.11861	transmembrane 4	TM, SS	2.67
	424687	JG3070	Hs.151738	matrix metallopro	fn2 hemopoetin, Popliteal_S9, TM, SS	2.66
25	439579	AW600291	Hs.5823	hypothetical pr	TM	2.65
	430832	AU073913	Hs.100695	ESTs, Weakly ai	TM, SS	2.65
	429170	NM_001394	Hs.2335	dial specific	DSP, Rhoanase, TM,	2.64
	450400	A1694722	Hs.27574	ESTs	TM	2.64
	453380	AA579001	Hs.192221	ESTs	Occludin, TM, SS	2.64
	432375	BE539069	Hs.2962	S100 calcium-bi	S_100, ehant, TM, SS	2.63
30	453700	AB003428	Hs.560	apoptoprotein	dCMP_cyt_0cam_sugar_7, TM, SS	2.63
	422538	NM_001009	Hs.1554	histone, TM	SS	2.63
	453134	AA032211	Hs.118493	ESTs	adh_short, TM, SS	2.63
	420727	H75701	Hs.99986	complement comp	sushi,	2.62
35	408658	AW292286	Hs.250509	ESTs	TM	2.62
	414672	BE263782	Hs.77955	KIAA0008 gene p	TM	2.62
	403055				flament, TM, SS	2.62
	447400	AK000322	Hs.18457	hypothetical pr	zf-C/HC4, TM,	2.61
40	413753	U17750	Hs.301103	Human DNA seque	laminin_EGF, laminin_N1em, SS	2.61
	432320	AU076192	Hs.131933	ESTs	TM	2.60
	432651	BE515085	Hs.5002	nuclear prote	TM, SS	2.60
	445988	Y09753	Hs.22785	gamma-aminobuty	neur_chain, TM, SS	2.60
	425453	AK000740	Hs.157985	hypothetical pr	TM	2.60
	435370	A1964074	Hs.225838	ESTs	EGF_fn3, fibronectin_C, TM, SS	2.59
45	432215	AU075509	Hs.7534	ribonucleotide	ribonucleo_red/bonus_red_7g, TM,	2.59
	409142	AL136877	Hs.50758	chromosome-asso	SMC_N, TM, SS	2.59
	443919	A1091284	Hs.135224	ESTs	adh_short, TM, SS	2.58
	413268	AL039079	Hs.75255	regulator of G-	RG5, TM,	2.58
	404519				defensins, SS	2.58
50	414988	NM_002543	Hs.77729	oxidized low de	TM	2.57
	425957	NM_003816	Hs.2442	a disintegrin a	TM, SS	2.57
	425841	A1052358	Hs.193725	ESTs	asp, TM, SS	2.57
	416786	AA363733	Hs.1032	regenerating is	lectin_C, SS	2.57
	417933	202208	Hs.82952	thymidylate syn	thymidylat_7ym, SS	2.56
55	441384	AA447849	Hs.288560	protease, serin	TM	2.56
	451939	U80455	Hs.27311	single-minded (PAC, PAS, BPLBPL_C, TM,	2.55
	418867	D31771	Hs.83404	msh (Drosophila	homeobox, TM,	2.55
	416925	BE267931	Hs.78995	proliferating c	TM	2.55
60	431890	X17033	Hs.271865	riegrin, alpha	5m, w/integrin_AFG-GAP, TM, SS	2.55
	407830	NM_001086	Hs.587	arylacetamide d	COEsterase_7m, 1, TM, SS	2.55
	454815	AF155582	Hs.46744	coret UDP-galac:	SS	2.54
	435647	AB53240	Hs.49623	ESTs	TM	2.54
	453505	AB578452	Hs.232688	ESTs, Weakly si	TM, SS	2.54
65	414361	AU06138	Hs.204044	ESTs	SS	2.54
	425782	U66468	Hs.159525	cell growth reg	SS	2.53
	415984	H38765	Hs.80705	diaphorase (NAD	TM	2.53
	431183	NM_008655	Hs.202696	KDEL (Lys-Asp-G	ER_lumen_receptLRR, DEAD, helicase_C, TM, SS	2.53
	456743	A630124	Hs.7434	ESTs	TM	2.53
70	410268	AA315181	Hs.51535	six transmembra	TM	2.52
	424905	NM_002497	Hs.153704	NIMA (never in	plaze, TM,	2.52
	432657	AA631615	Hs.270940	ESTs	TM	2.51
	430400	AB077016	Hs.154652	hypothetical pr	DL_CXXCXXGXG, TM, SS	2.51
	418969	W33191	Hs.28907	hypothetical pr	SH3, TM,	2.51
	431808	MM0703	Hs.270833	amphigutrin (s	EGF, TM, SS	2.51
75	426053	NM_000253	Hs.195799	microsomal trig	Vitellogenin_N, TM, SS	2.50
	447634	AB967952	Hs.5152	Homo sapiens cD	TM	2.50
	436393	AW022213	Hs.143617	ESTs	Galactosyl_T_2, TM, SS	2.50
	453751	R36752	Hs.101282	Homo sapiens mR	TM	2.49
	445465	A282584	Hs.146575	ESTs	SS	2.49
80	414683	AA926960	Hs.72560	CDC28 protein k	Cks, TM,	2.49
	436747	A925153	Hs.217493	anexin A2	TM	2.49
	446921	AB012113	Hs.165330	small inducible	IL8, SS	2.49
	426322	J05068	Hs.2012	transcobalamin	Cobalamin_bind, TM, SS	2.48

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	422515	AW500470	Hs.117950	multifunctional
	447030	AW444559	Hs.232184	ESTs
	448454	NM_005679	Hs.21254	TRAF interactin
5	415992	J05581	Hs.89603	mucin 1, trans
	409540	U78722	Hs.55461	zinc finger pro
	404171			
	414747	U30872	Hs.77204	centromere prot
	410406	A969703	Hs.301842	ESTs
	452220	BE158006	Hs.212095	ESTs
10	421483	BE020241	Hs.104825	ectodermal-neur
	446838	AV651640	Hs.208558	ESTs
	413816	AW658181	Hs.189998	ESTs
	436813	AA972891	Hs.192574	Homo sapiens cD
	432874	W94322	Hs.279551	melanoma inhib
15	422397	J04088	Hs.195345	topoisomerase (
	422363	T55979	Hs.115474	replication fac
	431924	AK000850	Hs.272203	Homo sapiens cD
	431457	NM_017211	Hs.255297	integrin, alpha
	416498	U33637	Hs.79351	potassium chann
20	428484	AF104032	Hs.184601	solute carrier
	431958	K53629	Hs.2877	cadherin 3, typ
	413833	Z15005	Hs.75573	centromere prot
	407243	AA058357	Hs.74466	carcinogen-induc
	410044	BE566742	Hs.58169	highly expresse
25	424273	W40450	Hs.144442	phospholipase A
	409533	AW969543	Hs.21261	nitrogen-activat
	419741	NM_007019	Hs.83002	ubiquitin anti
	409897	AW097949	Hs.184719	ESTs, Weakly ai
	431359	AB035896	Hs.150587	Kinesin-like pr
30	433396	BE562558	Hs.74346	ESTs, Weakly ai
	426427	M6689	Hs.168640	TK, protein kin
	434725	AK000796	Hs.4104	hypothetical pr
	433312	A241331	Hs.131765	ESTs
	407047	K65965	Hs.291759	griH-sapiens SO
35	418220	AA811938	Hs.78381	ESTs
	416530	U62801	Hs.79381	calyculin 6 (n
	435219	AA676349	Hs.190331	ESTs
	418322	AA284166	Hs.84113	cyclic-dependen
	404283			
40	422670	BE278891	Hs.194691	retinoic acid i
	418653	A1750878	Hs.87409	thrombospondin
	451237	AW600293		gb-EST00049 pGE
	407796	AA116021	Hs.38260	ubiquitin speci
45	437935	AW935591	Hs.5940	hypothetical pr
	419525	BE246743	Hs.288620	Homo sapiens cD
	435937	AA530893	Hs.119769	ESTs
	438993	AA828955		gb:cd77008.s1 N
	422082	AA016188	Hs.111244	hypothetical pr
50	450396	AU077002	Hs.24550	regulator of C-
	422578	AF239666	Hs.1545	caudal type hom
	428070	T63918	Hs.182313	retinol-binding
	416111	AA033813	Hs.79018	chromatin assem
	433345	AA581545	Hs.152982	Homo sapiens cD
55	427357	NM_002659	Hs.179557	glutamine-act
	423554	M90516	Hs.1674	glutamine-fruct
	453204	R10799	Hs.191990	ESTs
	425081	X74794	Hs.154443	minichromosome
	434682	AA427165	Hs.191598	ESTs
	414108	A1267592	Hs.75761	SFRS protein ki
60	417900	BE250127	Hs.82906	CDC20 (cell di
	428046	AW812795	Hs.155381	ESTs, Moderat
	448019	AW947164	Hs.195641	ESTs
	431753	X76029	Hs.2841	neurexedin U
65	410361	BE391804	Hs.62651	guanylate bindi
	418526	BE019020	Hs.85338	solute carrier
	444478	W07318	Hs.240	M phase phospho
	438861	AW375974	Hs.155704	ESTs
	408194	AA601038	Hs.191797	ESTs
	438578	AA811244	Hs.164168	ESTs
70	429163	AB014604	Hs.197925	KIAA0704 protei
	433900	AW001582	Hs.226414	ESTs, Weakly ai
	432877	AW974111	Hs.252477	ESTs
	451928	AA823801	Hs.30315	ESTs
	418245	AA088767	Hs.83883	transmembrane,
75	435196	AA108847	Hs.193380	ESTs, Highly ai
	432193	AA337264	Hs.273193	hypothetical pr
	449532	W74653	Hs.271593	ESTs
	409703	NM_006187	Hs.56009	Z-foligodendry
	419373	NM_003244	Hs.90077	TC-interacting
80	433507	W73428	Hs.8750	uncharacterized
	405818			
	444371	BE540274	Hs.239	forkhead box M1
	432675	A1791855	Hs.105854	ESTs

AIRC,SAICAP, synlTM,	2.48
TM	2.48
zf-C3HC4, TM,	2.48
SEA, TM,SS	2.48
zf-C2H2,SCAN, TM,	2.48
sod1c, TM,	2.47
SS	2.47
FGGY, TM,	2.47
FG-GAP, TM,SS	2.46
B19, G4b4, TM,	2.46
integrin_A,FG-GAP, TM,SS	2.46
AMP-binding, G_glu, transactin, TM,	2.45
TM,SS	2.45
SHL,SS	2.45
HATPase, c,SS	2.45
TM	2.45
SH3, TM,	2.44
integrin, alpha	2.44
FG-GAP, vna, TM,SS	2.44
TM	2.44
aa_permeases, TM,	2.43
cadherin, Cadherin_C_term, TM,SS	2.43
kinesin, TM,	2.43
TM,SS	2.43
TM,SS	2.43
phoslip, TM,SS	2.42
TM,SS	2.42
UQ, consulfand, TM,SS	2.42
ABC_tran, ABC_membrane, TM,	2.42
kinesin, Myosin_cat, TM,SS	2.42
SS	2.42
phox, TM,	2.41
TM	2.41
zf-C2H2, SS	2.41
sod1c, TM,	2.41
TM,SS	2.40
integrin, pto, isomerases, TM,SS	2.40
TM	2.40
SS	2.40
Nucleon, TM,SS	2.40
Thm, 3, TM,	2.40
EGF, TSPH, lbp_1, lbp_3, vnc, SS	2.39
TM	2.39
UCH-1, UCH-2, SS	2.39
TM,SS	2.39
TM	2.39
TM	2.39
integrin_B, TM,SS	2.38
TM	2.38
regulator of C-	2.38
homeobox, SS	2.38
lipocalin, TM,	2.38
TM,SS	2.37
TM	2.37
LIPAL, LV,SS	2.37
GATase, 2,SS, TM,SS	2.37
TM	2.37
MCM, TM,	2.36
TM	2.36
phox, TM,	2.36
WD40, TM,	2.36
ank, SS	2.36
ESTs	2.36
NMII, TM,SS	2.36
GBP, TM,SS	2.36
MCT, TM,SS	2.36
kinesin, SS	2.36
TM	2.35
TM	2.35
formyl_transf, AIRS, GARS, TM,	2.35
TM	2.35
TM	2.33
Etc, SAM_PNT, TM,	2.33
TM	2.33
mi_Rccept, a, TM,SS	2.33
TM	2.33
TM,SS	2.33
TM	2.33
NTP_transf_2, TM,SS	2.33
homeobox, SS	2.32
SS	2.32
TM,SS	2.32
Fork_head, SS	2.32
PDFAse, TM,	2.32

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411773	NM_006799	Hs.72026	protease, serin	trypsin,SS	2.31
434775	AA649883	Hs.212911	ESTs	TM,SS	2.31
426211	AA158177	Hs.118722	lucosyltransfer	SS	2.31
419493	AF001212	Hs.90744	proteasome (pro	SS	2.31
424435	AB011167	Hs.146857	KIAA0555 protei	TM	2.30
429622	AK000631	Hs.52556	hypothetical pr	WD40,TM,SS	2.30
428125	AA393071	Hs.182579	leucine aminope	Peptidase_M17,TM,SS	2.30
417655	AA780791	Hs.14014	ESTs, Weakly si	TM	2.29
407287	AJ678872	Hs.201658	ESTs, Weakly si	rac,TM,SS	2.29
429923	BE047598	Hs.188785	ESTs	TM,SS	2.28
422203	X57522	Hs.158154	ATP-binding cas	ABC_tran,ABC_membrane,TM	2.29
430402	AF208234	Hs.695	cystatin B (ste	cystatin,SS	2.29
418359	AL043202	Hs.90073	chromosome segm	TM,SS	2.29
415199	AW176401	Hs.27424	DEAD/D (Aap) pr	TM,SS	2.29
420811	AF219139	Hs.87726	KIAA0154 prote	Cobalamin_bnd,SS	2.29
420931	AF044197	Hs.100431	small inducible	IL8,TM,SS	2.28
425247	NM_005940	Hs.155324	matrix metallo	hemopexin,Peptidase_M10,TM,SS	2.28
438170	AJ916685	Hs.194601	ESTs	2-Haact_DH,TM	2.28
445378	AV65564	Hs.226946	ESTs	TM	2.28
428048	AA705745	Hs.185070	ESTs	AMP-binding,TM	2.28
414696	AF002020	Hs.76918	Niemann-Pick, di	Patched,TM,SS	2.27
433635	AF111106	Hs.3382	protein phospho	TM	2.27
421155	HF8789	Hs.102267	lysyl oxidase	Lysyl_oxidase,SS	2.27
405545				ABC_tran,ABC_membrane,TM,SS	2.27
446537	AJ245671	Hs.12844	EGF-like domain	EGF,SS	2.27
423634	AW959908	Hs.1690	heparin-binding	TM,SS	2.26
427742	AF186252	Hs.30084	sulfotransferase,SS	Sulfotransferase,SS	2.26
428330	L22524	Hs.2256	matrix metallo	Peptidase_M10,SS	2.26
429731	AK001592	Hs.212172	beta,beta-carot	TM	2.26
400514				p450,TM,SS	2.26
431846	BE019924	Hs.271580	uncgulin 1B	transmembrane4,TM,SS	2.26
428010	AA135653	Hs.1975	Homo sapiens cD	TM	2.26
437641	AA811452	Hs.291911	ESTs	TM	2.26
411393	AW979437	Hs.69771	B-factor, prope	sushi,trypsin,waa,DEAD,rm,EGF,fn3,thromogen,CS	2.26
414809	AA344699	Hs.77356	transferrin rec	PA,Fibronectin_S2,TM	2.25
415498	AJ316241	Hs.99891	nucleosiphonin	SS	2.25
434540	NM_015045	Hs.5184	TH1 disophila	TM	2.25
410196	AJ936442	Hs.59838	hypothetical pr	UBA/CT_repeat,TM	2.25
456844	AQ264155	Hs.152581	CDP-diacylglyce	Cytochrome,TM	2.25
428353	BE438838	Hs.44258	hypothetical pr	Fibronectin_S17,TM	2.25
448753	AL048858	Hs.224365	ESTs, Weakly si	TM	2.25
428479	Y00072	Hs.184572	cell division c	pkase,TM,SS	2.24
424971	AA479005	Hs.154036	tumor suppress	ion_trans,PH,TM	2.24
432673	AB028859	Hs.278605	ER-associated D	DJ,DJ_C,TM,SS	2.24
429432	DA9372	Hs.54450	small inducible	IL8,TM,SS	2.24
429925	NM_000786	Hs.226213	cytochrome P450	p450,TM,SS	2.24
445413	AA151342	Hs.12677	CGI-147 protein	UPF0999,TM,SS	2.23
447532	AK000614	Hs.18791	hypothetical pr	TM	2.23
423515	AA327077	Hs.102204	ESTs	SS	2.23
444743	AA045548	Hs.11817	nuclei (nucleosi	mult,TM	2.23
434518	H65995	Hs.37372	Homo sapiens DN	TM	2.23
435602	AF217515	Hs.283532	uncharacterized	TM,SS	2.23
449974	AW978948	Hs.269403	ESTs	TM	2.23
424927	AW973666	Hs.153850	hypothetical pr	TM	2.23
414420	AA043424	Hs.76095	immediate early	TM	2.23
431840	AA534908	Hs.2860	POU domain, cta	homeobox,pou,TM,SS	2.23
452300	AW195285	Hs.194087	ESTs	SS	2.23
435391	AJ227692	Hs.146274	ESTs	SS	2.23
439186	AW697274	Hs.6487	Xc2B, 2000top s	Epimerase,SS	2.23
414732	AW410976	Hs.77152	minichromosome	MCM4,TM	2.22
411855	U29343	Hs.72550	hyaluronan-medi	TM	2.22
438923	AA781171	Hs.244051	gli-a24405 s1 S	myosin_head,TM	2.22
450149	AW969781	Hs.293440	ESTs, Moderat	TM	2.22
401519				filament,TM	2.22
441794	AW197794	Hs.253338	ESTs	ank,TM	2.22
408901	AK001330	Hs.48655	hypothetical pr	TM	2.21
434423	NM_006769	Hs.3844	Uln domain only	LIM,TM	2.21
432140	AK000404	Hs.272688	hypothetical pr	SS	2.21
423453	AW450737	Hs.128791	CGI-09 protein	Gravin,CDP-OH_P_trans,TM	2.21
429438	NM_001955	Hs.2271	endostatin 1	endostatin,TM,SS	2.21
421473	BE281191	Hs.1378	annexin A3	annexin,TM,SS	2.21
440381	AA917608	Hs.190495	ESTs	TM,SS	2.20
453779	N35187	Hs.42388	ESTs	TM,SS	2.20
433627	AF078866	Hs.284296	Homo sapiens cD	SURF4,TM	2.20
417944	AA007196	Hs.82985	collagen, type	COL1A1,Collagen,wc,TM,SS	2.20
422689	AW856655		gbr-3-CTD257-2	SNF2_N,TM	2.20
448457	H65629	Hs.245997	ESTs	TM,SS	2.20
426125	X87241	Hs.166994	FAT tumor suppr	EGF_cadherin,Jammin_G,TM,SS	2.20
435053	AA148164	Hs.247280	HBV associated	zf,CHCA,TM	2.20
425774	BE281191	Hs.154462	minichromosome	MDA,TM	2.20
452679	Z42387	Hs.42999	Homo sapiens cD	TM	2.20
410519	BE512730	Hs.65114	keratin 18	filament,TM	2.20
424332	AA338919	Hs.101615	ESTs	SS	2.20

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	418561	NM_001949	Hs.1189	Human mRNA for	E2F_TOP1,MM5	
	415341	N71463	Hs.118888	ESTs, Weakly as	UPF0076,MM5S	
	427920	Z11502	Hs.181107	annexin A13	annexin, TM	
	403208				hrech_c1,MM5S	
5		AF063811	Hs.119533	Z Sdf-godomy	abiquitin, SS	
	444261	AA298958	Hs.10724	MD5023 protein	TM	
	423401	NM_001952	Hs.128087	coagulation fac	TM, 1,MM5S	
	453450	AW797827	Hs.85474	ADP-ribosylatio	SS	
	444334	BE294793	Hs.10848	KIAA1817 gene p	SS	
10		437616	A1571153	Hs.207554	SAC,NT,MM5S	
	451937	WS2854	Hs.27099	DKF ZP564J0863 p	TM	
	430441	BE360951	Hs.6590	DKF ZP434D155 p	TM	
	411578	A1907114	Hs.71465	squalene epoxid	Myonogenesis, TM	
	452291	AF0115362	Hs.28853	CDCT (cell divi	lamp, TM	
15		444342	NM_143638	Hs.13887	similar to hpa	TM
	451099	RS2795	Hs.25954	interleukin 13	tm3, TM, SS	
	425873	NM_013390	Hs.150417	transmembrane p	TM	
	417404	NM_007350	Hs.82101	plectrokin homo	TM	
	445995	AJ55012		ghyql16010.x1N	TM	
20		439561	AA857451	Hs.269656	ESTs	TM
	429125	AA446854	Hs.271004	ESTs	TM	
	407103	AA242481	Hs.256301	ESTs	TM	
	415116	AA160353	Hs.265556	ESTs	ER, lumen_recept, TM, SS	
	440052	KR33744	Hs.195648	ESTs	PAC, TM, SS	
25		423961	D13666	Hs.136348	Fosducin, TM, SS	
	431070	AW408164	Hs.249184	transcription f	PHA, SS	
	443569	AJ075559	Hs.134125	ESTs	TM	
	427258	AA420091	Hs.38421	ESTs	TM	
	418113	A1272141	Hs.83484	SRY (sex determ	TM	
	450335	BE262773	Hs.25584	hypothetical pr	ArmG_box, TM	
	449357	AB303784	Hs.22541	KIAA1363 protei	TM	
	448113	Y12005	Hs.23521	HM1T1 (puRNP-nucl	TM, SS	
	424653	AW977534	Hs.151465	calcium/calmodu	TM	
35		431341	AA307211	Hs.251531	proteasome (pro	TM
	452965	A1824046	Hs.115657	ESTs	TM	
	432785	D25381	Hs.3104	AA10042 gene p	TM	
	436580	AA811282	Hs.295202	ESTs	SS	
	422192	AA305159	Hs.113019	fts485	SS	
	425607	U05960	Hs.155333	protease, serin	TM	
40		447289	AW427017	Hs.36578	melanoma antig	TM
	447674	BE276440	Hs.19192	cyclin-dependent	TM	
	441021	AW575716	Hs.7544	H1 histone fami	TM	
	426471	M22440	Hs.170005	transforming pr	TM	
	431941	AK000105	Hs.272227	Homo sapiens cD	inkar, histone, TM	
45		414761	AJ077228	Hs.77256	enhancer of cas	SET, TM
	410407	X66835	Hs.63297	carbonic anhydr	car_anhydrase, TM, SS	
	420900	AL045633	Hs.44269	ESTs	TM	
	415236	AA448183	Hs.184598	Homo sapiens cD	AK_Xan_oh_CFDA_binding_5, TM	
50		452721	AJ265529	Hs.30377	Homo sapiens ES	TM
	410644	NM_006033	Hs.65370	lipase, endothe	TM	
	452335	AK001269	Hs.30738	hypothetical pr	Ribosomal_L27,up,PLAT, TM, SS	
	452952	BE245374	Hs.77842	hypothetical pr	TM	
	401708				Acyltransferase, TM, SS	
	411400	AA311919	Hs.69851	GAR1 protein	SS	
55		448526	AB028546	Hs.21361	KIAA1023 protei	TM
	421175	A1879509	Hs.102397	GIOT-3 for gona	TM	
	413611	A6271778	Hs.75412	Arginine-rich p	z-C2H2/KRAB, TM, SS	
	422945	AL043583	Hs.271387	ESTs, Weakly sti	TM	
	418552	X66229	Hs.284153	Fanconi anemia	PK, SS	
60		425298	AK000209	Hs.155556	hypothetical pr	TM
	450956	AW153531	Hs.205547	ESTs, Moderatel	TM	
	419559	A971551	Hs.51143	pegged 1 (Abag	TM	
	421508	NM_054833	Hs.105115	absent in muscu	TM	
	413670	AB000115	Hs.75470	hypothetical pr	TM	
65		422783	AA598956	Hs.120439	ethanolamine ki	TM
	410418	DJ1382	Hs.63325	transmembrane p	TM	
	414860	BE285583	Hs.77502	methionine aden	TM	
	425860	L29339	Hs.1564	solute carrier	TM	
	414839	X63692	Hs.77462	DNA (cytosine-5	TM	
70		437050	AA756420	Hs.251606	ESTs	TM
	430217	N47863	Hs.182450	ribosomal prote	TM	
	405012	AL117435	Hs.46725	DKF ZP434216 p	TM	
	428365	AA295331	Hs.183851	Homo sapiens cD	TM	
	410839	NM_000849	Hs.55581	protein disulf	TM	
75		430510	AA010056	Hs.242958	ESTs	TM
	427475	AA401351	Hs.191605	ESTs	SS	
	433748	R12244		ghyC3c12.r1 S	TM	
	415138	C18358	Hs.78045	tissue factor p	TM	
80		414788	X78342	Hs.77133	cyclin-dependent	TM
	415474	NM_014252	Hs.78457	solute carrier	TM	
	416472	AA180756	Hs.193094	ESTs, Moderatel	TM	
	410718	A1520783	Hs.191435	ESTs	TM	
	425811	AL038104	Hs.155557	karyophen atp	TM	

E2F_TDP, TM, SS	220
UPF0016, TM, SS	220
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lecitin_c, TM, SS	219
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SMC_N, TM, SS	218
TM	218
TM	218
Monooxygenase, TM	218
pkase, TM	218
Lamp, TM, SS	218
Ins3, TM, SS	218
TM	217
TM	217
TM	217
ER_lumen_recept, TM, SS	217
PAC, TM, SS	217
Fascidin, TM, SS	217
PHA, SS	216
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TM	216
ArfGAP, SS	216
TM	216
Guanylate_kin, PDZ, pkase, SH3, TM	216
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PMP22, Claudin, TM, SS	216
TM	216
pkase, TM	216
SS	215
kl_recept_a, trypsin, CUB, SRCR, MAM, SEA, TM, SS	215
3beta_HSD, Epimerase, AA, GE, TM	215
phage, TM	215
linker_histone, TM	215
EGF, TM, SS	215
phage, Funn-like, TM, SS	215
SET, TM	215
carb_anhydrase, TM, SS	215
Ald_Xan_4h, CFAD, binding_5, TM	215
TM	215
TM	215
zC2H2, KRAB, TM, SS	213
TM	213
PK, SS	213
TM	213
TM	213
pkase, TM, SS	213
EGF, DSL, TM, SS	213
TM	213
TM	213
Choline_kise, TM	213
hypoxin, kl_recept_a, TM, SS	213
S-Hsd, kl_cylin, SS	213
SSF, Ribosomal_S17e, TM	213
zC, CXC, BAH, TM, SS	213
TM	213
TM, SS	213
RhoGEF, TM	212
TM	212
thored, TM	212
TM, SS	212
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AMP-binding, TM	212
Kunitz_BPTI, C-gamma, TM, SS	212
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miso_cen, TM	211
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SGS_PSY, TM, SS	211
Armadillo_seg, IBB, TM, SS	211

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	447197	R36075	gbyh8501.s1 S	SDF, TM	2.11	
	431621	AW292329	Hs.163481	ESTs	2.11	
	433849	BE465884	Hs.280728	ESTs	2.11	
5	438308	AV712629	Hs.194161	ESTs, Weakly si	2.11	
	422032	AA476966	Hs.110857	polymerase (RNA	2.11	
	409717	AA452871	Hs.56043	CCG-115 protein	TM	2.11
	445837	AI261700	Hs.145544	ESTs	TM	2.11
	423880	BE278111	Hs.134200	DKF2P564C166 pr	TM	2.10
	421574	AJ000152	Hs.105924	defensin, beta, TM,SS	2.10	
	437133	AW119408	Hs.152940	ESTs	Choline_Se, TM	2.10
	450747	AI064821	Hs.48306	ESTs, highly si	nm, TM	2.10
	437333	AW248364	Hs.5408	RNA polymerase	TM	2.10
	417640	D30857	Hs.82363	protein C recep	TM	2.10
	431120	AA492588	gkng9p68.s1 H	hypothetical pr	TM, SS	2.10
15	438510	AW162916	Hs.241576	hypothetical pr	TM	2.10
	429669	BE165499	Hs.2471	KIAA0020 gene p	TM	2.10
	407881	AW072003	Hs.40968	heparan sulfate	SS	2.10
	436415	BE265254	Hs.5181	proliferation a	TM	2.10
	407887	AA575568	Hs.41072	serine (or cyst	serpin, TM	2.10
20	447615	AI432199	Hs.247084	ESTs	LIM, TM	2.09
	432474	AA628539	Hs.116252	ESTs, Moderatel	nm, TM, SS	2.09
	411571	AA122393	Hs.70811	hypothetical pr	SS	2.09
	442526	AF152382	Hs.145845	ESTs	phala, TM	2.09
	423750	AF165883	Hs.132415	peldolin 2	TM	2.09
25	446199	AI050122	Hs.196988	ESTs	ras, TM	2.09
	415363	AI670947	Hs.78406	phosphatidylyno	PP5P, phos, TM, SS	2.09
	418462	BE301596	Hs.62565	integrin, beta	integrin_B, h3, TM, SS	2.09
	430336	D80007	Hs.239469	KIAA0165 protei	S1, TM	2.09
	443450	N65045	Hs.133529	ESTs	TM	2.08
30	418753	BE217818	Hs.87016	Homo sapiens cD	TM	2.08
	438018	AW309882	Hs.26538	ESTs, Weakly si	TM, SS	2.08
	431628	AF144277	Hs.255561	CD2-associated	SH3, SS	2.08
	446528	AJ075640	Hs.15243	nuclear prote	Nol1_Nop2_Sun, TM	2.08
	411372	AI147861	Hs.213289	low density lip	EGF_RL_recept_aM_recept_h, TM, SS	2.08
35	450319	NM_000599	gk-Homo sapiens	BRCA2_reseal, TM	2.08	
	426730	AI060717	Hs.47144	CHK2P58A0616 p	TM, SS	2.08
	409220	BE243313	Hs.51233	tumor necrosis	TNF_R_c, death, TM	2.08
	429504	X99133	Hs.204238	lipocalin 2 (on	lipocalin, SS	2.08
	409866	AK000002	Hs.55879	Homo sapiens mR	ABC_tran, ABC_membrane, TM	2.08
	413082	AA128065	Hs.118665	ESTs	EGF, TM, SS	2.08
	413715	AW051121	Hs.75467	Homo sapiens cD	cystin, TM	2.08
	423020	AA363092	Hs.1608	replication pro	TM	2.07
	438378	AW970529	Hs.86434	Homo sapiens cD	TM, SS	2.07
	432125	AW972667	Hs.287510	Homo sapiens cD	Band_41, TM, SS	2.07
45	448370	AK002114	Hs.23495	hypothetical pr	TM, SS	2.07
	454011	M31008	Hs.37009	alkaline phosph	alk_phosphatase, TM, SS	2.07
	427876	AI464291	Hs.111977	ESTs	TM	2.07
	422501	R81936	Hs.121576	aspartate beta-	SS	2.07
	449207	AL044222	Hs.73255	nucleophin 155	TM, SS	2.07
50	408243	Y00787	Hs.624	interleukin 5	IL8, TM, SS	2.07
	446546	BE167887	Hs.166628	ESTs	Selftransferr, TM, SS	2.07
	423472	AF041260	Hs.129057	breast carcino	TM	2.07
	435211	AF001581	Hs.80961	polymerase (DNA	gk-EST351283 MA	2.06
55	455157	AW075153	Hs.148968	EST	transmembrane4, TM	2.06
	407143	C14076	Hs.248968	EST	TM	2.06
	432440	X63597	Hs.2996	sucrase-isomalt	Glyco_hydro_31, intol, TM, SS	2.06
	410668	BE379794	Hs.65403	hypothetical pr	TM	2.06
	42785	AW489701	Hs.1578	baculoviral IAP	BIR, TM	2.06
	439632	TB1829	Hs.14670	ESTs	SS	2.06
60	445318	AW509552	Hs.200885	ESTs	TM	2.06
	439981	A034767	Hs.124636	ESTs	TM, SS	2.06
	426307	V27393	Hs.183648	protein tyrosin	TM	2.06
	432504	AA308809	Hs.41039	Homo sapiens cD	SS	2.06
65	433027	AF191018	Hs.279923	putative nucleo	MMR_HSR1, TM	2.06
	433716	AA608808	Hs.225118	ESTs	TM	2.06
	429412	NM_006235	Hs.2407	PCU domain, cda	TM	2.06
	449026	BE509046	Hs.289106	ESTs	TM	2.06
	437016	AJ076916	Hs.5398	guanine monophos	GAase, GMP_synth, C, TM	2.06
	442547	AA306997	Hs.268362	ESTs, Weakly si	SS	2.06
70	455778	BE098746	gk-CMO-810693-2	gk	TM	2.06
	439975	AW328091	Hs.6817	Homo sapiens pr	TM, SS	2.06
	433337	NM_014158	Hs.279938	HSPC067 protein	TM	2.06
	440086	NM_005402	Hs.288757	v-rat simian le	ras, TM	2.06
	436414	BE264633	Hs.143638	WID repeat domai	WD40, TM	2.05
75	411770	NM_014278	Hs.71392	heat shock prot	HSP70, TM	2.05
	409459	D06407	Hs.544491	low density lip	EGF_RL_recept_aM_recept_h, TM, SS	2.05
	436238	AK002163	Hs.301724	ESTs, Highly si	MMR_HSR1, TM	2.05
	400517	AF242388	Hs.145855	lengsin	TM	2.05
	421904	BE143533	Hs.109339	hypothetical pr	SS	2.05
80	417850	AA215734	Hs.52741	primase, polye	SS	2.05
	417491	AW376842	Hs.1085	guanylate cycl	pkase, guanylate_cyc, ANF_receptor, TM, SS	2.05
	453775	NM_002216	Hs.35120	replication fac	AAA, TM, SS	2.05
	435525	AI831297	Hs.123310	ESTs	TM	2.05

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5	412627	BE391959	Hs.14276	chloride intrac	G patching,MUS_C,TM	2.05
	438702	AW085526	Hs.134182	ESTs	A2M,SS	2.05
	440006	AK005517	Hs.6844	hypothetical pr	TM	2.05
	417308	H60720	Hs.81892	KIAA0101 gene p	TM	2.05
	446311	AW007294	Hs.148795	ESTs, Weakly si	pknox,TM	2.05
10	427871	AW982405	Hs.59622	ESTs, Weakly si	SS	2.05
	453804	AA300204	Hs.35276	KIAA0952 protein	TM,SS	2.05
	449939	T86420	Hs.272139	ESTs	DIL,myosin_head,TM,SS	2.05
	417819	A1253112	Hs.133540	ESTs	TM	2.04
	427747	AW411425	Hs.19055	ser-nucleosin	phox,TM	2.04
15	415009	C75253	Hs.220950	ESTs	TM	2.04
	437829	A1368522	Hs.270188	ESTs	TM	2.04
	482753	AW939252	Hs.192527	hypothetical pr	TM	2.04
	446475	A1908188	Hs.235245	ESTs	OPR,TM	2.04
	411394	AK000692	Hs.223251	HERV-H LTR-asso	ig,TM,SS	2.04
20	423701	AA329856	Hs.143022	ESTs	TM	2.04
	422369	AF005216	Hs.115541	Janus kinase 2	SH2,ptkase,TM	2.04
	432481	AW451645	Hs.151504	Homo sapiens cD	TSPN,Collagen,TM,SS	2.04
	443746	AW611370	Hs.195022	ESTs	TM	2.04
	400792	AA635062	Hs.50094	Homo sapiens mR	zf-C3HC4,CARD,BIR,TM	2.04
25	428343	AL043021	Hs.12705	ESTs, Weakly si	TM	2.04
	419329	AY007220	Hs.288598	S100-type calci	TM	2.04
	423485				filament,TM	2.04
	413313	NM_002047	Hs.75280	ghey-1RNA syn	WHEP-1RS,TM,2,TM,SS	2.04
	433326	A079496	Hs.159430	ESTs	TM	2.03
30	440246	W62010	Hs.191379	ESTs	serpin,TM	2.03
	444006	BE1395085	Hs.10086	type I transmem	TM,SS	2.03
	452705	H46905	Hs.240025	ESTs	TM	2.03
	421724	AB037832	Hs.107287	KIAA1411 protein	TM	2.03
	447474	AW614220	Hs.189402	ESTs	SS	2.03
35	418852	BE531703	Hs.27254	hypothetical pr	TM	2.03
	431842	NM_005764	Hs.271473	epithelial prot	TM,SS	2.03
	440773	AA352702	Hs.37747	hypothetical pr	TM	2.03
	443425	A1056776	Hs.133397	ESTs	TM,SS	2.03
	407975	X89426	Hs.41716	endothelial cel	IGFBP,SS	2.03
40	428299	AL338004	Hs.29419	ESTs	TM,SS	2.03
	415757	AA830854	Hs.187810	ESTs	TM	2.03
	432559	AW452948	Hs.257631	ESTs	PAC,TM,SS	2.03
	425912	AL137629	Hs.162189	serine/threonin	in3,pg,PH,RhoGEF,TM,SS	2.02
	419395	BE286326	Hs.90280	S-aminomethylaz	AICARF1_MP-C-Haz,MGS,TM	2.02
45	417576	AA333449	Hs.82285	phosphorylase	APRS,formyl_trans,GARG,TM	2.02
	418559	AA225404	Hs.104207	ESTs	TM	2.02
	410855	X97795	Hs.66718	RAD54 (S.cerev	SNF2_Nucleicase_C,TM	2.02
	422072	A801825	Hs.111138	KIAA0712 gene p	TM	2.02
	419546	AA241199	Hs.930055	gibco2055-s1 N	Y_phosphatase,TM	2.02
50	450516	AA902656	Hs.21943	NIF3 (Nigo 1 inte	DUF3A,TM	2.02
	419807	R77402		gby75111.1 S	TM	2.02
	438192	AB59065	Hs.16908	ESTs, Weakly si	TM,SS	2.02
	401866				filament,TM,SS	2.02
	443129	R16075	Hs.21658	ESTs	TM,SS	2.02
55	424783	AA913909	Hs.153088	TATA box bindin	TM	2.01
	413293	AL047483	Hs.75270	GTP-binding pro	ras,TM,SS	2.01
	435787	AW162767	Hs.100914	hypothetical pr	SS	2.01
	422599	BE387202	Hs.119368	non-metastatic	NDK,SS	2.01
	431630	NM_002204	Hs.265829	integrin, alpha	FG-GAP,Integrin_A,TM,SS	2.01
60	448275	BE514434	Hs.20830	synaptic Ras CT	kinesin,PHD,aldehydease_2,TM,SS	2.01
	404584				filament,SS	2.01
	435469	AK001455	Hs.51598	Down syndrome c	TM	2.01
	451273	NM_014811	Hs.26163	KIAA0649 gene p	TM	2.01
	432378	AI493046	Hs.146133	ESTs	TM	2.01
65	419981	AA957581	Hs.128773	ESTs	SH_Sno,SS	2.01
	445808	AV655234	Hs.28083	ESTs	sush,TM,SS	2.01
	453787	H73505	Hs.117874	ESTs	Papilloma_S4,P,TM	2.01
	430466	AF052573	Hs.241517	polymerase (DNA	TM	2.01
	422790	AA809875	Hs.25933	ESTs	TM	2.01
70	443303	U67319	Hs.9216	casease 7, spop	ICE_p10ICE_p20,TM	2.01
	410068	AA079552	Hs.127832	ESTs	fg-m20h12.s1 S	2.01
	440774	AI420611	Hs.127832	ESTs	zf-MYND,TM,SS	2.01
	442961	BE614474	Hs.289074	Homo sapiens cD	TM	2.00
	424420	BE614743	Hs.146688	prostaglandin E	MAPEG,TM,SS	2.00
75	410240	AL157424	Hs.61289	synaptobilin 2	TM	2.00
	435014	BE560898	Hs.10026	ribosomal prote	Ribosomal_L17,TM	2.00
	406752	AI285598	Hs.217493	annexin A2	TM	2.00
80	TABLE 41B					
	Play:	Unique Eos probest identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
80	Play	CAT number	Accession			
	410008	116812_1	AA079552 BE142525 BE142527			
	418546	176677_1	AA224827 T59708 T59843 BE156903			
	419546	185766_1	AA244199 AA244272 H57440			

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419837	188252_1	F77402 AA262462 AA250968 F06794
422689	219896_1	AW556665 AA315006 AW954733
431120	328264_1	AA492588 AA492498 AA452571
433748	37385_1	R12244 H171290 AH10058 AF090916 AF075357 AA011531
438223	452646_1	AA71171 A122139 A120209
438993	467651_1	AA628995 AA834579 A926361
466955	702207_1	A135012 AW812856
447197	711623_1	R36075 A1365546 R36167
450193	827655_1	U13367 AW191555 U151771 A0686285
451237	863593_1	AW602923 A167468
455778	1364506_1	BE068746 BE08802 BE088755 BE088876 BE088947 BE088881 BE088952
456157	158261_1	AW979153 AA176967 AA26015

TABLE 41C:

Key: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: indicates DNA strand from which exons were predicted.
 Nt_position: indicates nucleotide positions of predicted exons.

Key	Ref	Strand	Nt_position
406514	979699A	Minus	78944-79025,80950-80991,89754-89941,93750-93891
401519	6649315	Plus	152115-157950
401708	2951946	Plus	154511-155298
401866	8018106	Plus	73126-73823
402076	8117407	Plus	121967-122035,122804-122921,124019-124161,124455-124610,125672-129076
402555	874890A	Minus	109532-110225
403208	7630829	Minus	147706-147903,148667-148804
403422	9665041	Minus	151169-151561
404385	9966528	Plus	2808-3001,3199-3532,3655-4117
404376	7770611	Minus	1414-1513,1634-1756
404171	9530793	Plus	173667-173783,176876-177055
404253	9367202	Minus	55975-56055
404519	8152000	Plus	12817-13000
404567	7249169	Minus	101320-101501
405484	5922025	Plus	199214-199379,199672-199920,200262-200455
405545	1054740	Plus	116677-116807,119091-119296,121626-121823
405818	4071056	Plus	29058-29196
406399	9256288	Minus	63449-63554

TABLE 42A: ABOUT 561 GENES UP-REGULATED IN STOMACH CANCER

Table 42A lists about 561 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 40A except using various non-malignant stomach specimens in determining the denominator value.

Key: Unique Eos probe set identifier number
 ExAccess: Exon/Accession number, Genbank accession number
 UnigenelID: Unigene number
 Unigene Title: Unigene gene title
 RT: Ratio of tumor to normal tissue

Key	ExAccess	UnigenelID	Unigene Title	RT
428368	BE440042	HS.83326	matrix metalloproteinase 3 (stromelysin)	60.4
448933	AW024854	HS.226320	Human sapiens cDNA: FLJ23537 f5, clone L	26.6
428564	AK001666	HS.189805	similar to SALL1 (cat (Drosophila)-like)	26.8
422330	D30783	HS.115263	epigargin	22.0
415989	AI267700	HS.111128	ESTs	21.2
439979	AW600291	HS.6823	hypothetical protein FLJ10430	19.0
451059	RS2795	HS.29554	interleukin 13 receptor, alpha 2	17.1
437776				14.9
424905	NM_002497	HS.153704	NIMA (never in mitosis gene a)-related k	14.8
414132	AB011235	HS.48480	ESTs	14.2
450375	AA005647	HS.8550	a disintegrin and metalloproteinase domain	12.2
453922	AF053306	HS.36708	building uninhibited by benzimidazoles 1	13.8
436032	AA150797	HS.109276	lactoxin protein	13.1
427555	D31152	HS.179729	collagen, type X, alpha 1 (Schmid metaph	12.5
416681	AI834543	HS.79440	ICF-3 mRNA-binding protein 3	12.2
414672	BE263782	HS.77655	KIAA0096 gene product	9.9
445900	AF070526	HS.13429	Homo sapiens clone 24767 mRNA sequence	10.5
446619	AU076643	HS.313	secreted phosphoprotein 1 (osteopontin,	10.5
441377	BE218239	HS.202656	ESTs	10.2
415423	D38486	HS.50315	KIAA007 protein	9.8
451538	C18356	HS.78045	tissue factor pathway inhibitor 2	9.6
424639	AI917494	HS.121329	ESTs	9.4
412472	AW975398	HS.253836	ESTs	9.4
447046	AI1833863	HS.226320	Homo sapiens cDNA: FLJ23537 f5, clone L	8.9
416379	AA218940	HS.132516	edgfin-like 1	8.8
423020	AA383092	HS.1608	replication protein A3 (14kD)	8.6
408938	BE296227	HS.48915	serine/threonine kinase 15	8.5
419946	AB041035	HS.33847	NAD(P)H oxidase 4	8.3
411750	BE522298	HS.71327	HOADN1 protein, homolog of yeast ribos	8.3
411479	AW848047		gb1L3.C7C124.291299-052-A12 CT0214 Homo	8.1
420900	AL045633	HS.44269	ESTs	8.0
449347	AW649748	HS.295901	ESTs	8.0

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450401	AB033025	Hs.50061	KJAA1159 protein	8.0
450480	X82125	Hs.25040	zinc finger protein 239	7.6
417655	AA780791	Hs.14014	ESTs, Weakly similar to KJAA0673 protein	7.6
453878	AW664440	Hs.19025	ESTs	7.6
430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	7.5
427961	AW293165	Hs.143134	ESTs	7.4
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	7.3
426235	A0831964	Hs.34447	ESTs	7.1
452291	AF015592	Hs.28653	CDCC (cell division cycle 7, S. cerevisiae)	7.0
415205	L27715	Hs.53780	tropomyosin 1, skeletal, fast	7.0
409757	NM_001898	Hs.123114	cystatin SN	6.9
430044	AA464510	Hs.152812	ESTs	6.6
444763	AK001468	Hs.52180	anillin (Drosophila Scraps homolog), act	6.5
416209	AA236716	Hs.79076	MAZD (mitotic arrest deficient, yeast, h	6.5
419020	A0621170	Hs.192699	ESTs	6.3
431958	X53629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.8
434656	AA643687	Hs.149425	Homo sapiens cDNA FLJ11960 fs, clone HE	5.7
424345	AK001390	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT	5.6
428227	AA321649	Hs.2248	small inducible cytokine subfamily 6 (C)	5.4
434551	BC387162	Hs.280658	ESTs, Highly similar to XPS_HUMAN DNA-RE	5.3
427660	AT741320	Hs.114121	Homo sapiens cDNA: FLJ23226 fs, clone C	5.0
424960	BE245386	Hs.153552	5' nucleotidase (CD73)	4.9
400268				4.8
408427	AW194270	Hs.177236	ESTs	4.7
453785	AI368236	Hs.283732	ESTs	4.7
411274	NM_002776	Hs.69423	kallikrein 10	4.7
424717	H03754	Hs.152213	wingless-type MMTV integration site fam	4.7
415752	BC314524	Hs.78776	putative transmembrane protein	4.6
434370	AF130988	Hs.58346	downless (mouse) homolog	4.6
431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamily	4.6
402265				4.6
427938	NM_001809	Hs.1594	cathepsin protein A (17kD)	4.5
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.4
453160	AI263307	Hs.146228	ESTs	4.4
446871	AA331906		g0E5T35805 Embryo, 6 week 1 Homo sapien	4.4
431211	M86493	Hs.5566	gap junction protein, beta 2, 26kD (conn	4.4
465638	AL133063	Hs.15763	Homo sapiens mRNA: cDNA DKFZp434P1115 (f	4.3
406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.3
411560	AW851186		gbl.3.CT0220-150200-071-H05 CT0220 Homo	4.1
433159	AB033098	Hs.190587	kinasin-like protein 2	4.1
446142	AT754693	Hs.145968	ESTs	4.1
414727	BE468904		g0E5T35803 x1 NOL_CGAP_CG6 Homo sapiens	4.1
422285	A081033		g0E5T35803 x1 Soares_NthHMVp_S1 Homo sapi	4.1
451807	VS2854	Hs.27899	DNFZP364A0863 protein	4.1
411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	4.0
415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.0
409420	T15006	Hs.54451	laminin, gamma 2 (nicotin 100kD), latini	3.9
452009	NM_015368	Hs.30865	parvovirus 1	3.9
443211	AT12838	Hs.143655	ESTs	3.9
442696	R37725	Hs.261108	ESTs	3.8
407768	BE514982	Hs.38991	S100 calcium-binding protein A2	3.8
406671	AA129547	Hs.287574	met proto-oncogene (hepatocyte growth fa	3.8
421155	H87879	Hs.102267	lysozyme	3.8
420652	AK000492	Hs.98906	hypothetical protein	3.8
420727	H57501	Hs.99886	complement component 4-binding protein,	3.7
422655	AJ018182	Hs.119018	transcription factor NFR	3.7
441425	AY953747	Hs.18573	xylophosphatase 1, erythrocyte (common)	3.7
417715	AY906567	Hs.86368	ESTs	3.7
460676	AL390179	Hs.137011	Homo sapiens mRNA: cDNA DKFZp47P134 (fr	3.6
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fs, clone PL	3.6
412723	AA848459	Hs.179912	ESTs	3.6
452461	NT8223	Hs.108106	transcription factor	3.6
453321	AT040665	Hs.8895	ESTs	3.6
406434				3.6
417956	AA210704	Hs.190465	ESTs	3.6
416162	AY6245508	Hs.279727	Homo sapiens cDNA FLJ114035 fs, clone HE	3.6
426471	M22440	Hs.170009	transforming growth factor, alpha	3.5
425782	U66468	Hs.155925	cell growth regulatory with EF-hand doma	3.5
442556	AL137761	Hs.8379	Homo sapiens mRNA: cDNA DKFZp596L2424 (f	3.5
426957	AA393676	Hs.97459	ESTs, Weakly similar to KJAA0819 protein	3.5
448105	AY0591433	Hs.170675	ESTs, Weakly similar to TM62_HUMAN TRANS	3.5
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (oxLDL)	3.5
442942	AW167087	Hs.121562	ESTs	3.4
416291	AI878527	Hs.79284	mesoderm specific transcript (mouse) hom	3.4
423230	AI034344	Hs.238020	Homo sapiens cDNA FLJ11796 fs, clone HE	3.4
408243	Y00787	Hs.624	interleukin 8	3.4
412978	AA431708	Hs.820	homeo box CG	3.4
412851	AR26502	Hs.106149	ESTs	3.4
417720	AA205625	Hs.205067	ESTs	3.4
414812	X27255	Hs.72567	monokine induced by gamma interferon	3.4
453884	AA355925	Hs.36232	KJAA0166 gene product	3.4
436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fs, clone HE	3.4
425921	NM_007231	Hs.162211	solute carrier family 5 (phosphorotransfer	3.4

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	420092	AA814043	Hs. B8045	ESTs	3.3
	423441	R68649	Hs. 278359	absent in melanoma 1 like	3.3
	421787	AA227068	Hs. 108301	nuclear receptor subfamily 2, group C, m	3.3
5	447342	A119928	Hs. 19322	ESTs	3.3
	430178	AW49512	Hs. 152475	ESTs	3.3
	452826	BE245286	Hs. 301636	ESTs, Moderately similar to PEX5_HUMAN P	3.3
	414821	M63835	Hs. 77424	Fc fragment of IgG, high affinity Ia, re	3.3
	413339	A818080	Hs. 194290	ESTs	3.3
	445756	A173651	Hs. 171480	ESTs	3.3
10	421944	425831	Hs. 111758	heratin 5A	3.3
	431453	AW573917	gb.RC0-CT0299-291109-014-F02 CT0299 Homo	3.3	
	438538	AA832203	Hs. 261955	ESTs	3.3
	439759	AL339555	Hs. 67709	Homo sapiens mRNA full length insert cDN	3.3
	431721	AB032206	Hs. 268044	KIA1170 protein	3.3
15	436391	AJ27892	Hs. 146274	ESTs	3.3
	442025	AV887434	Hs. 11810	ESTs, Weakly similar to CD4.2 [C.elegans	3.3
	418007	M13509	Hs. 83169	matrix metalloproteinase 1 (interstitial	3.2
	411678	AB07114	Hs. 27465	spatene epoxidase	3.2
	422586	BE545072	Hs. 122570	hypothetical protein FLJ10461	3.2
20	450400	AB64722	Hs. 279744	ESTs	3.2
	453857	AL080235	Hs. 35861	DKFZP586E1621 protein	3.2
	425528	AB011137	Hs. 129740	KIA0565 gene product	3.2
	442559	AF134160	Hs. 7327	clausin 1	3.2
	441085	AW138551	Hs. 181245	Homo sapiens cDNA FLJ12532 fls, clone NT	3.2
25	412022	U005043	Hs. 26143	ESTs	3.2
	418203	XS4942	Hs. 83758	CC28 protein kinase 2	3.1
	415111	AA033813	Hs. 79018	chromatin assembly factor 1, subunit A (3.1
	408633	AW963372	Hs. 46577	PRO2000 protein	3.1
	445808	AV555234	Hs. 298083	ESTs	3.1
30	414618	AT040400	Hs. 95978	ESTs	3.1
	421340	FT7783	Hs. 1365	dcn-4 accelerating factor for complement	3.1
	422689	AW556665	gb.RC3-CT029/-290100-013-003 CT0297 Homo	3.1	
	456508	AA502764	Hs. 123469	ESTs, Weakly similar to AF208555 1 BM-01	3.1
	420759	T11832	Hs. 127797	ESTs	3.1
35	452637	AW971231	Hs. 251020	ESTs	3.1
	415857	AA486115	Hs. 301546	Homo sapiens cDNA FLJ11381 fls, clone HE	3.1
	439451	AF086270	Hs. 278554	heterochromatin-like protein 1	3.1
	424051	AL110203	Hs. 138411	Homo sapiens mRNA, cDNA DKFZP586J1922 (f	3.1
40	440138	AB033023	Hs. 6362	hypothetical protein FLJ10201	3.1
	454456	AW555964	gb.L3-CT0220-150200-050-H08 CT0220 Homo	3.0	
	429125	AA46854	Hs. 271004	ESTs	3.0
	408031	AA081395	Hs. 421173	Homo sapiens cDNA FLJ10366 fls, clone NT	3.0
	438394	BE379623	Hs. 27893	CG-124 protein	3.0
45	405361	NM_005982	Hs. 54416	sine oculis homeobox (Desophila) homolo	3.0
	439453	BE264874	Hs. 6556	thyroid hormone receptor 13	3.0
	414696	AF020200	Hs. 76918	Niemann-Pick disease, type C1	3.0
	422746	NM_004484	Hs. 119651	glycocalyx 3	3.0
	424947	R77952	Hs. 239625	integral membrane protein 2B	3.0
	453775	NM_002916	Hs. 35120	replication factor C (activator 1) 4 (37	3.0
50	445386	AA001308	Hs. 193213	ESTs	3.0
	430587	BE274217	Hs. 249247	heterogeneous nuclear protein similar to	2.9
	428852	NM_000346	Hs. 2316	SRY (sex-determining region Y)-box 9 (ca	2.9
	401747				2.9
55	429682	NM_006306	Hs. 211602	SMC1 (structural maintenance of chromoso	2.9
	444735	BE019923	Hs. 243122	hypothetical protein FLJ13057 similar to	2.9
	413385	M34455	Hs. 840	indoleamine-pyrrole 2,3 dioxygenase	2.9
	436222	AQ208737	Hs. 122810	Homo sapiens cDNA FLJ11489 fls, clone HE	2.9
	442961	BE514474	Hs. 288074	Homo sapiens cDNA FLJ13086 fls, clone Y7	2.9
60	454798	AAW81295	gb.PM3-ST0307-241299-002-g03 ST0307 Homo	2.9	
	421650	AA781795	Hs. 122587	ESTs	2.9
	434358	AA121098	Hs. 3638	serum-inducible kinase	2.9
	420153	N02120	Hs. 75277	hypothetical protein FLJ13910	2.9
	435706	W31254	Hs. 7045	GLD04 protein	2.9
65	416065	BE267931	Hs. 78996	proliferating cell nuclear antigen	2.9
	423250	BE061916	Hs. 125849	chromosome B open reading frame 2	2.8
	423453	A815865	Hs. 125963	alkylglyoxal-oxidizing enzyme E20 1 (homo	2.8
	432422	U66669	Hs. 235642	3-hydroxyisobutyryl-Coenzyme A hydrolase	2.8
	436411	AW574352	gb.baf3/07-y1 NH_MGC_12 Homo sapiens cd	2.8	
	411770	NM_014278	Hs. 71992	heat shock protein (hsp110 family)	2.8
70	437834	AA769294	gb.mbc36/g01s1 NCI_CGAP_G061 Homo sapiens	2.8	
	400440		Hs. 93367	nebulin	2.8
	444743	AA045548	Hs. 11817	nucleotide diphosphate linked moi	2.8
	428725	AI565937	Hs. 59692	ESTs	2.8
	417771	AA804698	Hs. 82547	retinoic acid receptor responder (taccar	2.8
75	449420	AI554552	Hs. 186562	ESTs, Highly similar to TS24 MOUSE PROTE	2.8
	433929	A1374509	Hs. 27379	ESTs	2.8
	430287	AW182459	Hs. 125759	ESTs, Weakly similar to tumor suppressor	2.8
	423346	AI267617	Hs. 127416	synaptotagmin 1	2.8
	407824	AA147884	Hs. 5812	ESTs	2.8
80	005482	NM_000676	Hs. 45743	adenosine A2b receptor	2.8
	425188	AK002052	Hs. 155071	hypothetical protein FLJ11190	2.8
	456999	AA331978	Hs. 172247	eukaryotic translation elongation factor	2.8
	408875	NM_015434	Hs. 48604	DKFZP4340168 protein	2.8

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40	7839	AA045144	Hs.161566	ESTs	2.7
	409012	AL117435	Hs.49725	DKFZP4340216 protein	2.7
	410762	AF226053	Hs.66170	HSKM-B protein	2.7
5	428925	NM_001196	Hs.172894	EH3 interacting domain death agonist	2.7
	410115	AW638671	Hs.58636	squamous cell carcinoma antigen recogniz	2.7
	428398	AI249368	Hs.98558	ESTs	2.7
	400048			AFX control_YE0020z/WBP1	2.7
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (robkines	2.7
10	435664	AK032087	Hs.259819	ESTs	2.7
	405695				2.7
	456655	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	2.7
	408670	AF160967	Hs.46784	potassium large conductance calcium-acti	2.7
	422576	BE546555	Hs.116564	CGI-83 protein	2.7
15	431379	AA504264	Hs.182537	peptidylglycyl isomerase A (cytoplasm	2.7
	429540	MB5776		gb:EST02297 Fetal brain, Stratagene (cat	2.7
	426874	N67325	Hs.247132	ESTs	2.7
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.7
	409902	AI337658	Hs.150351	ESTs	2.7
20	422336	AW161322	Hs.115285	dihydropteroate 5-acetyltransferase (E2	2.7
	408434	AW195317	Hs.107716	Homo sapiens cDNA: FLJ22344 f1a, clone H	2.7
	432328	AI572739	Hs.195471	6-phosphogluco-2-kinase/fructose-2,6-bi	2.7
	407633	NM_007096	Hs.37189	similar to rat HREVI07	2.6
	419216	AI076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.6
25	422363	TS5979	Hs.115474	replication factor C (activator 1) 3 (3)	2.6
	445564	AB028957	Hs.12896	KIAA1034 protein	2.6
	401644				2.6
	417479	AI057052	Hs.133564	ESTs	2.6
	434217	AW014795	Hs.23349	ESTs	2.6
30	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	2.6
	414800	BE539630		gb:67064676F1 NH_MGC_10 Homo sapiens c	2.6
	420289	X07832	Hs.2258	matrix metalloproteinase 10 (matrilysin)	2.6
	412146	U39845	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	2.6
	450387	AW582962	Hs.307061	ESTs, Highly similar to AF151805 1 CG14	2.6
35	428048	AA705745	Hs.185070	ESTs	2.6
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.6
	440052	AE633744	Hs.195648	ESTs	2.6
	433077	AA314262	Hs.289008	Homo sapiens cDNA: FLJ21814 f1a, clone H	2.6
40	424047	AA221036	Hs.285026	HERV-H LTR-associated 1	2.6
	423401	NM_007115	Hs.25352	tumor necrosis factor, alpha-induced pro	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	410889	X31662	Hs.66744	twist (Drosophila) homolog (acrocephalos	2.6
	440100	BE382685	Hs.158549	ESTs	2.6
45	413746	AA132343	Hs.171553	ESTs	2.6
	414737	AI160386	Hs.125087	ESTs	2.6
	422063	BE156476		gb:Q90-HT0368-040100-082-c05 HT0368 Homo	2.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (iso	2.6
	437641	AA811452	Hs.291911	ESTs	2.6
50	436027	A864053	Hs.38972	ESTs, Weakly similar to 138588 reverse I	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CAS4_HUMAN COLLA	2.6
	452571	W31518	Hs.34665	ESTs	2.6
	452862	AW378065	Hs.8867	ESTs	2.6
55	411984	NM_005419	Hs.72968	signal transducer and activator of trans	2.6
	446440	AV558411	Hs.42656	Homo sapiens cDNA FLJ12567 f1a, clone NT	2.6
	448663	BE614599	Hs.106823	Hsapiens gene from PAC 42616, similar I	2.6
	426427	MB6859	Hs.168840	TTK protein kinase	2.6
	445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 unkno	2.6
	420022	AA256253	Hs.120817	ESTs	2.6
60	451418	BE387730	Hs.26369	hypothetical protein FLJ20287	2.6
	428953	AA306610	Hs.194676	DKFZP434C013 protein	2.6
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.6
	417863	AB000450	Hs.62771	vaccinia related kinase 2	2.6
	414987	AA524334	Hs.165544	ESTs	2.6
	440249	AI046590	Hs.125325	ESTs	2.6
65	407966	AA295052	Hs.38616	ESTs	2.6
	406885	M18728		gb Human nonspecific crossreacting antiq	2.5
	403204				2.5
	436961	AW375974	Hs.156704	ESTs	2.5
70	422260	AA315953	Hs.105454	ESTs, Weakly similar to LITE_HUMAN LITHO	2.5
	444471	AB026884	Hs.112121	KIAA3977 protein	2.5
	430290	AI734110	Hs.136355	ESTs	2.5
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	2.5
	421928	AF013758	Hs.109543	polyadenylate binding protein-interactin	2.5
	439580	AF086401	Hs.253847	ESTs	2.5
75	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.5
	457065	AA176318	Hs.192480	ESTs	2.5
	439521	AI808955	Hs.58248	ESTs	2.5
	420711	AA383471	Hs.180669	coronovirus gene amplified in osteosarcoma	2.5
80	422631	BE118919	Hs.118793	hypothetical protein FLJ10086	2.5
	417866	AW057903	Hs.82772	odlagin, type XI, alpha 1	2.5
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lym	2.5
	415947	U04045	Hs.78934	mMuS (E. coli) homolog 2 (colon cancer,	2.5
	454678	AW813089		gb:RC3-ST0186-249400-111-b05 ST0186 Homo	2.5

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5	424080	AW189983	Hs.139119	Homo sapiens cDNA FLJ10967 fs, clone PL	2.5
	425572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.5
	440594	AW445167	Hs.126036	ESTs	2.5
	428764	AA424839	Hs.38484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	408750	BE240469	Hs.35381	hypothetical protein FLJ10512	2.5
10	451177	A360016	Hs.13034	ESTs	2.5
	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog gbr34007.x1 NC1_CGAP_Ov23 Homo sapiens	2.5
	434414	A1798376			2.5
	400240				2.5
	410519	AW612264	Hs.131705	ESTs	2.5
15	440953	A1683036	Hs.124135	KIAA1618 protein	2.5
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.5
	444476	W07316	Hs.240	M-phase phosphoprotein 1	2.5
	442285	A1827488	Hs.224398	Homo sapiens cDNA FLJ11469 fs, clone HE	2.5
	420894	AA744597	Hs.88854	ESTs	2.5
20	410054	BE147897	Hs.55593	general transcription factor IIF, polype	2.4
	413998	AW103907	Hs.243933	ESTs	2.4
	412281	A1810054	Hs.14119	ESTs	2.4
	418105	AW933486	Hs.17000	ESTs	2.4
	447335	BE617695	Hs.286192	protein phosphatase 1, regulatory (inhib	2.4
25	466852	AW451643	Hs.257479	ESTs, Weakly similar to AF147747.1 BOC25	2.4
	408915	NM_016651	Hs.48950	hepatocellular carcinoma novel gene-3 pro	2.4
	442991	BE261236	Hs.6885	hypothetical protein FLJ29424	2.4
	410193	A1132592	Hs.59757	zinc finger protein 281	2.4
	410664	NM_006033	Hs.65370	spase, endothelial	2.4
30	445264	A1637648	Hs.196105	ESTs	2.4
	423453	AW450737	Hs.120791	CS1-09 protein	2.4
	433757	A1949074	Hs.152670	ESTs	2.4
	411598	BE336654	Hs.70937	H3 histone family, member K	2.4
	431657	A1345227	Hs.105448	ESTs, Weakly similar to B34067 hypothetical	2.4
35	429663	M62074	Hs.211587	phospholipase A2, group IVA (cytosolic, leukemia inhibitory factor (cholinergic	2.4
	426242	H55708	Hs.5220	ring finger protein	2.4
	419559	Y07628	Hs.51096	phospholipase A2, group VII (platelet-ac	2.4
	419839	U24577	Hs.93304	nucleoside diphosphate linked moi	2.4
	419713	AW968058	Hs.92381	ESTs	2.4
40	413281	AA661271	Hs.34396	ESTs	2.4
	402819				2.4
	431457	NM_012211	Hs.256297	imagin, alpha 11	2.4
	422654	A148006	Hs.222120	ESTs	2.4
	434523	BE241717	Hs.9676	uncharacterized hypothetical protein HT0	2.4
45	407242	M18726		gh-human nonspecific crossreacting antiq	2.4
	408235	AA168827	Hs.7868	ESTs, Weakly similar to endo-alpha-D-man	2.4
	408938	AA059013	Hs.22607	ESTs	2.4
	422158	I10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.4
	422217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.4
50	408321	AW405882	Hs.44205	coristatin	2.4
	419086	NM_000216	Hs.85991	Kallmann syndrome 1 sequence	2.4
	425945	AW978167	Hs.31086	Homo sapiens mRNA for cytochrome b5, par	2.4
	425234	AW084176	Hs.223296	ESTs	2.4
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.4
55	403059	A1916284	Hs.195671	ESTs	2.4
	450737	AW007152	Hs.203330	ESTs	2.4
	428513	BE220806	Hs.104697	Homo sapiens clone 23785 mRNA sequence	2.4
	405454				2.4
	422168	AA566894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.3
60	421462	AF016495	Hs.104624	aquaporin 9	2.3
	423416	A1744626	Hs.301506	ESTs, Highly similar to KIAA0554 protein	2.3
	422038	BE567832	Hs.12146	hypothetical protein	2.3
	446968	Y09763	Hs.22785	gamma-aminobutylic acid (GABA) A recepto	2.3
	429145	A1694923	Hs.49031	ESTs	2.3
65	423198	M81933	Hs.1634	cell division cycle 25A	2.3
	442914	AW188551	Hs.99519	Homo sapiens cDNA FLJ14007 fs, clone Y7	2.3
	449042	AW294985	Hs.301148	potassium voltage-gated channel, lks-rel	2.3
	421308	AA687322	Hs.192843	ESTs	2.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.3
70	429992	AL050533	Hs.227397	Homo sapiens mRNA, cDNA DKFZp566E103 (f	2.3
	440501	NE2409	Hs.126688	ESTs	2.3
	446232	A1281848	Hs.165547	ESTs	2.3
	410174	AA306007	Hs.59461	DKFZP434C245 protein	2.3
	452110	T47657	Hs.28005	Homo sapiens mRNA, cDNA DKFZp564G2453 (f	2.3
75	422493	AW414183	Hs.233816	ESTs	2.3
	407047	X65985		gh.H.sapiens: SOD-2 gene for manganese su	2.3
	411096	U80034	Hs.65583	mitochondrial intermediate peptidase	2.3
	426457	AW894667	Hs.169965	chimerin (chimerin) 1	2.3
	442029	AW656888	Hs.14458	neurite precursor cell expressed, develop	2.3
80	446545	AA431796	Hs.164192	ESTs, Weakly similar to Y161_HUMAN HYPOT	2.3
	427094	AF129535	Hs.272027	F-box only protein 5	2.3
	421933	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	2.3
	430001	AF500056	Hs.36992	ESTs	2.3
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.3
	402053			v-myb avian myeloblastosis viral oncogen	2.3
	415666	H72693	gh.yb03c11.1 Soares fetal liver spleen	2.3	
	432743	A1146966	Hs.101656	ESTs	2.3

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	433409	A1278902	Hs.25661	ESTs	2.3
	408330	AW182602	Hs.249954	ESTs	2.3
	407807	AL031427	Hs.40054	Human DNA sequence from clone 157A19 on	2.3
5	436972	AA284679	Hs.25640	claudin 3	2.3
	436747	AK0977192	Hs.291343	ESTs	2.3
	433730	AK022135	Hs.3542	hypothetical protein FLJ111273	2.3
	414839	X53692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	2.3
	438192	A859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.3
10	415338	NM_015156	Hs.78398	KIAA0771 protein	2.3
	405339	W80630	Hs.58445	ESTs	2.2
	412651	AA115333	Hs.107968	ESTs	2.2
	450556	AW193531	Hs.205647	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	430335	D80007	Hs.239499	KIAA185 protein	2.2
15	417849	AK251587	Hs.52733	ribogen 2	2.2
	454945	AW045375		gh:CMV-C10179-050200-090-09 C10179 Homo	2.2
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	2.2
	408349	BE546947	Hs.44276	homeo box C10	2.2
	424704	AJ263293	Hs.152096	cytochrome P450, subfamily III (parachloro	2.2
20	419432	AA814807	Hs.7305	hypothetical protein FLJ21932	2.2
	409532	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	2.2
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (F540, chr	2.2
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.2
	403137				2.2
25	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	2.2
	403200	BE613337	Hs.234996	germinin	2.2
	437345	AF075320	Hs.29980	Homo sapiens clone HQ0270	2.2
	425390	AJ026254	Hs.155114	protein tyrosine phosphatase, non-recept	2.2
	400380	AF123050	Hs.44532	dibucetin	2.2
30	422424	AI186431	Hs.116577	prostate differentiation factor	2.2
	431548	A1834273	Hs.9711	Homo sapiens cDNA FLJ13018 fs, clone NT	2.2
	400299	AA302279	Hs.61635	six transmembrane epithelial antigen of	2.2
	428771	AB028992	Hs.193143	KIAA1059 protein	2.2
	411571	AA122393	Hs.70811	hypothetical protein FLJ220516	2.2
	425737	H83395	Hs.7567	Homo sapiens cDNA: FLJ21962 fs, clone H	2.2
35	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	2.2
	412530	AA160584	Hs.265273	Homo sapiens cDNA FLJ13345 fs, clone OV	2.2
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.2
	408432	AW195262		gh:sm67005.x1 NC1_CGAP_CML1 Homo sapiens	2.2
40	404283	AF132892	Hs.190489	ESTs	2.2
	429568	AC088991	Hs.208141	Homo sapiens mRNA: cDNA DKFZp564D0472 ff	2.2
	424033	BE274117	Hs.137505	Homo sapiens BAC clone RP11-120J2 from 7	2.2
	425300	AW601773	Hs.270259	ESTs	2.2
	448568	AA149121	Hs.71947	ESTs	2.2
	419229	AB27237	Hs.283884	ESTs	2.2
45	420982	AW578160	Hs.100725	KIAA0592 protein	2.2
	403258				2.2
	439553	AW021103	Hs.6531	hypothetical protein FLJ20373	2.2
	426827	AW067805	Hs.172655	methyltetrahydrofolate dehydrogenase	2.2
50	444514	AB529205	Hs.270431	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	426298	AW968508	Hs.111583	ESTs	2.2
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	2.2
	421652	NM_014141	Hs.106552	cell recognition molecule Casp2	2.2
	412805	AA874491	Hs.21734	ESTs	2.2
55	438708	AA825716		gh:cm210.s1 NC1_CGAP_GGB1 Homo sapiens	2.2
	429058	AF138953	Hs.194827	hypothetical protein FLB6421	2.2
	423104	AJ005273	Hs.123547	antigenic determinant of reca protein (m	2.2
	410406	AP69703	Hs.301842	ESTs	2.2
	443100	RI5875	Hs.70945	ESTs	2.2
60	419235	AW470411	Hs.288433	neurotrophin	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.2
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.2
	415058	AW902848	Hs.273829	ESTs	2.2
	418049	AF211467	Hs.190468	hypothetical protein FLJ10120	2.2
65	436209	AW850417	Hs.254020	ESTs, Moderately similar to unannotated prot	2.2
	409042	AL049233	Hs.42244	Homo sapiens mRNA: cDNA DKFZp564A0023 (lr	2.2
	423682	D80041	Hs.153556	H-acetyltransferase 1 (paralamin N-acyl	2.2
	409565	NM_003731	Hs.52777	Fukuyama type congenital muscular dystro	2.2
	428157	AF738719	Hs.296668	ESTs	2.2
	410480	R97457	Hs.63984	cadherin 13, N-cadherin (hear)	2.2
70	429732	U20138	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	2.2
	414747	U30872	Hs.77204	centromere protein F (CENPO/NUD, mitosi	2.2
	425843	BE313280	Hs.150627	death associated protein 3	2.2
	445299	AB10382	Hs.118727	Homo sapiens cDNA FLJ13692 fs, clone PL	2.1
	436251	BE515065	Hs.5092	nuclear protein (PKED repeat)	2.1
75	430066	AB295059	Hs.237625	signal recognition particle 72ND	2.1
	422516	BE226862	Hs.117950	multifunctional polypeptide similar to S	2.1
	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	2.1
	416109	AA420311	Hs.126530	suppressor of K+ transport defect 1	2.1
80	427528	AU077413	Hs.179565	mitochondrion maintenance deficient (S	2.1
	448089	AW467945	Hs.173636	ESTs	2.1
	441790	AW254909	Hs.132208	ESTs	2.1
	400222			AFFX control: STAT1	2.1
	428728	NM_016625	Hs.191381	hypothetical protein	2.1

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	414366	BE549143	gb:501076456F1 NH_MGC_12 Homo sapiens c	2.1
	409929	R38772	Hs.172619 KIAA1106 protein	2.1
	405264			2.1
5	445625	BE246743	Hs.285529 Homo sapiens cDNA: FLJ22635 fs, clone H	2.1
	409949	AF189011	Hs.49153 initiator tRNAserine III	2.1
	424513	BE385864	Hs.145894 mitochondrial translational initiation I	2.1
	433683	AI817723	Hs.22678 hypothetical protein FLJ21832	2.1
	442952	AI743261	Hs.131860 ESTs	2.1
	441020	W52823	Hs.33562 ESTs	2.1
10	446770	AV60309	Hs.154986 ESTs, Weakly similar to AF137386 1 plasm	2.1
	432378	AI493046	Hs.146133 ESTs	2.1
	447769	AW873704	Hs.487654 ESTs	2.1
	417654	AF93480	Hs.29553 Homo sapiens cDNA FLJ11896 fs, clone HE	2.1
	445669	AE570830	Hs.174070 ESTs	2.1
15	417979	AL077284	Hs.83061 GTP cyclohydrolase I feedback regulatory	2.1
	433849	BE465884	Hs.280728 ESTs	2.1
	437928	NM_005476	Hs.5920 UDP-N-acetylglucosamine-2-epimerase/N-ac	2.1
	457341	BE181718	gb:CV14470639-150506-198-ctd H19369 Homo	2.1
	452833	BE559681	Hs.30736 KIAA0124 protein	2.1
20	403055			2.1
	414581	AA256213	Hs.72010 ESTs	2.1
	432840	AF001403	Hs.779521 hypothetical protein FLJ20538	2.1
	418994	AA256520	Hs.89548 selectin E (endothelial adhesion molecu	2.1
	440908	AI915225	Hs.126735 ESTs	2.1
25	417621	AV654694	Hs.82316 interferon-induced, hepatitis C-associated	2.1
	438985	AF037335	Hs.5338 carbonic anhydrase XII	2.1
	453716	BE070263	gb:CV4-BT0421-280100-299-ctd BT0407 Homo	2.1
	408420	NM_006915	Hs.299481 Homo sapiens mRNA; cDNA DKFZ568E0118 f	2.1
	435849	BE305242	Hs.112442 ESTs, Weakly similar to CLDE_HUMAN CLAU	2.1
30	424308	AW975531	Hs.154443 minichromosome maintenance deficient (S	2.1
	433844	AW342028	Hs.256112 ESTs	2.1
	400020			2.1
	434054	AL048045	Hs.180758 AFFX control: STAT1	2.1
	410560	AI061118	Hs.65328 hypothetical protein PRO0082	2.1
35	404076			2.1
	441382	BE514410	Hs.23044 Fanconi anemia, complementation group F	2.1
	422515	AV502470	Hs.117950 RAD51 (S. cerevisiae) homolog (E coli Re	2.1
	444863	AW384082	Hs.301323 multifunctional polypeptide similar to S	2.1
40	445867	AF272563	Hs.13405 ESTs	2.1
	441021	AV515716	Hs.7644 gephyrin	2.1
	446595	TS7448	Hs.15467 H1 histone family, member 2	2.1
	417515	L24203	Hs.82237 hypothetical protein FLJ20725	2.1
	412429	AV550282	Hs.75765 ataxia-telangiectasia group D-associated	2.1
	446927	AL044222	Hs.23255 GRO2 oncogene	2.1
45	412095	AE24707	Hs.5921 nucleosporin 155d	2.1
	400861			2.1
	448826	AI580252	Hs.293246 Homo sapiens cDNA: FLJ21592 fs, clone C	2.1
	440591	AA431599	Hs.132799 ESTs, Weakly similar to putative p150 (H	2.1
50	425181	AA371422	Hs.69644 Homo sapiens cDNA: FLJ23451 fs, clone H	2.1
	452880	AA028332	Hs.87549 ESTs, Weakly similar to dJ151N21.1 (H) se	2.1
	421878	AA299552	Hs.111496 ESTs	2.1
	442104	L20971	Hs.1188 Homo sapiens cDNA FLJ11643 fs, clone HE	2.1
	427224	AL135554	Hs.101637 phosphodiesterase 4B, cAMP-specific (fun	2.1
55	446921	AB012113	Hs.16530 sine oculis homolog (Drosophila) (homolo	2.1
	432487	AA550988	Hs.221472 small inducible cytokine subfamily A (Cy	2.1
	429534	AW976987	Hs.163327 ESTs	2.1
	446025	BE048061	Hs.153315 ESTs	2.1
	444700	AA431328	Hs.291179 ESTs, Weakly similar to topoisomerase I	2.1
60	422575	BE018517	Hs.119140 eukaryotic translation initiation fac	2.1
	415173	AW501735	Hs.253015 ESTs	2.1
	425170	AL007315	Hs.154970 transcription factor GP2	2.1
	453751	R03672	Hs.101262 Homo sapiens mRNA; cDNA DKFZp434B102 (fr	2.1
	426783	NM_003837	Hs.169139 kynureninase (L-tryptophan hydroxylase)	2.1
65	417874	BE616160	Hs.82829 protein tyrosine phosphatase, non-recept	2.1
	449555	AW450288	Hs.195390 ESTs	2.1
	439689	AF086334	Hs.187561 ESTs, Moderately similar to ALU1_HUMAN A	2.1
	427413	BE547647	Hs.177781 superoxide dismutase 2, mitochondrial	2.1
	424673	AA345051	Hs.294092 ESTs	2.1
70	407802	D84145	Hs.39913 novel RGD-containing protein	2.0
	423834	AI638627	Hs.106685 ESTs	2.0
	438895	AW007021	Hs.82894 ESTs	2.0
	446035	NM_006508	Hs.13565 Sam68-like phosphotyrosine protein, T-ST	2.0
	406981	S71129	Hs.206844 Acetylcholinesterase (A4 E5 domain) (huma	2.0
75	427001	NM_006482	Hs.173135 dual-specificity tyrosine-(Y)-phosphoryl	2.0
	439223	AW236799	Hs.225945 ESTs	2.0
	432343	NM_002960	Hs.2961 S100 calcium-binding protein A3	2.0
	414890	BE281095	Hs.77573 uridine phosphorylase	2.0
	423019	AI540185	Hs.225816 ESTs	2.0
	435905	AW987484	Hs.8003 KIAA0456 protein	2.0
80	422778	AF072873	Hs.114218 ficuzel (Drosophila) homolog 6	2.0
	439608	AW864696	Hs.26198 Homo sapiens cDNA: FLJ23363 fs, clone H	2.0
	432114	AL036021	Hs.225597 ESTs	2.0
	405545			2.0

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	418201	AA214345	Hs.58445	Homo sapiens cDNA FLJ21652 fls. clone C	2.0
	442528	AF150317	Hs.134217	ESTs	2.0
	446237	AW270515	Hs.149596	ESTs	2.0
5	428074	BE187770	Hs.182278	colony stimulating factor 2 receptor, al	2.0
	423430	AF112461	Hs.128501	R0534, S. cerevisiae, homolog of, B	2.0
	435767	H71505	Hs.117874	ESTs	2.0
	432945	AL043683	Hs.271357	ESTs. Weakly similar to unpaired protein	2.0
	428792	BE359555	Hs.193602	chromosome condensation protein G	2.0
	404170				2.0
10	410286	AJ739159	Hs.61898	DkF2P586N2124 protein	2.0
	434565	TS2172	Hs.1547	gp.v22001.1.1 Stratiagene fetal spleen (9	2.0
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	2.0
	417933	X02008	Hs.25962	thymidylate synthetase	2.0
15	441354	AJA47849	Hs.268640	protease, serine, 23	2.0
	437403	AG208149	Hs.121196	ESTs	2.0
	412673	AL042957	Hs.31845	ESTs	2.0
	414020	NM_002994	Hs.75703	small inducible cytokine A4 (homologous	2.0
	438426	AA635936	Hs.269763	ESTs	2.0
20	413943	AW034416	Hs.144687	ESTs	2.0
	449001	AI619957	Hs.189854	ESTs	2.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	2.0
	433425	H16263	Hs.31416	ESTs	2.0
	433364	AJ075407	Hs.290983	ESTs	2.0
25	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	2.0
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comelin)	2.0
	428746	X03626	Hs.2057	uridine monophosphate synthetase (protal	2.0
	411943	BE520436	Hs.7962	ESTs. Weakly similar to positive E-clip	2.0
	414266	BE267834	gb.601124428F1 NIH_MGC_8 Homo sapiens cd	2.0	
30	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-glucosamine poly	2.0
	405034	AI570189	Hs.25132	KIAA0470 gene product	2.0
	446715	AJ377335	Hs.173919	ESTs	2.0
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TABLE 42B:

Play:

CAT number:

Accession:

Unique Eos probest identifier number

Gene cluster number

Genbank accession numbers

Play

CAT number

Accession

408432

1058687_1

114179

1247077_1

AW195262

278688

AW811262

AW648047

AW648202

AW848631

AW848142

AW848702

AW848121

AW848632

AW848140

AW848571

AW348009

AW348067

AW848059

AW848605

AW648214

AW851186

AW996967

BE143456

BE267834

BE514180

BE185406

BE185406

BE277344

BE520436

BE185406

BE185406

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5	402053	8083229	Plus	62703-63179
	402819	6729581	Plus	29217-29422
	403055	8748904	Minus	109532-110225
	403137	9211454	Minus	92349-92572,92598-93084,93579-93712,93919-94072,94591-94748,95214-95337
	403204	7627392	Plus	16214-16439
10	403258	7770439	Minus	156251-156619
	403776	7770611	Minus	1414-1513,1624-1756
	404075	9931752	Minus	3849-3967
	404170	9930783	Plus	168036-169248
	405264	7329374	Plus	28556-28684
15	406454	7556675	Plus	133807-134053
	405345	1054740	Plus	118677-118807,119091-119296,121626-121823
	405695	4309958	Plus	51860-52162
	405434	5256551	Minus	17803-17931

TABLE 43A: ABOUT 339 GENES UP-REGULATED IN STOMACH CANCER

Table 43A lists about 339 genes up-regulated in stomach cancer compared to normal stomach that are likely to be extracellular or cell-surface proteins. Those were selected as Table 43A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g., p, h3, egl, 7in domains). Predicted protein domains are noted.

Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
Unique Esq probset identifier number, Genbank accession number					
Exemplar Accession number, Genbank accession number					
Unigene gene title					
Protein Structural Domain					
Ratio of tumor to normal tissue					
25	Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain
	426368	8E440042	Hs.83326	hemopexin,Peptidase_M10_SS	60.4
	426664	AK001666	Hs.189055	zrC2H2, TM,SS	26.8
	422330	D30783	Hs.115263	EGF_TM,SS	22.0
	435670	AW050291	Hs.6823	TM	19.0
	451099	R52795	Hs.25954	h3, TM,SS	17.1
	403776			IL8, TM,SS	14.9
30	424605	NM_002497	Hs.153704	NIMA (never in budding uninhib	phosphatase, TM
	425922	AF053306	Hs.36708	blevin protein	TM
	427585	D31152	Hs.179729	collagen, type	Clq, Collagen, TM,SS
	418651	AA634543	Hs.79340	IGF-1 mRNA-bi	KH-domain, TM
40	414972	8E263782	Hs.77895	KO domain gene p	TM
	446619	AU076543	Hs.313	osteopontin	Osteopontin, TM,SS
	415138	C18356	Hs.78345	interleukin-8	Kunitz_BPTL-G-gamma, TM,SS
	423020	AA383092	Hs.1608	replication pro	TM
45	406908	BE296227	Hs.46915	serine/threonin	phosphatase, TM,SS
	418948	AB041035	Hs.53547	ADPH co-recept	FcRn, inducible, TM,SS
	411750	8E562208	Hs.71827	NADPH oxidase 1	SS
	429900	AL045633	Hs.44269	ESTs	AK_Xan_dh_C_FAD_binding_5, TM
	454380	X92125	Hs.25040	zinc finger pro	zrC2H2, TM,SS
50	417655	AA780791	Hs.14014	ESTs, weakly st	TM
	430403	AF033390	Hs.241382	tumor necrosis	TM,SS
	428330	L22524	Hs.2256	matrix metallo	Peptidase_M10_SS
	452291	AF015592	Hs.28853	CDK7 (cyclin de	kinase, TM
	418205	L21715	Hs.83760	protein, 1, 2	TM
55	420757	NM_001898	Hs.123114	cystatin, SS	SS
	444783	AK001468	Hs.62180	anilin (disoca	PH, TM
	416209	AA236776	Hs.79078	MAO2 (Mocap	HORMA, SS
	411958	X63629	Hs.2877	cadherin 3, 5	cadherin, Cadherin_C_term, TM,SS
	404345	AK001180	Hs.145479	Homo sapiens c	TM,SS
	428927	AA321549	Hs.2248	small, inducib	IL8, TM,SS
60	424960	BE245380	Hs.153552	S' nucleotidase	S' nucleotidase, TM,SS
	402098				Myosin_tail, SS
	411274	NM_002776	Hs.69423	kallikrein 10	tyrosinase, TM
	415752	8E314524	Hs.78776	pulvative trans	TM
	431806	AF186114	Hs.270737	tumor necrosis	TM,SS
65	402005				SS
	422338	NM_001809	Hs.1594	centromere pro	histone, TM
	426687	N31126	Hs.272620	pregnancy spec	hemopoetin, TM
	423871	AA331906		TM	TM
70	431211	M86849	Hs.5566	gap junction pr	connexin, TM
	446238	AL130063	Hs.15783	Homo sapiens m	TM
	400741	AA058357	Hs.74465	carcinoembryon	h3, TM,SS
	411560	AW851186	Hs.150587	gbl3_C10220-1	TM
	433159	AB035898	Hs.150587	kinesin-like pr	kinesin Myosin_tail, TM,SS
	422285	AB031033	Hs.150587	gh-141	TM
75	451807	WS2854	Hs.70799	DMF-255A4083 p	TM
	411558	AA102670	Hs.70725	gamma-aminobu	neur_chan, TM,SS
	415701	NM_003878	Hs.78519	gamma-glutamyl	TM,SS
	409420	Z15008	Hs.54451	gamma-aminobu	TM
	425209	NM_015368	Hs.30985	pancreatin 1	pancreatin_1, SS
80	407788	HE141492	Hs.38991	S100-calculin bi	TM
	421155	H97879	Hs.102267	lysyl oxidase	Lysyl_oxidase, SS
	420552	AK000492	Hs.98806	hypothetical pr	SS
	402072	H15701	Hs.99886	complement pro	sushi,

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	422965	AJ011812	Hs.119018	transcription f	R3H,G-pitch,GTP_CDC,TM,SS	3.7
	447425	A963747	Hs.18573	acylphosphatase	Acylphosphatase,TM	3.7
	460076	AL390179	Hs.137011	Homo sapiens mR	TM	3.6
	406434				heme,1TM	3.6
	417565	AA210704	Hs.194855	ESTs	auth,,SS	3.6
	411012	AW248508	Hs.197277	Homo sapiens cD	TM,SS	3.6
	426471	M22440	Hs.170009	transforming gr	EGF,TM,SS	3.5
	425782	U66468	Hs.159525	cell growth reg	SS	3.5
	428587	AA393656	Hs.97459	ESTs, weakly si	SS	3.5
	448105	AW691433	Hs.170075	ESTs, weakly si	hypoxia,TM	3.5
	414598	NM_002543	Hs.77729	oxidized low de	TM	3.5
	442942	AW167087	Hs.131562	ESTs	kinase,TM,SS	3.4
	416391	A878927	Hs.79284	mesoderm specifi	abhyfolase,TM,SS	3.4
	424230	AL334344	Hs.296620	Homo sapiens cD	Fort, heat,TM	3.4
	438243	Y00787	Hs.624	interleukin 8	IL8,TM,SS	3.4
	412978	A431708	Hs.820	homeo box C6	homeobox,TM	3.4
	412851	A1826502	Hs.106149	ESTs	TM,SS	3.4
	414812	X72755	Hs.77267	monokine inducib	IL6,SS	3.4
	453984	AA355925	Hs.26222	KIAA0198 gene p	TM	3.4
	425921	NM_007231	Hs.162211	solute carrier	SNF,TM	3.4
	421787	AA227068	Hs.108301	nuclear recepto	TM	3.3
	447342	A191268	Hs.19322	ESTs	TM,SS	3.3
	453626	BE245286	Hs.301638	ESTs, Moderate	AAA,TM	3.3
	414521	ME3835	Hs.77424	Fr fragment of	lg,TM,SS	3.3
	448756	A739241	Hs.171480	ESTs	TM	3.3
	421948	L42583	Hs.111758	keratin 6A	filament,TM	3.3
	435833	AA632203	Hs.291365	ESTs	TM	3.3
	435391	AJ227892	Hs.146274	ESTs	SS	3.3
	418007	MT3509	Hs.83169	matrix metallo	hemopexin,Peptidase_M10,,SS	3.2
	411678	A1907114	Hs.71465	squalene epoxid	Monooxygenase,TM	3.2
	422656	BE545072	Hs.122579	hypothetical pr	TM	3.2
	450400	A854722	Hs.279744	ESTs	TM	3.2
	440659	AF134160	Hs.7327	claudin 1	PMP22,Claudin,TM,SS	3.2
	418203	XS4942	Hs.83758	CDC28 protein k	CKS,TM	3.1
	416111	AA033813	Hs.79018	chromatin assem	TM,SS	3.1
	445908	AF553234	Hs.298063	ESTs	sushi,TM,SS	3.1
	421340	F07783	Hs.1368	decay accelerat	sushi,,SS	3.1
	422689	AF086665		gb:RC3-C10297-2	SNF2_N,TM	3.1
	438451	AF096270	Hs.278554	heterochromatin	chromo.Chromo,,shadow,,SS	3.1
	424456	AW085884		gb:3-C10220-1	hs3,TM,SS	3.0
	429125	AA44854	Hs.271004	ESTs	TM	3.0
	409361	NM_005982	Hs.54416	sine oculis hom	homeobox,,SS	3.0
	439453	BE264874	Hs.6556	thyroid hormone	AAA,TM	3.0
	414696	AF002020	Hs.76918	Niemann-Pick d	Patched,TM,SS	3.0
	422746	NM_004484	Hs.115951	glypican 5	Glypican,TM,SS	3.0
	453775	NM_002916	Hs.35120	replication fac	AAA,TM,SS	3.0
	428862	NM_000346	Hs.2316	SRY (sex-determ	HMG_box,TM	2.9
	401747				filament,TM	2.9
	422682	NM_005306	Hs.211602	SMC1 (structura	SMC,,C_SMC,,N,TM	2.9
	413386	MC3445	Hs.840	indoleamine-pyr	IDO,,TM	2.9
	442961	BE514474	Hs.289074	Homo sapiens cD	TM	2.9
	421650	AA781795	Hs.122587	ESTs	TM	2.9
	434398	AA121098	Hs.3838	serum-inducible	kinase,POLO_box,TM	2.9
	435706	W01254	Hs.7945	GLOD4 protein	POCase,TM	2.9
	416065	BE267931	Hs.78996	proliferating c	TM	2.9
	423453	A1815965	Hs.120883	ubiquitin-conju	UQ,,cont,,SS	2.8
	430242	U66669	Hs.239642	3-hydroxyisobut	TM	2.8
	411770	NM_012478	Hs.71692	heat shock prot	HSP70,TM	2.8
	400440	XS3957	Hs.83870	nebulin	TM	2.8
	444743	AA045648	Hs.11817	nuclei (nucleos	mult,TM	2.8
	417771	AA804698	Hs.82547	retinoic acid r	TM,SS	2.8
	430287	AW182459	Hs.125759	ESTs, weakly si	TM	2.8
	405462	NM_000676	Hs.45743	adenosine A2-7	7m,,1TM,SS	2.8
	425188	AK002052	Hs.155071	hypothetical pr	TM	2.8
	456999	AA319798	Hs.172247	eukaryotic tran	SS	2.8
	408875	NM_015434	Hs.48804	DICP2-4348168 pr	TM	2.8
	409012	AL117435	Hs.49725	DICP2-434816 pr	RINGEF,TM	2.7
	410762	AF226053	Hs.66170	HSKM-B protein	zfMYND,,SS	2.7
	426925	NM_001196	Hs.172894	Bh3 interacting	TM	2.7
	410116	AW030671	Hs.58636	squamous cell c	TM,SS	2.7
	426398	A245368	Hs.38558	ESTs	SS	2.7
	412140	AA219691	Hs.73625	RAB6 interactin	kinasin,TM,SS	2.7
	456655	A378735	Hs.111779	secreted protei	kazal,,SS	2.7
	408670	AF160967	Hs.46784	potassium large	TM,SS	2.7
	422576	BE548555	Hs.118554	Cdx-83 protein	basalase_B,,SS	2.7
	431379	AA54264	Hs.182637	pepdylopyl	TM	2.7
	433183	AF231338	Hs.222024	transcription f	HLH,PAS,TM,SS	2.7
	423228	A572739	Hs.195471	6-phosphofructo	PGAMRP2K,TM	2.7
	407633	NM_007069	Hs.37189	similar to rat	TM,SS	2.6
	419216	AJ075718	Hs.164021	small inducible	IL8,TM,SS	2.6
	422363	TS5979	Hs.115474	replication fac	TM	2.6
	401644				zf-C2B2,TM	2.6
	417479	AW07052	Hs.133554	ESTs	CARD,TM	2.6

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426514	BE615633	Hs.301122	bone morphogene	TGF-beta,TGFb_propeptide,TM,SS	2.6
400289	X07830	Hs.2758	matrix metallo	hemopexin_SS	2.6
418478	U38945	Hs.1174	cyclin-dependen	ank,TM,SS	2.6
421246	AW982662	Hs.300561	ESTs, Highly si	PolyA_pos,TM	2.6
420045	AA705745	Hs.155070	Hs.155070	AMP-binding,TM	2.6
420592	BE245374	Hs.27942	hypothetical pr	Acyltransferase,TM,SS	2.6
400562	AJ633744	Hs.195648	ESTs	PAC,TM,SS	2.6
458061	NM_007115	Hs.29352	tumor necrosis	XenCUB,TM,SS	2.6
451813	NM_016117	Hs.27182	phospholipase A	WDC4_SS	2.6
410880	XY1662	Hs.66744	nest (Drosoph)	HLH,TM	2.6
422063	BE156476	Hs.27942	gb.QV04-HTC950-0	SS	2.6
418250	U29926	Hs.83918	adonisein monop	A_desaminase,TM	2.6
417401	AA611452	Hs.291511	ESTs	TM	2.6
422571	W01518	Hs.34955	ESTs	TM	2.6
411984	NM_005419	Hs.77988	signal transduc	SH2,STAT_SS	2.6
426427	M86599	Hs.169840	TTK protein kin	kinase,TM	2.6
425840	AA774824	Hs.13377	Homo sapiens cf	TM	2.6
420222	AA252523	Hs.120817	ESTs	SS	2.6
451418	BE387790	Hs.26369	hypothetical pr	TM	2.6
428953	AA306610	Hs.194675	DKFZP434C013 pr	ar,TNFR_cf,DEAD,Stathmin,TM,SS	2.6
429008	RC2740	Hs.137555	pulvative chemok	7tm_1,TM	2.6
417863	AE000459	Hs.82771	vacuina relate	kinase,TM,SS	2.6
430961	AW375974	Hs.155704	ESTs	TM	2.5
413670	AB000115	Hs.75470	hypothetical pr	TM	2.5
421528	AF013758	Hs.105943	polyadenylate b	SS	2.5
433963	AA247529	Hs.6793	platelet-activa	PAF-AW43HBW_bgg,kinase,TM	2.5
427111	AA383471	Hs.183659	conserved gene	TM	2.5
422631	BE218919	Hs.118793	hypothetical pr	TM	2.5
417866	AW057903	Hs.82772	collagen_type	TSPN,Collagen,COLFL_SS	2.5
416975	NM_004131	Hs.1051	granzyme B (gra	tyrosin_SS	2.5
415947	UO-045	Hs.78594	musE (E coli)	MXS_C,MLM_SS,TM	2.5
456478	AW813089	Hs.27942	gb.RC3-ST0186-2	TPR,Ribosomal_SS,TM,SS	2.5
426572	AB037783	Hs.170623	hypothetical pr	PH,FYVE,TM	2.5
428254	AA424839	Hs.96484	ESTs, Weakly si	TM	2.5
444478	W07316	Hs.240	M-phase cyclin	Kiegin_SS	2.5
442295	AB27248	Hs.224388	Homo sapiens cD	Collagen,COLFL,wvc,TM,SS	2.5
410094	BE147897	Hs.58593	general transpo	TFIIF_beta,TM	2.4
413998	AW103807	Hs.243633	ESTs	TPR,TM,SS	2.4
412281	AB100584	Hs.14119	ESTs	Ribosomal_S7a,TM	2.4
446852	AW451543	Hs.257479	ESTs, Weakly si	TM	2.4
428915	NM_019551	Hs.48950	hepatocellular c	TM,SS	2.4
429991	BE281238	Hs.8886	hypothetical pr	TM	2.4
410193	AJ132592	Hs.59575	zinc finger pro	zfC2H2,TM	2.4
410684	NM_026053	Hs.55370	lipase, endothe	Ribosomal_L22,ipase,PLAT,TM,SS	2.4
423453	AW405737	Hs.128701	CGI-05 protein	Gnase,COP-ON_P_trans,TM	2.4
411598	BE336654	Hs.70937	H3 histone limi	histone_SS	2.4
429663	M08874	Hs.211597	phospholipase A	C2,PLA2_B,TM	2.4
428642	H57109	Hs.2200	leukemia inhibi	UF_OSM,TM	2.4
419559	Y07838	Hs.91096	ring finger pr	zfC2HC4_zfp8_box,TM	2.4
419839	U24577	Hs.93304	phospholipase A	SS	2.4
402819				IBR,TM	2.4
431457	NM_012211	Hs.256297	integrin, alpha	FG-GAP,wva,TM,SS	2.4
443883	BE241717	Hs.9575	uncharacterized	DUF157,TM	2.4
422158	L10343	Hs.112341	protease inhibi	wap_SS	2.4
423217	NM_000094	Hs.1640	collagen_type	ln3,Collagen,Kunitz_BPTI,wva_SS	2.4
408321	AW405882	Hs.44205	corstatin	corstatin	2.4
419086	NM_002216	Hs.89591	Kallmann syndro	ln3,wap_SS	2.4
427722	AK000123	Hs.189479	hypothetical pr	PH_SS	2.4
405454				TM	2.4
422108	AA506894	Hs.112408	S100 calcium-bi	ctfand,TM	2.3
427462	AF016495	Hs.104624	equopom 9	MP,TM	2.3
403416	AF144626	Hs.301506	ESTs, highly si	SS	2.3
448988	Y09763	Hs.22785	gamma-aminobuty	neur_chan,TM,SS	2.3
423198	MB1933	Hs.1634	cell division c	Rhodanesa_SS	2.3
419926	AW900992	Hs.93796	DKFZP586D2223 p	SS	2.3
429992	AL050053	Hs.277987	Homo sapiens mR	ln3,TM,SS	2.3
446212	A0261848	Hs.155547	ESTs	7tm_3,TM	2.3
422493	AW474183	Hs.233816	ESTs	TM	2.3
407047	X65955	Hs.1634	gltR.sapiens SO	sodie,TM	2.3
411096	U00034	Hs.68933	mitochondrial i	Popilliaae_M3	2.3
026457	AW894667	Hs.169965	chemokine (chem)	CAG_Fc-and_PhoGAP,TM	2.3
446545	AI431798	Hs.164192	ESTs, Weakly si	TM	2.3
422094	AF129535	Hs.272027	F-box only prot	TM	2.3
421933	RR8881	Hs.106655	sex comb on mid	SAM,TM	2.3
430001	AI500266	Hs.98922	ESTs	TM	2.3
420802	U22276	Hs.1334	v-myb avian mye	TM	2.3
420553				gpdh_SS	2.3
432743	AI146966	Hs.101656	ESTs	SS	2.3
433499	A278802	Hs.26661	ESTs	PMPNP_PHD_bromodomain,TM	2.3
408330	AW162092	Hs.249984	ESTs	TM,SS	2.3
407807	AL031427	Hs.40094	Human DNA seque	T4_deoxynase,TM	2.3
436972	AA284679	Hs.25640	claudin 3	PMP22_Claudin,TM,SS	2.3
433730	AK002135	Hs.3542	hypothetical pr	TM,SS	2.3

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414839	X63692	Hs.77462	DNA (cytosine-5	zf-CXXC,BAH,TM,SS	2,3
438192	A859065	Hs.16808	ESTs, Weakly si	TM,SS	2,3
415339	NM_015156	Hs.78398	KIAA0071 protein	ELM2, TM	2,3
449539	M60351	Hs.58446	ESTs	kinase, Favin like, Recop, L_domain, TM,SS	2,2
420956	AW193331	Hs.20564	ESTs, Moderate	plasma, TM,SS	2,2
430335	D80007	Hs.239499	KIAA0185 protein	S1, TM	2,2
417849	AWG91587	Hs.82733	nidogen 2	EGF_ML_recept, b, hyroglobulin, 1, TM,SS	2,2
412326	R07566	Hs.73817	small inducible	IL8, SS	2,2
426349	BC545847	Hs.44276	homo box C10	homodimer, TM	2,2
424704	A0263293	Hs.152096	cytochrome P450	p450, SS	2,2
409632	W74001	Hs.55279	serine (or cyst	serpin, TM	2,2
415323	BC269352	Hs.949	neutrophil cyto	SH3, TPR, TM	2,2
417531	NM_003157	Hs.1087	serum/threonin	kinase, TM	2,2
403137				mm, TM,SS	2,2
428479	Y00272	Hs.184572	cell division c	kinase, TM,SS	2,2
430200	BE613337	Hs.234896	germinin	TM,SS	2,2
425190	A0026294	Hs.156114	protein tyrosin	g_Opioid, neurop, TM,SS	2,2
402360	AF123050	Hs.44332	disubiquitin	ubiquitin, TM, 3, ANF_receptor, sushi, 7, tm, 1, TM	2,2
424242	A1186431	Hs.116577	prostate differ	TGF_beta, SS	2,2
400298	AA032279	Hs.61635	six transmembra	TM	2,2
411571	AA122983	Hs.70811	hypothetical pr	SS	2,2
412802	U41518	Hs.74602	aquaporin 1 (ch	MAP, TM	2,2
414761	AU077228	Hs.77256	enhancer of cas	SET, TM	2,2
408432	AW155262		gban57b05.5.1 N	TM,SS	2,2
429558	A088691	Hs.209414	Homo sapiens mR	mito_carr, TM	2,2
425300	AK601773	Hs.210259	ESTs	TM	2,2
439653	AW021103	Hs.5931	hypothetical pr	TM,SS	2,2
426827	AW067805	Hs.172955	methyltransfera	THF_DHG_CYH_FTHFS, TM	2,2
444514	A1682905	Hs.270431	ESTs, Weakly si	cnMP_binding, TM,SS	2,2
425322	U53630	Hs.155537	protein kinase,	MCM, TM	2,2
421652	NM_014141	Hs.105552	cell recogniti	aminin, G, TM,SS	2,2
438788	AA825716		gluc29a10.5.1 N	ant, death, RHD, TM	2,2
429058	AF138863	Hs.194827	hypothetical pr	TM	2,2
423104	AJ005273	Hs.123547	antigenic deter	TM	2,2
419406	A169703	Hs.301842	ESTs	FGGY, TM	2,2
421379	Y15221	Hs.103982	small inducible	IL8, TM,SS	2,2
422805	AK001379	Hs.121028	hypothetical pr	IQ, TM	2,2
418049	AA211467	Hs.190458	hypothetical pr	TM	2,2
436205	AW655417	Hs.254020	ESTs, Moderate	TM,SS	2,2
408042	AJ045223	Hs.42244	Homo sapiens mR	TM	2,2
425692	D50041	Hs.155956	N-acetyltransfe	Acetyltransf, TM	2,2
409655	NM_006731	Hs.55777	Fukuyama type c	SS	2,2
428157	AJ738719	Hs.258658	ESTs	hexokinase, TM	2,2
410480	R07457	Hs.63584	cadherin 13, H	cadherin, TM,SS	2,2
429732	U20158	Hs.2488	lymphocyte cyto	SH2, TM	2,2
414747	U30872	Hs.77204	centromere prot	SS	2,2
425843	BE313280	Hs.159527	death associate	TM	2,2
445298	AJ013062	Hs.118727	Homo sapiens cD	HLA, TM	2,1
435251	BE515065	Hs.5922	nucleolar prote	Nop, TM,SS	2,1
430066	A1929559	Hs.237825	signal recognit	TPR, SS	2,1
427528	AU077143	Hs.179555	minichromosome	MCM, TM,SS	2,1
448089	A1467945	Hs.173696	ESTs	TM,SS	2,1
428728	NM_016625	Hs.151381	hypothetical pr	TM	2,1
409529	R38772	Hs.172619	KIAA1105 protein	TM	2,1
405264				SS	2,1
445625	BE245743	Hs.285529	Homo sapiens cD	TM	2,1
408949	AF189211	Hs.49163	putative ribonu	Ribonuclease_3, TM,SS	2,1
424513	BE385864	Hs.149894	mitochondrial t	GTP_EFTU, IF2, TM	2,1
433583	A0181723	Hs.22678	hypothetical pr	SS	2,1
424952	AJ743261	Hs.131860	ESTs	TM	2,1
432378	A1693496	Hs.146133	ESTs	TM	2,1
417979	AU077284	Hs.83881	GTP-cytohydrol	TM,SS	2,1
433849	BE465884	Hs.280728	ESTs	SS	2,1
437928	NM_005476	Hs.5920	UDP-N-acetylglu	ROK, Epimerase, 2, TM	2,1
403055				flament, TM,SS	2,1
432840	AK001403	Hs.279521	hypothetical pr	TM	2,1
418994	AA296520	Hs.85546	selectin E (end	EGF, lectin, s_sushi, TM,SS	2,1
440908	A1915225	Hs.126735	ESTs	TM	2,1
417621	AV054694	Hs.82316	interferon-indu	TM	2,1
436855	AF031335	Hs.5338	carbonic anhydr	carb_anhydrase, TM,SS	2,1
408420	NM_006915	Hs.295481	Homo sapiens mR	kinase, TM,SS	2,1
434064	AL049405	Hs.180758	hypothetical pr	cadherin, TM,SS	2,1
404076				RenaAD, TM	2,1
422515	AW504070	Hs.117950	multifunctional	AIRC, SNAICAR, syn, TM	2,1
445867	AJ727263	Hs.13406	glypican	glypican, TM	2,1
441021	AW578716	Hs.7614	H1 histone fam	histone, histone, TM	2,1
446595	T57448	Hs.15467	hypothetical pr	TM,SS	2,1
417515	L24203	Hs.82267	ataxia-telangi	zf, b, box, SS	2,1
412429	AV050262	Hs.75165	GRO2 oncogene	IL8, TM,SS	2,1
445207	AL044222	Hs.23265	nucleopoin 155	TM,SS	2,1
412095	A1524707	Hs.5921	Homo sapiens cD	TM,SS	2,1
400861				kinase, TM	2,1
440591	AA431599	Hs.132799	Homo sapiens cD	TM	2,1

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442104	L20971	Hs	188	phosphodiesterase	PDEase, TM,	2.1
446521	AB012113	Hs	16530	small inducible	IL8, SS	2.1
446051	BE048061	Hs	153315	ESTs	Reprtyrsn_Pep_M128_propep, TMSS	2.1
42675	BE018517	Hs	119140	eukaryotic Irfn	off-Sa, TM	2.1
425170	AU077315	Hs	154570	transcription 1	TM	2.1
435751	R36762	Hs	101282	Homo sapiens mR	TM	2.1
426263	NM_003937	Hs	169139	lynnenase (L	TM	2.1
417874	BE616160	Hs	82829	protein tyrosin	Y_phosphatase, TM,	2.1
446555	AW450268	Hs	155390	ESTs	TM	2.1
436699	AF066534	Hs	187561	ESTs, Moderatel	TM	2.1
427413	BE547647	Hs	177781	superoxide dism	sodfe, TM,	2.1
407802	D84145	Hs	35913	novel RGD-conta	hexapep, TM, SS	2.0
440035	NM_006558	Hs	13565	Sam68-like phos	TM	2.0
400681	ST1129	Hs	256644	Acylcholinester	COesterase, TM, SS	2.0
432343	NM_002960	Hs	2961	S100 calcium-bi	S_100, ethanol, TM, SS	2.0
414590	BE281055	Hs	77573	uridine phospho	PNP_UDP_1, TM, SS	2.0
423019	AI540185	Hs	225616	ESTs	SS	2.0
422278	AF072873	Hs	114218	hizited (Droso	P_2, Fuzized, TM, SS	2.0
405645					ABC_tran, ABC_membrane, TM, SS	2.0
446237	AW270515	Hs	145596	ESTs	bZIP, TM,	2.0
428074	BE387770	Hs	182378	colony stimulat	SS	2.0
423430	AF112461	Hs	128501	PAD5A, S. cerev	SNF2_Nucleosce_C, TM,	2.0
435767	HT3086	Hs	117874	ESTs	Pepidase, SRP, TM,	2.0
432945	AI043683	Hs	271357	ESTs, Weakly si	PK, SS	2.0
404170					sodfe, TM,	2.0
422610	AF153820	Hs	1547	potassium inwar	IK, TM,	2.0
417533	X02308	Hs	82962	thymidylate syn	thymidylat_synth, SS	2.0
441384	AA447845	Hs	288660	protease, serin	TM	2.0
414020	NM_002984	Hs	75703	small inducible	IL8, SS	2.0
427674	NM_003026	Hs	2178	H2D histone lam	histone, TM, SS	2.0
435425	H16083	Hs	31416	EST	TM	2.0
427972	NM_005754	Hs	220689	Ras-GTPase-acti	mm, NTF2, SS	2.0
417356	BE18289	Hs	1075	small proline-r	Cornfin, TM,	2.0
426746	J03626	Hs	2057	uridine monopho	Phibosyltran, OMPdecase, TM,	2.0
432677	NM_004482	Hs	278611	UDP-N-acetyl-s	Glycos_transf_2, Rcin_B_lectin, TM	2.0

TABLE 43B:

Play:	Unique Eos probe(s) identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Play	CAT number	Accession
408432	1058667_1	AW195252 R27868 AW611262
411580	1249443_1	AW851186 AW996957 BE143456
422063	210852_1	BE156475 BE156473 BE156474 BE156475 AA302839
422285	214659_1	AI803103 AI851433 AI470793 AW450703 AI090784 AW271587 AW236950 AW242783
422689	215896_1	AW856665 AA315006 AW954733
422871	232749_1	AA331908 AA322484
428788	455159_1	AA825716 AW918653 AA828841
454456	1207088_1	AW650584 AW752836 M66124
454678	1228915_1	AW813089 W28102

TABLE 43C:

Play	Unique number corresponding to an Eos probe(s)
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al" refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:469-495.
Strand:	Indicates DNA strand from which exons were predicted.
NT_position:	Indicates nucleotide positions of predicted exons.

Play	Ref	Strand	NT_position
400861	9757506	Plus	163855-164016
401644	8576130	Plus	82655-83559
401747	9785672	Minus	118596-118816, 119119-119244, 119609-119761, 120422-120990, 130161-130381, 130408-130593, 131097-131258, 131866-131932, 132451-132575, 133680-134011
402053	8083229	Plus	62703-63179
402819	6728561	Plus	25217-29427
403055	8748954	Plus	106532-110225
403137	9211454	Minus	92349-92572, 92958-93084, 93579-93712, 93949-94072, 94561-94748, 95214-95337
403776	7770611	Minus	1414-1513, 1624-1756
404076	9531752	Minus	3848-3967
404170	9530793	Plus	168306-169248
405264	7329374	Plus	28556-28684
405454	7656675	Plus	133807-134053
405545	1064740	Plus	118677-118807, 119091-119296, 121626-121823
406434	9256551	Minus	17803-17931

TABLE 44A: ABOUT 314 GENES DOWN-REGULATED IN STOMACH CANCER

Table 44A lists about 314 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 42A, except that the numerator and denominator were switched.

Play:	Unique Eos probe(s) identifier number
Ex/Accession:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number

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Unigene Title: R1	Unigene gene title Ratio of tumor to normal tissue	Unigene Title	R1
5	Pleky 142859 NM_000705 145447 Z91711 427469 AA003084 407486 S69741 428602 AL137479 402751 BE387521 443547 AW271273 430130 AL137311 435473 NS3559 455826 BE144228	Unigene ID HS.813 HS.78454 HS.269347 HS.186955 HS.108980 HS.23767 HS.234074 HS.260881 HS.151017 HS.61255 HS.61255	Unigene Title ATPase, H+K+-exchanging, beta polypep myosin, trabecular meshwork inducible ESTs ghnSGG-3stomach cancer gene-3 (oncogen Homo sapiens mRNA; cDNA DKF2p544a0223 f chaperonin containing TCP1, subunit 7 (e Homo sapiens cDNA FLJ12696 fs, clone NT Homo sapiens mRNA; cDNA DKF2p751G02121 (E ESTs ghAFD-HT0165-140200-009-004 HT0165 Homo
10	402015 430664 AW969834 445151 AW204908 425201 XQ3178 344424 AB11202 450940 A1744943 400811 AF219139 424596 AB028939 403670 10234 NM_003837 407462 AJ252011	402015 430664 AW969834 445151 AW204908 425201 XQ3178 344424 AB11202 450940 A1744943 400811 AF219139 424596 AB028939 403670 10234 NM_003837 407462 AJ252011	ESTs gh.EST1381912 MAGE resequences, MAGK Homo ESTs group-specific component (vitamin D bind Homo sapiens cDNA: FLJ23523 fs, clone L ESTs, Moderately similar to ALU7_HUMAN A KIAA0154 protein; ADP-ribosylation facto estrogen-related receptor gamma fructose-1,6-bisphosphatase 2 ghHomo sapiens partial mRNA for amilor
15	405110 402760 408947 AL080093 413724 AA131469 431514 AW972363 451103 FC2804 452033 AW273741 440058 AB32662 405845	405110 402760 408947 AL080093 413724 AA131469 431514 AW972363 451103 FC2804 452033 AW273741 440058 AB32662 405845	ESTs ESTs microsomal triglyceride transfer protein ESTs lipase, gastric sulfotransferase family, cytosolic, 2A, cholecystokinin B receptor ESTs ESTs
20	429593 NM_000253 445627 AW518475 426679 XQ5997 417296 L36196 443537 D13305 436654 AW139612 406326	429593 NM_000253 445627 AW518475 426679 XQ5997 417296 L36196 443537 D13305 436654 AW139612 406326	Homo sapiens mRNA; cDNA DKF2p564N1662 f Homo sapiens cDNA FLJ12696 fs, clone NT gh.EST384454 MAGE resequences, MAGL Homo DKF2p564D205 protein ESTs ESTs ESTs
25	454120 AB032990 455841 AW993005 453889 MG3962 407261 LQ3172 451062 AL110125 428350 AT54634 411021 FQ0055 412121 AW242447 450572 AT700863 449322 AS921750 421362 AA530594 427432 NM_005136	454120 AB032990 455841 AW993005 453889 MG3962 407261 LQ3172 451062 AL110125 428350 AT54634 411021 FQ0055 412121 AW242447 450572 AT700863 449322 AS921750 421362 AA530594 427432 NM_005136	hypothetical protein KIAA1164 gc.RC2-BN0032-160200-013-004 BN0032 Homo ATPase, H+K+-exchanging, alpha polypep gh-Homo sapiens cell-type 1-cell immunog Homo sapiens mRNA; cDNA DKF2p564C1416 f ESTs itin ESTs, Weakly similar to lactase phlorizi Homo sapiens cDNA FLJ13245 fs, clone OV Homo sapiens cDNA FLJ13752 fs, clone PL ghrelin precursor potassium voltage-gated channel, Isk-rel phospholamban
30	418421 RS8670 424104 AA669515 422282 AA312650 417332 AW972717 432440 XE3597 448520 AB002367 401989	418421 RS8670 424104 AA669515 422282 AA312650 417332 AW972717 432440 XE3597 448520 AB002367 401989	ESTs gc.EST183335 Jurkat T-cells VI Homo sapi Homo sapiens cDNA: FLJ21511 fs, clone C sucrase-isomaltase doubtcorin and CaM kinase-like 1 ESTs ESTs
35	452528 412559 HS3789 434779 AF153815 406255	452528 412559 HS3789 434779 AF153815 406255	ESTs ESTs, Weakly similar to KIAA0638 protein potassium inwardly-rectifying channel, s ESTs
40	452528 412559 HS3789 434779 AF153815 406255	452528 412559 HS3789 434779 AF153815 406255	ESTs ESTs, Weakly similar to KIAA0638 protein potassium inwardly-rectifying channel, s ESTs
45	419393 AA1745282 428649 AL045716 410036 RS7171 414502 AL137321 432113 AA935065 413808 JQ2887 451406 AI694320 347445 AW974445 420444 AB055985 445200 AA084460 415314 NS8802	419393 AA1745282 428649 AL045716 410036 RS7171 414502 AL137321 432113 AA935065 413808 JQ2887 451406 AI694320 347445 AW974445 420444 AB055985 445200 AA084460 415314 NS8802	ESTs Homo sapiens cDNA FLJ11003 fs, clone PL caldesmon 2, cardiac muscle ESTs ESTs caldesmon 1 ESTs, Weakly similar to T17248 hypotheli ESTs, Weakly similar to HsEMAP (H sapien ESTs somatostatin glycoprotein M6B hypothetical protein FLJ10570
50	431152 AW970998 423206 Y18207 401775	431152 AW970998 423206 Y18207 401775	gc.EST383083 MAGE resequences, MAGK Homo protein phosphatase 1, regulatory (inhib ESTs ESTs ESTs
55	440559 AW67335 436089 AA804957 447071 AW239857 435504 AA525379	440559 AW67335 436089 AA804957 447071 AW239857 435504 AA525379	ESTs ESTs ESTs uncharacterized bone marrow protein BMD4
60			
65			
70			
75			
80			

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5	423968	AF098277	Hs.135529	solute carrier family 23 (nucleoside tra	0.32
	445487	A006287	Hs.201217	ESTs	0.32
	421296	NM_002666	Hs.103253	porlipin	0.32
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	0.33
	449816	T5625	Hs.290221	ESTs	0.33
10	446393	AW014174	Hs.151707	ESTs	0.33
	446632	A033565	Hs.159073	diacylglycerol kinase, eta	0.33
	428070	T53918	Hs.182313	retinol-binding protein 2, cellular	0.33
	421451	AA291377	Hs.50831	ESTs	0.33
	408117				0.33
15	454790	AW820852		gb:RC2-ST0301-120200-011-112 ST0301 Homo	0.33
	413679	BE156755		gb:RC1-HT0370-120100-012-c09 HT0370 Homo	0.34
	404121				0.34
	433564	M18079	Hs.782255	faty acid binding protein 2, intestinal	0.34
	413079	BE064382		gb:RC4-BT0310-110300-015-c12 BT0310 Homo	0.34
20	403059				0.35
	458987	AW750067	Hs.205386	ESTs	0.35
	429609	AF002246	Hs.210953	cell adhesion molecule with homology to	0.35
	423371	AJ076819	Hs.1650	solute carrier family 25, member 3	0.35
	424765	AA428711	Hs.284256	hypothetical protein FLJ14003 similar to	0.35
25	451818	A019018		gb:t5401.x1 NCL_GGAP_K48 Homo sapiens	0.35
	433380	T06430	Hs.6194	chondralin sulfate proteoglycan BGA4b	0.35
	405742				0.35
	403429				0.35
	443522	A1911527	Hs.11805	ESTs	0.36
30	404973				0.36
	444567	AV654020	Hs.184261	ESTs. Weakly similar to putative type II	0.36
	412228	AW603785	Hs.73792	complement component (3d/Epstein Barr vi	0.36
	407110	AA018042	Hs.95078	ESTs	0.36
	411671	BE049054	Hs.278567	ESTs	0.36
35	430800	NM_000805	Hs.2681	gelsin	0.36
	454560	AW607291		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	0.36
	444536	A1161068	Hs.14780	ESTs	0.36
	454042	H2570	Hs.172572	hypothetical protein FLJ20093	0.37
	444102	AA467953	Hs.282379	ESTs	0.37
40	421421	AA335593	Hs.115147	ESTs	0.37
	452093	AA447453	Hs.27950	Homo sapiens mRNA; cDNA DKFpZ585M0723 (f	0.37
	436277	R88520	Hs.120917	ESTs	0.37
	450350	BE246762	Hs.59459	arachidonate 5-lipoxygenase	0.37
	451027	AW615024	Hs.40806	ESTs	0.37
45	426784	U03746	Hs.172216	chromogranin A (parathyroid secretory pr	0.38
	410023	A0017169	Hs.57929	slit (Drosophila) homolog 3	0.38
	436802	N34486	Hs.170504	ESTs	0.38
	448142	AS21768	Hs.164596	ESTs	0.38
	442378	RS4033	Hs.21245	ESTs	0.38
50	444006	A0535681	Hs.25248	ESTs	0.38
	455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	0.38
	424903	T26477	Hs.22883	ESTs. Weakly similar to ALUS_HUMAN ALU S	0.38
	405714	AJ219304	Hs.283108	hemoglobin, gamma G	0.39
	434340	AJ193043	Hs.128685	ESTs	0.39
55	406036				0.39
	431078	U82627	Hs.249195	homeo box A13	0.39
	457863	AW371846	Hs.118119	ESTs	0.39
	451880	A021032	Hs.200387	ESTs	0.39
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.39
60	446414	W93246	Hs.59187	ESTs	0.39
	442317	AW15599	Hs.128225	ESTs	0.39
	447281	NM_006991	Hs.17917	lymphatic vessel endothelial hyaluronan	0.39
	439599	AW602166	Hs.222399	CEGP1 protein	0.39
	433485	AJ493076	Hs.78183	aldo-keto reductase family 1, member C1	0.40
65	432753	NM_014075	Hs.278915	PRC0693 protein	0.40
	420200	A271429	Hs.88142	ESTs	0.40
	421853	A050797	Hs.108972	Homo sapiens mRNA; cDNA DKFpZ34P228 (fr	0.40
	453950	AA156998	Hs.211568	eukaryotic translation initiation factor	0.40
	407408	AF054830		gb:Homo sapiens interferon-1 type I rec	0.40
70	410732	AW994328		gb:PM3-HN0010-050400-001-h12 HN0010 Homo	0.40
	456272	AJ797360	Hs.264899	ESTs. Weakly similar to ALUS_HUMAN ALU S	0.40
	401514	AF147186		gb:AF147186 Homo sapiens library (Schere	0.40
	436363	AA843926	Hs.124434	ESTs	0.40
	434445	AG49306	Hs.11782	ESTs	0.40
75	413212	AA127923	Hs.282356	ESTs	0.40
	402681	N51508	Hs.143718	ESTs	0.40
	454554	AW847505		gb:RC0-CT0210-280999-021-c10 CT0210 Homo	0.40
	450891	AJ743118	Hs.238914	ESTs. Weakly similar to neurogranin-4 sho	0.40
	452078	AW027620	Hs.52170	ESTs	0.41
80	416278	AJ076799	Hs.1247	apolipoprotein A-IV	0.41
	433637	AW024214	Hs.135405	ESTs	0.41
	449923	BE258051		gb:60111034F1 NIH_MGC_16 Homo sapiens c	0.41
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (arcom	0.41
	451319	AA330620	Hs.240859	ESTs	0.41
85	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFpZ34C1915 (f	0.41
	437931	AA249468	Hs.145274	ESTs	0.41
	402759				0.41

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5	452888	AIW021446	Hs.80714	ESTs	0.41
	417318	AW653837	Hs.12891	ESTs	0.41
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	0.41
	424884	AW299437	Hs.225717	ESTs	0.41
	439224	R06696	Hs.35598	ESTs	0.42
10	423232	AF038556	Hs.132183	solute carrier family 16 (monocarboxylic gb:zm7803.1.1 Stratigene neuroepithelium	0.42
	409300	AA126190		Human DNA sequence from clone RP4-788L20	0.42
	444237	AA336878	Hs.9842	solute carrier family 5 (sodium/glucose	0.42
	425860	L29339	Hs.1954	ESTs	0.42
	447021	AJ355584	Hs.161405	protein tyrosine phosphatase-lke (prol	0.42
15	422270	AF114494	Hs.114062	ESTs	0.42
	407850	AW086230	Hs.244912	ESTs	0.42
	449884	AI673110	Hs.222195	ESTs	0.42
	436327	AA813075	Hs.120181	ESTs	0.42
	419872	HT1436	Hs.262201	ESTs	0.42
20	400917			ESTs	0.43
	435309	AW089050	Hs.157993	ESTs	0.43
	425860	WY9027	Hs.271762	ESTs	0.43
	445577	W05096	Hs.146077	ESTs	0.43
	411069	AL133092	Hs.68055	hypothetical protein DKFZp340A28	0.43
25	440286	U29589	Hs.7138	cholinergic receptor, muscarinic 3	0.43
	451123	AB272724	Hs.213480	ESTs	0.43
	457151	AW052119	Hs.235338	ESTs	0.43
	459185	AJ908222		gb:RC-BT165-300399-020 BT155 Homo sapien	0.43
	411607	AW853498		gb:RC1-CT0252-170200-025-h02 CT0252 Homo	0.43
30	424815	AA347287	Hs.104673	ESTs	0.43
	429704	AA504440	Hs.165812	ESTs	0.43
	411057	AI651006	Hs.301543	ESTs	0.43
	430172	AA468591	Hs.161889	ESTs	0.43
	435124	AA725382	Hs.120456	ESTs	0.43
35	445965	L17330	Hs.286	p53-TAK1 cell associated protein	0.43
	443741	AW451759	Hs.145420	ESTs	0.43
	415275	H42823	Hs.155742	glyoxylate reductase/hydroxyphenylacetate red	0.44
	451138	W52287	Hs.40258	ESTs	0.44
	409138	T97430	Hs.50002	small inducible cytokine subfamily A (Cy	0.44
40	426733	AL440738		gb:CKFZp340B1615_r1 434 (synonym: hies3)	0.44
	410055	AL117584	Hs.58419	DKFZP558L024 protein	0.44
	427965	D00306	Hs.183864	elastase 3B	0.44
	418026	BE379727	Hs.63213	fatty acid binding protein 4, adipocyte	0.44
	409479	DE470209	Hs.144463	ESTs	0.44
45	457594	AW130239	Hs.132922	ESTs	0.44
	435564	AF210652	Hs.16614	5(3)-deoxynucleotidylase (dNT-2); nucl	0.45
	430659	AF755910	Hs.54560	vascular endothelial junction-associated	0.45
	434399	AA878845	Hs.125769	ESTs	0.45
	415797	AJ291896	Hs.72800	ESTs	0.45
50	430264	AA470519		gb:nc71110.s1 NOL_CGAP_P1 Homo sapiens	0.45
	408435	AI810721	Hs.95424	ESTs	0.45
	433542	AA598669	Hs.173770	ESTs	0.45
	455400	AW535342		gb:CA4-DT0021-281299-0704-12 DT0021 Homo	0.45
	412047	AA534389	Hs.48595	ESTs	0.45
55	443648	T56148	Hs.9997	Homo sapiens mRNA full length insert cDN	0.45
	450307	AW450335	Hs.201783	ESTs	0.45
	434300	AF143877	Hs.215047	Homo sapiens clone IMAGE:113431 mRNA seq	0.45
	420460	AA262331	Hs.135503	ESTs	0.45
	450752	AA012986	Hs.60466	ESTs	0.45
60	418138	AA213525	Hs.130204	EST	0.45
	441088	AA316546	Hs.126546	ESTs	0.46
	410590	AW812929		gb:RC3-ST0186-250200-018-c05 ST0186 Homo	0.46
	438211	T08401		gb:EST05292 Infant Brain, Benton Soares H	0.46
	434349	NM_015678	Hs.3821	neurobeachin	0.46
65	406824	AW501063		gb:U1HF-BP09-alc-c-01-U1r1 NIH_MGC_S	0.46
	403279			ESTs	0.46
	434882	AW574752	Hs.269497	ESTs	0.46
	406429			ESTs	0.46
	427393	AB029018	Hs.177636	KIAA1095 protein	0.46
70	454651	AW612091		gb:RC4-ST0173-151099-032-504 ST0173 Homo	0.46
	401992			ESTs	0.46
	452725	AA463422	Hs.209431	ESTs	0.46
	403710			guanylate cyclase activator 1A (mlna)	0.46
	419726	L36651	Hs.92858	guanylate cyclase activator 1A (mlna)	0.46
75	421075			ESTs	0.46
	421387	AF059566	Hs.103083	solute carrier family 5 (sodium iodide s	0.46
	453404	AA035446	Hs.261224	ESTs	0.46
	407208	T10695	Hs.102948	enigma (LIM domain protein)	0.46
	444081	AW448696	Hs.166547	ESTs	0.46
80	454206	AW810279		gb:NR4-ST0125-151299-029-a09 ST0125 Homo	0.47
	402466			ESTs	0.47
	429936	N00822	Hs.48909	ESTs	0.47
	403980			gb:z26005.r1 Soares_MH4M4V_S1 Homo sapi	0.47
	428151	AA422028		gb:z802003.r1 Soares_senescenc1_fibroblas	0.47
	410495	N95428		ESTs	0.47
	402851			ESTs	0.47
	438421	AA806907	Hs.194451	ESTs	0.47

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5	454661	BE244138		gb:TCBP1E1218 Prostatic pre-B cell acut	0.47
	408753	A0337152	Hs.47438	SH3 domain binding glutamic acid-rich pr	0.47
	405106	AW037854	Hs.177386	ESTs	0.47
	413159	M62843	Hs.75236	ELAV [embryonic lethal, abnormal vision,	0.47
	442799	A564739	Hs.68565	ESTs	0.47
10	457955	A209886	Hs.143945	ESTs	0.47
	458147	AW752597		gb:IL3-CT0214-161299-045-B06 CT0214 Homo	0.47
	407938	AA905087	Hs.85060	phospholamban	0.47
	414141	BE25083		gb:501111390F1 NIH_MGC_16 Homo sapiens c	0.47
	440869	A792798	Hs.12496	ESTs	0.47
15	400749			ESTs	0.47
	458745	AW207347	Hs.211101	ESTs	0.48
	418437	AA771738	Hs.295351	ESTs	0.48
	452286	A356570	Hs.123376	ESTs	0.48
	430369	AA477631	Hs.119484	ESTs	0.48
20	453572	AA382590	Hs.31848	ESTs, Weakly similar to hypothetical pro	0.48
	455175	AW993247		gb:RC2-8N0033-180200-014-109 BN0033 Homo	0.48
	445705	AV655102	Hs.117266	ESTs	0.48
	400322	AF045576	Hs.247768	officary receptor, family 5, subfamily	0.48
	412526	M60366	Hs.73982	zona pellucida glycoprotein 2 (sperm rec	0.48
25	407586	U32659	Hs.41724	interleukin 17 (cytotoxic T-lymphocyte-a	0.48
	455479	AW948512		gb:RC0-MT0015-280300-021-004 MT0015 Homo	0.48
	455038	A852571	Hs.201681	ESTs	0.48
	411149	N68715	Hs.265128	ESTs	0.48
	453982	AW014252	Hs.252637	ESTs	0.48
30	410971	AW812258		gb:RC0-ST0174-191099-031-602 ST0174 Homo	0.48
	410639	NM_006649	Hs.65581	protein disulfide isomerase	0.48
	421553	AA530060	Hs.97302	ESTs	0.48
	442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12229 fls, clone MA	0.48
	454754	AW819191		gb:CM1-ST0283-071299-061-608 ST0283 Homo	0.48
35	447858	AW080339	Hs.211811	ESTs	0.49
	422639	A1929377	Hs.173724	creatine kinase, brain	0.49
	420449				0.49
	420440	NM_002407	Hs.97644	mammaglobin 2	0.49
	435056	AW023337	Hs.5422	glycoprotein M6B	0.49
40	419543	AA344170	Hs.188719	ESTs	0.49
	407033	U78628		gb:Human leukemia inhibitory factor rece	0.49
	437468	AA457619		gb:aa69d11.1 Stratagene fetal retina 93	0.49
	412639	AW961284	Hs.296235	ESTs	0.49
	405109				0.49
45	404519				0.49
	410285	AA083609		gb:zmf63005.r1 Stratagene fibroblast (937	0.49
	400938				0.49
	414290	A1968601	Hs.717721	ESTs	0.49
	432433	AW014734	Hs.157969	ESTs	0.49
50	405273				0.49
	454736	BE072139		gb:PM1-8T0533-291299-002-605 BT0533 Homo	0.49
	414383	BE279406		gb:50115798F1 NIH_MGC_21 Homo sapiens c	0.49
	445911	A585587	Hs.145645	ESTs, Moderately similar to JALU1_HUMAN A	0.49
	451241	A767545	Hs.209572	ESTs	0.49
55	428336	AA503115	Hs.183752	microseminoprotein, beta-	0.49
	418310	AA814100	Hs.88693	ESTs	0.49
	452152	AL046755	Hs.28219	protein phosphatase 2 (formerly 2A), reg	0.49
	454869	AW836004		gb:PM04L70019-170200-001-411 LT0019 Homo	0.49
	400332	S66407	Hs.248032	FLT4	0.49
60	452280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	0.49
	408221	AA912183	Hs.47447	ESTs	0.50
	440179	A690151	Hs.125904	ESTs	0.50
	425360	BE547704		gb:601076309F1 NIH_MGC_12 Homo sapiens c	0.50
	406600				0.50
65	416594	A1733063	Hs.187619	ESTs	0.50
	432126	AA127221	Hs.117037	ESTs	0.50
	458611	A1268407	Hs.211458	ESTs	0.50
	426495	NM_0010151	Hs.2043	soluble carrier family 25 (mitochondrial	0.50
	441068	AA913897	Hs.233569	ESTs	0.50
70	428108	AA421452	Hs.164851	ESTs	0.50
	400803				0.50
	439996	AA915555	Hs.221675	ESTs	0.50

TABLE 44B

Phy: Unique Eas probaset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

75	Phy	CAT number	Accession
		005300	111676_1 AA126190 AA074486 AA074707 AA070059 AA084886
		409824	1155499_1 AW501063 AW503034 AW501523
		410285	119128_1 AA083609 AA083796 AA112048
		410495	120548_1 H54238 W24040 AW751366 H51987
80		410732	1218556_1 AW084328 AW584322 AW984318 AW984330 R58427 AW984332 AW199897 AW984321
		410571	1228216_1 AW812258 AW812252 AW812261 AW812263 AW812285 AW812277 AW812264
		410590	1228645_1 AW812929 AW812779 AW813088

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	411607	1251251_1	AWB53498 AWB53442 AWB53590 AWB53433 AWB53592
	413075	1348528_1	BE154382 BE064381 BE064385 BE064381 BE153367 BE153366 BE153401 BE153385 BE064372
	413679	1382784_1	BE156765 BE156767 BE156767 BE156769 BE156803 BE156802 BE156847 BE156847 BE156836 BE156792 BE156834 BE156779 BE156789 BE156833 BE156844 BE156831 BE156849 BE156797 BE156794 BE156801 BE156843 BE156793 BE156852
5	414141	1420715_1	BE255083 BE257634
	414383	1440279_1	BE279406 BE280100
	422582	218132_1	AA312660 AA474863
	425350	250531_1	BE547704 AA355909
	425730	271055_1	AL040736 AA355983
10	428151	287158_1	AA422036 WT1911
	430254	315008_1	AA470219 BE300310 BE300254 BE384120
	430654	321423_1	AW956834 AA528493 AA83165 AW959842
	431152	328675_1	AW970598 AW971004 AA574217 AA493538
	431514	334213_1	AW972363 AA350635 AD17445
15	437468	43742_1	AA425219 AL280167
	438211	45225_1	TD8401 253934 T15897
	449923	81926_1	BE258051 RA45758 AA04732 BE255126
	451818	867271_1	AB119018 R05492 W27615
20	454205	1050948_1	AWB10279 BE146804 BE166903 BE146594 BE146679 AWB10472 AWB10208 AWB10356 AWB10153 AW178838 AW178837 AW178857 AWB10515 AWB10330 AWB10514 AWB10441 AWB10358 AW178852 AWB10359 AWB10332 AWB10327 AWB10211 AW178835 AWB10635 AWB10288 AWB10253 AWB10325 AWB10443 AWB10198 AWB10321 AWB10265 AWB10567 AWB10447 AWB10328 AWB10513 BE146674 AWB10257 AWB10185 AWB10281 AWB10258 BE052400 AWB10323 AWB10253 BE146652 AWB10516 BE146689 AWB10289 AWB10566 AWB10636 AW178942 BE062434 BE146653 AWB10536 AWB46445
25	454554	1223842_1	AWB47365 AWB11792 BE061442 BE061433 AWB47506 AWB06999 AWB06996 BE061436 BE061430 BE142460 BE148499 AWB06994 AWB06155 AWB02591 AWB14282 AWB06992 BE061669 AWB07002 BE146659 AWB06995 AWB07000 AWB45743 AWB45747 AWB47504 BE142458 AWB061431 BE061435 AWB47507 BE146650 BE142470 AWB14096 AWB07012 BE061438 AWB07011 AWB06993 BE142455 BE142459 BE142462 AWB061434 AWB065331 BE061434 BE061731 BE142464 AWB47501 AWB07001 BE142463 AWB11800 BE061437 AWB11802 BE061440 AWB06997 AWB06998 BE061745 BE061753
	454550	1223940_1	AWB07281 AWB07092 AWB07425 AWB07330 AWB07174 AWB07171 AWB07274 AWB07275 AWB07367
30	454651	1228069_1	AWB12051 AWB12228 AWB12105 AWB36581 AWB12080
	454661	1228527_1	BE244138 BE244727 AWB12636 AWB12647
	454738	1234445_1	BE027139 BE157917 BE12794 AWB05794 AWB17778
	454754	123380_1	AWB1191 AWB19522 AWB19183 AWB19175 AWB19177 AWB19186 AWB19180 BE158470 AWB19242 AWB19269 AWB19244 AWB19190 AWB19265 AWB19268 AWB19246 BE152602 AWB19249 AWB19251 AWB19253 AWB19194
35	454790	123452_1	AWB20852 AWB20773 AWB21088
	454853	1238137_1	AWB20304 AWB32587 AWB32163 AWB36152 AWB36085 AWB36084 AWB36079 AWB36083 AWB36082 AWB36086 AWB36088 AWB36166 AWB36164 BE061745 BE061753
	455175	1257335_1	AW592247 AWB91464
	455400	1288135_1	AW5936342 AWB59336
40	455479	1250163_1	AWB48312 AWB48286 AWB48289 AWB48291 AWB48279 AWB48295
	455541	1331705_1	AWB59302 AWB59326 AWB593240
	455753	1356070_1	BE075124 BE075229 BE075278
	455826	1373392_1	BE144228 BE144291
	458147	488021_1	AW752597 AWB48781 AWB49062 AWB48490 AW752699 AW752604 AW752700
45	459185	922623_1	AWB08222 AWB08224 AWB08217

TABLE 44C

Play:	Unique number corresponding to an Eos probe
Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22". Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

	Play	Ref	Strand	NL_position
55	420749	7331445	Minus	9102-9293
	420803	8567875	Minus	18267-19088
	420917	7283186	Minus	173258-173631
	420938	7628980	Minus	52074-52423
	421035	3887273	Plus	81218-81365
60	421514	7628235	Plus	32224-32292,94913-95065,95163-95334
	421775	9966311	Minus	110228-110340
	421889	4309964	Minus	118611-118621
	421992	4153058	Plus	31452-31649
65	422015	7417802	Minus	48791-49043,50038-50205,51530-51672,54448-54565,55933-56073
	422449	5796674	Plus	59867-60039,52988-62828,53466-53623,64952-65108
	422495	9795919	Plus	57659-57866,58839-58908
	422759	5213869	Plus	134117-134281
	422760	9213865	Plus	136829-136952,137336-137521
70	422851	9550753	Minus	63022-63126,63683-63783
	423069	8954192	Minus	69553-69702
	423279	8072597	Plus	162568-162768,163918-164168
	423429	9719550	Minus	52789-52917
	423670	7259739	Minus	88377-88537
	423680	7331517	Minus	157184-157415
75	423710	6437516	Plus	27413-26978
	424121	9798219	Plus	59256-59401
	424519	8152000	Plus	12817-13000
	424529	9795555	Plus	55584-55796
	424873	3213020	Plus	101805-102591
	425110	8298408	Minus	118910-119100
80	425273	4155137	Minus	98141-98754
	425545	4928854	Minus	92231-92380,92724-92869
	425742	7283744	Minus	54424-54488

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5	405817	4071056	Plus	19914-20112.29555-25810
	405914	6758904	Minus	23738-24076
	406036	6758919	Plus	17942-18163
	406109	9127147	Minus	56328-58485
	406255	7117728	Plus	2959-3207
	405326	8212185	Plus	94508-84655
	406600	8249616	Minus	36296-36610

TABLE 45A. ABOUT 947 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL ADULT TISSUES
Table 45A lists about 947 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 56680 probesets on the Affymetrix/Eos Hu3.0 GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" stomach cancer level was set to the 50th percentile amongst various stomach cancers. The "average" normal adult tissue level was set to the 50th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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Pkey: Unique Eos probe/identifier number
ExAccon: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
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Rt: Ratio of stomach cancer compared to normal stomach

	Pkey	ExAccon	UnigeneID	Unigene Title	Rt
	418302	M13509	Hs.53169	matrix metalloproteinase 1 (interstitial)	66.80
	411243	AB038896	Hs.69319	CA11	61.16
25	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin)	42.36
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metallo)	35.80
	425679	XQ5697	Hs.159177	lipase, gastric	26.34
	405041	AB033025	Hs.52081	Ki6A-1199 protein	26.91
	452121	NM_004081	Hs.70936	deleted in azoospermia	26.22
30	403776			NA	25.00
	444783	AK001468	Hs.52180	anilin (Drosophila Scraps homology), act	23.90
	422556	BE545072	Hs.122579	hypothetical protein FLJ10461	23.90
	409187	AF154830	Hs.50996	cartilaginous phosphatase synthesize 1, mitochond	23.35
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	22.26
35	430759	AL350055	Hs.67709	Home sapiens mRNA full length insert cDN	21.05
	415989	AB267700	Hs.317584	ESTs	20.72
	415209	AA281776	Hs.78078	MDM2 (mitotic arrest deficient, yeast, h	19.84
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	15.50
	438639	AI278360	Hs.31409	ESTs	15.16
40	428427	M86699	Hs.159840	TYK protein kinase	14.54
	443032	AA045573	Hs.22900	nuclear factor (erythroid derived 2) like	14.26
	443211	AI128388	Hs.143655	ESTs	14.22
	421470	R27496	Hs.1378	annexin A3	13.96
	400792	AA616562	Hs.50054	Home sapiens mRNA; cDNA DKFpZ34400515 (f	13.94
45	424086	AI351010	Hs.102267	lysyl oxidase	13.73
	457789	AI591344	Hs.127812	ESTs, Weakly similar to T17330 hypothe	13.38
	409757	NM_001898	Hs.123114	cystatin SN	13.33
	447033	AI357412	Hs.157601	ESTs	13.20
50	447164	AF026391	Hs.17518	Home sapiens cpg mRNA, partial sequence	12.80
	420159	AS27490	Hs.99785	Home sapiens cDNA: FLJ21245 fs, clone C	12.66
	423296	AJ224741	Hs.278461	matrin 3	12.64
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	12.46
	413582	AW295847	Hs.71331	hypothetical protein MGC3350	12.32
55	423020	AA330022	Hs.1988	replication protein A3 (RAD)	12.16
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	11.74
	442660	AW138174	Hs.130651	ESTs	11.73
	441693	AA384673	Hs.7943	RbB5-mediated protein	11.16
	453221	AA328102	Hs.24641	cytoskeleton associated protein 2	11.08
	414142	AK036387	Hs.150042	Home sapiens cDNA FLJ14438 fs, clone HE	10.30
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.48
	443715	AI563187	Hs.9700	cyclin E1	10.44
	420503	AL045633	Hs.44269	ESTs	10.38
	453922	AF063306	Hs.39738	binding uninhibited by benzimidazoles 1	10.36
65	415076	NM_000867	Hs.77890	guanylate cyclase 1, soluble, beta 3	10.20
	452291	AF015592	Hs.28853	CDC7 [cell division cycle 7, S. cerevisi	10.18
	410366	AF373210	Hs.43247	Home sapiens cDNA FLJ13585 fs, clone PL	10.14
	414422	AA147224	Hs.332322	ESTs	10.12
	405269	AA576953	Hs.22972	hypothetical protein FLJ13352	10.02
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.02
70	418882	NM_004996	Hs.85433	ATP-binding cassette, sub-family C (CFTR	9.80
	428365	AA265331	Hs.183681	Home sapiens cDNA FLJ20942 fs, clone CO	9.72
	416661	AA634543	Hs.79440	KIF-II mRNA-binding protein 3	9.68
	400195	NA		NA	9.66
	418738	AW388633	Hs.6582	solute carrier family 7, (cationic amino	9.64
75	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	9.60
	414259	W44433	Hs.301296	Home sapiens cDNA: FLJ21311 fs, clone L	9.58
	417517	AF001176	Hs.82238	PDP4 (processing of precursor, S. cerev	9.34
	446998	N95013	Hs.16762	Home sapiens mRNA; cDNA DKFpZ564D2062 (f	9.26
80	420486	AF153827	Hs.203963	hypothetical protein FLJ10339	9.16
	428227	AA321649	Hs.22448	small inducible cytokine subfamily B (Cy	8.95
	411810	X67155	Hs.270845	irinotecan-like 5 (irinotecan-like 5)	8.84
	419261	X07876	Hs.85791	wingless-type MMTV integration site fami	8.80
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.78

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424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT	8.69
413268	AL039079	Hs.75256	regulator of C-protein signalling 1	8.68
417801	AA417383	Hs.62582	Integrin, beta-like 1 (with EGF-like rep	8.68
452461	N75223	Hs.108106	transcription factor	8.68
425916	NM_008706	Hs.152200	urosterin 2	8.64
422805	AA346899	Hs.121017	H2A histone family, member A	8.54
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	8.52
441377	BE218230	Hs.202656	ESTs	8.41
445891	AK391342	Hs.199490	ESTs	8.31
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	8.30
436521	AI608955	Hs.58248	ESTs	8.30
425087	R62424	Hs.126059	ESTs	8.28
424653	AY977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.22
441795	N38115	Hs.21137	ADQ24 protein	8.02
427678	C05766	Hs.181022	CGI-07 protein	8.00
413583	AI.120806	Hs.5888	ESTs	7.98
407653	AA336797	Hs.40499	dickekopf (Xenopus laevis) homolog 1	7.98
425628	HI5302	Hs.169550	Homo sapiens mRNA, cDNA DKFZp566A1046 (f	7.97
404996			NA	7.96
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.96
419044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	7.94
417655	AA780791	Hs.14014	hypothetical protein FLJ14813	7.92
452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.91
418895	AA84638	Hs.14560	ESTs	7.90
446155	A553495	Hs.159422	Homo sapiens cDNA FLJ13957 fs, clone Y7	7.86
423123	NM_012247	Hs.126027	SELENOPHOSPHATE SYNTHETASE, Human selen	7.82
434539	AW748078	Hs.214419	ESTs, Weakly similar to MUC22/HUMAN MUC20	7.80
447505	AL049266	Hs.18724	Homo sapiens mRNA, cDNA DKFZp564F093 (f	7.72
418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.70
447289	AK247017	Hs.38978	melanoma antigen, family A, 3	7.70
443354	AW974672	Hs.52417	protein kinase, AMP-activated, alpha 1 c	7.69
427718	AI798980	Hs.25333	ESTs	7.66
434032	AW009951	Hs.206892	ESTs	7.60
427738	NM_000316	Hs.160612	peroxisomal membrane protein 3 (3MD, Ze	7.58
452480	X82125	Hs.25240	zinc finger protein 239	7.51
418678	NM_001327	Hs.167319	carcinosarcoma antigen	7.49
431494	AA991355	Hs.236312	hypothetical protein DKFZp434A1315	7.44
452705	H49805	Hs.240005	ESTs	7.36
443546	AB085198	Hs.164285	ESTs	7.32
425420	BE538911	Hs.234543	hypothetical protein HUF2R	7.30
420617	AK001652	Hs.99423	ATP-dependent RNA helicase	7.28
421155	H87879	Hs.102267	lysyl oxidase	7.24
450715	AC66484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.24
447254	NM_004153	Hs.17938	origin recognition complex, subunit 1 (y	7.22
435473	N53550	Hs.206881	ESTs	7.20
413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	7.14
443347	AV649748	Hs.295901	KIAA0493 protein	7.11
452281	TS3590	Hs.28792	Homo sapiens cDNA FLJ11941 fs, clone PL	7.11
408936	BE296227	Hs.258822	serine/threonine kinase 15	7.11
408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 fert	7.10
453888	AW381270	Hs.194110	hypothetical protein PRO2730	7.02
426890	AA393167	Hs.41294	ESTs	6.98
404440			NA	6.97
426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	6.96
431723	AW058350	Hs.16762	Homo sapiens mRNA, cDNA DKFZp564E2062 (f	6.95
413833	Z15005	Hs.75573	centromere protein E (312kD)	6.94
426249	F05422	Hs.166352	nucleoside-like protein 1	6.94
441421	AA356792	Hs.334824	hypothetical protein FLJ14825	6.92
402096	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.85
423603	M57765	Hs.17121	interleukin 11	6.84
431041	AA495667	Hs.197555	KIAA0704 protein	6.74
417266	U94332	Hs.61791	tumor necrosis factor receptor superfam	6.74
426921	AA037145	Hs.172665	cleavage stimulation factor, 3' pre-RNA,	6.70
407771	AL138272	Hs.62713	ESTs	6.69
433383	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.66
407162	NS3855	Hs.142634	zinc finger protein	6.64
411343	U77949	Hs.85653	CDCE (cell division cycle 6, S. cerevisi	6.64
427920	Z11502	Hs.181107	annexin A13	6.59
430159	AT072416	Hs.200771	ESTs, Moderately similar to A Chain A, T	6.58
427401	U20562	Hs.21449	actin like protein	6.55
447702	BE187434	Hs.98471	ESTs, Weakly similar to T18712 hypoteli	6.54
431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	6.54
435159	AA668879	Hs.116649	ESTs	6.54
440209	H05049	Hs.22269	neurexin 3	6.54
416134	AA307869	Hs.86617	ESTs	6.50
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.47
448494	AW977850	Hs.23856	hypothetical protein MGCS297	6.40
422955	AL120982	Hs.124165	ESTs	6.34
426010	AA136563	Hs.18715	hypothetical protein FLJ21007	6.32
44696	AF002020	Hs.78918	Niemann-Pick disease, type C1	6.31
408380	AF123050	Hs.44532	diubiquitin	6.31
420218	AW958037	Hs.286	ribosomal protein L4	6.29
405817	NA		NA	6.28

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406747	AI025153	Hs.217493	annexin A2	6.24
448743	AB032962	Hs.21896	KIAA1136 protein	6.24
434636	AA0283764	Hs.6101	hypothetical protein MGC3178	6.20
424602	AK002055	Hs.151046	hypothetical protein FLJ111193	6.17
412861	H32860	Hs.24611	ESTs, Weakly similar to 154374 gene NF2	6.16
	401644		NA	6.15
423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.13
427335	AA448542	Hs.751677	G antigen T8	6.12
460375	AA009647	Hs.8650	a disintegrin and metalloproteinase doma	6.07
472420	U03336	Hs.1534	tumor necrosis factor (ligand) superfamily	6.06
419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	6.06
413573	AI733859	Hs.145089	ESTs	6.06
406758	NM_003686	Hs.47504	exonuclease 1	6.02
444188	A1383165	Hs.659	peptidyl-lysine isomerase B (cyclophilin	6.02
407746	AK001962	Hs.38114	hypothetical protein FLJ111100	6.00
446354	AB006624	Hs.14912	KIAA266 protein	5.98
418939	AW630903	Hs.89497	lamin B1	5.90
424639	AI911494	Hs.9612	Homo sapiens cDNA FLJ14388 fs, clone HE	5.86
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fs, clone HE	5.86
419863	AW952691	Hs.93485	Homo sapiens mRNA, cDNA DKFZp761D191 (fr	5.84
430849	AI940727	Hs.270556	ESTs, Highly similar to AF156779 1 A58-4	5.82
428872	V02416	Hs.30715	potassium voltage-gated channel, tol-rd	5.80
448776	BE324654	Hs.30067	MRG1 (S. cerevisiae)-like, magnesium hom	5.74
442957	AI949662	Hs.49397	ESTs	5.72
444577	AZ07721	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.72
424565	AW107223	Hs.75295	granulate cytochrome 1, soluble, alpha 3	5.71
433330	AW027034	Hs.132816	hypothetical protein MGC14801	5.68
428818	AA085360	Hs.160199	NAADPH oxidase, EF hand calcium-binding d	5.68
432867	AW016936	Hs.233364	ESTs	5.64
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakabins	5.62
433133	AB027249	Hs.104741	PQZ-binding kinase; T-cell originated pr	5.63
418379	AA371840	Hs.137516	fibrogen-like 1	5.57
434551	BE387162	Hs.280658	ESTs, Highly similar to AS3561 DNA excis	5.57
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	5.56
427386	AW636261	Hs.337717	ESTs	5.54
429550	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.52
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	5.51
448370	AK002114	Hs.23495	hypothetical protein FLJ11252	5.50
431118	BE264901	Hs.250302	carbonic anhydrase VIII	5.50
423673	BE033254	Hs.1695	matrix metalloproteinase 12 (macrophage	5.50
435831	AL121278	Hs.25144	ESTs	5.49
409044	AI125986	Hs.33033	hypothetical protein FLJ14623	5.48
436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.45
446336	RS3846	Hs.44976	ESTs	5.44
454018	AW016992	Hs.100855	ESTs	5.42
457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	5.42
412246	AI160873	Hs.69233	zinc finger protein	5.40
432193	AA372264	Hs.273193	hypothetical protein FLJ10706	5.40
431319	BE105958	Hs.56406	Homo sapiens cDNA FLJ13549 fs, clone PL	5.40
427860	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone C	5.40
452862	AW378065	Hs.8687	ESTs	5.38
408327	LA1162	Hs.53563	collagen, type IX, alpha 3	5.36
412611	H05382	Hs.21400	ESTs	5.34
443390	AI035414	Hs.21068	hypothetical protein	5.32
428187	AI667303	Hs.285529	G protein-coupled receptor 49	5.30
450434	AA166950	Hs.195870	hypothetical protein FLJ14991	5.28
434265	AA845811	Hs.130554	Homo sapiens cDNA: FLJ23089 fs, clone L	5.26
407811	AW190002	Hs.40098	cystine knot superfamily 1, BMP antagon	5.27
446638	AL133063	Hs.15783	Homo sapiens mRNA: cDNA DKFZp434P1115 (f	5.26
444743	AA045648	Hs.301957	rudix (nucleoside diphosphate linked mo	5.25
424902	NM_003686	Hs.153687	inositol polyphosphate 4-phosphatase, ty	5.24
457150	W42480	Hs.260864	ESTs	5.24
432695	AI753709	Hs.152484	ESTs, Weakly similar to U80022 hypophos	5.22
453382	AA709285	Hs.5997	hypothetical protein FLJ13078	5.22
447048	AW393080	Hs.228320	hypothetical protein FLJ23537	5.22
426518	Z43039	Hs.170719	KIAA0009 gene product	5.22
453884	AA355925	Hs.36332	KIAA0166 gene product	5.20
429625	AA455568	Hs.193814	ESTs	5.17
413472	BE247870	Hs.75379	solute carrier family 1 (glut high affi	5.20
449318	AW030021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	5.19
444059	RB0743	Hs.118774	integrin, alpha 1	5.18
409432	DI9372	Hs.54560	small inducible cytokine subfamily A (Cy	5.17
412719	AW016610	Hs.129911	ESTs	5.15
444342	NM_014396	Hs.10867	similar to lysosome-associated membrane	5.14
425739	T15016	Hs.159410	methylenetetrahydrofolate synthase	5.12
427198	AB087560	Hs.6310	ESTs, Weakly similar to U80022 hypophos	5.12
445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	5.10
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fs, clone HE	5.09
424296	AB631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	5.08
441645	AI222778	Hs.201555	ESTs, Weakly similar to T22405 hypophos	5.06
412723	AA648459	Hs.335951	hypothetical protein AF301222	5.06
448811	AI590371	Hs.174759	ESTs	5.05
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	5.04

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411835	U29343	Hs.72550	hyaluronan mediated mobility receptor (R)	5.04
421373	AA808229	Hs.167771	ESTs	5.04
448991	AW771565	Hs.185954	ESTs	5.02
425370	P19597	Hs.89709	glutamate-cysteine ligase, modifier subu	5.00
454036	AA374756	Hs.53550	Homo sapiens mRNA for KIAA1771 protein,	4.98
405770			NA	4.96
421110	AJ250717	Hs.1355	cathespain E	4.92
452988	AA889120	Hs.110637	homoeo box A10	4.96
431519	AB033698	Hs.150587	vinculin-like protein 2	4.91
420952	AA282067	Hs.88972	ESTs, Moderately similar to A46010 X-in	4.88
408321	AW405882	Hs.44205	coristatin	4.87
441801	AW242799	Hs.86366	ESTs	4.84
450568	AL505078	Hs.25159	Homo sapiens cDNA FLJ10784 fts, clone NT	4.83
452609	NM_015368	Hs.105865	pancrein 1	4.82
409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.82
451105	A1761324	Hs.81376	glt-w60b11.1 x1 NC1_CGAP_Co16 Homo sapiens	4.80
417168	AL133117	Hs.83758	Homo sapiens mRNA; cDNA DKF2p586L1121 (f	4.80
116203	X54947	Hs.83758	CDC20 protein kinase 2	4.80
118994	AA296520	Hs.89546	selectin E (endothelial adhesion molecuol	4.78
345682	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	4.78
422874	W94322	Hs.279651	melanoma inhibitory activity	4.78
440351	AF039933	Hs.7119	RAD1 (R. pomtie) homolog	4.78
431956	AK000032	Hs.272245	Homo sapiens cDNA FLJ11170 fts, clone PL	4.77
442980	AA857025	Hs.8878	kinesin-like 1	4.76
432437	W07088	Hs.293685	ESTs	4.76
414869	AA157291	Hs.21479	ubonectin 1	4.74
446254	BE179829	Hs.179932	Homo sapiens cDNA FLJ12832 fts, clone NT	4.74
118380	AA425473	Hs.84429	KIAA0971 protein	4.74
419343	AA460245	Hs.85503	down-regulated by Cimb1, a	4.74
416478	U10845	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	4.72
425813	AA364135	Hs.210553	hypothetical protein DKF2p761122	4.71
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.71
412733	AA984472	Hs.74554	KIAA0080 protein	4.68
444325	AW152618	Hs.16757	ESTs	4.66
407638	AJ404672	Hs.334463	hypothetical protein FLJ23571	4.66
450345	AK000252	Hs.239691	hypothetical protein FLJ20275	4.66
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	4.64
449448	D60730	Hs.57471	ESTs	4.62
409732	NM_016122	Hs.56148	NY-REN-38 antigen	4.62
432415	T16971	Hs.269014	ESTs, Weakly similar to A43632 mucin 2 p	4.62
421987	AI133161	Hs.786131	CGI-101 protein	4.60
430217	N47863	Hs.336901	ribosomal protein S24	4.58
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	4.57
425932	NA1650	Hs.1968	semenogelin 1	4.57
408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.56
428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	4.55
451254	AS71016	Hs.172967	ESTs	4.54
422426	W79117	Hs.158558	ESTs	4.54
439453	T69900	Hs.58323	Homo sapiens cDNA FLJ11613 fts, clone HE	4.53
435420	AA928513	Hs.59203	ESTs	4.53
447519	U46258	Hs.339665	ESTs	4.52
424176	AL137273	Hs.142307	hypothetical protein	4.52
414812	X72755	Hs.77367	monokine induced by gamma interferon	4.51
438069	N80701	Hs.33790	ESTs	4.50
450096	AA82088	Hs.79375	holocarboxylase synthetase (biotin-prop	4.50
438159	Z53947	Hs.10687	gdi H sapiens mRNA; clone CD 117	4.50
433925	AI183551	Hs.26481	SIBP76 protein	4.48
417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.48
433384	AI021992	Hs.124244	ESTs	4.47
421863	AA952677	Hs.108972	Homo sapiens mRNA; cDNA DKF2p34P228 (r	4.47
453941	U59817	Hs.336820	Bloom syndrome	4.45
423401	NM_001062	Hs.129087	coagulation factor II (thrombin) recepto	4.44
430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.43
424084	AA940675	Hs.20914	hypothetical protein FLJ23056	4.42
459587	AA031956	Hs.190485	glt-ct15c04 s1 Soares_pregnant_uterus_Nbr	4.42
417956	AA210704	Hs.190485	ESTs	4.42
449433	AA672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	4.42
421477	AI904743	Hs.104650	hypothetical protein FLJ10292	4.42
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.41
451813	NM_016117	Hs.27182	phospholipase A2-activating protein	4.41
415091	AL044872	Hs.177910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.40
425142	AW554397	Hs.154762	HIV-1 rev binding protein 2	4.40
441720	AA346487	Hs.28739	ESTs	4.40
409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	4.39
411571	AA122883	Hs.70811	hypothetical protein FLJ20516	4.38
430044	AA446510	Hs.152812	ESTs	4.37
436246	AA450963	Hs.119991	ESTs	4.37
409582	R27430	Hs.271555	ESTs	4.37
453652	AA002640	Hs.28368	ESTs, Moderately similar to S56557 alpha	4.35
425211	N18967	Hs.1867	progastrin (progastrinogen C)	4.34
448692	AA013907	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.34
402459	D68407	Hs.54481	low density lipoprotein receptor-related	4.34
424270	AA273860	Hs.5739	ESTs	4.33

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441804	AA134329	Hs.24170	Homo sapiens, clone IMAGE3685398, mRNA.	4.32
428957	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	4.31
436395	A1683487	Hs.152213	wingless-type MMTV integration site fami	4.31
433397	AW078766	Hs.134880	ESTs, Weakly similar to unnamed protein	4.30
417576	AA339449	Hs.82285	phosphoribosylglycamide formyltransferase	4.29
413278	BE553285	Hs.833	interferon-stimulated protein, 15 kDa	4.29
451592	A1805416	Hs.213897	ESTs	4.28
453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.28
428952	AA568776	Hs.121553	hypothetical protein FLJ20641	4.26
431699	NM_001113	Hs.267831	Rho GTPase activating protein 5	4.26
428380	AW115714	Hs.283127	ESTs, Weakly similar to T11201 hypotheti	4.24
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-con	4.23
409913	BE243442	Hs.236077	retroviral P4.1-associated protein, unc	4.22
445537	AJ245671	Hs.12844	EGF-like domain, multiple 5	4.21
455640	AW956625	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.20
422232	D43945	Hs.113274	transcription factor EC	4.18
402655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	4.18
443281	BE387335	Hs.263713	ESTs, Weakly similar to S6A054 hypotheti	4.16
434217	AW014755	Hs.23349	ESTs	4.16
413384	NM_000401	Hs.75334	exonuclease (multiple) 2	4.14
407758	AW002841	Hs.29475	ESTs	4.14
419188	AJ336132	Hs.33718	Homo sapiens cDNA FLJ112641 f1, clone NT	4.13
402165	AL133573	Hs.43143	Homo sapiens mRNA, cDNA DKFZ556A2463 (f	4.12
443691	A1081724	Hs.17267	ESTs	4.12
409640	U78722	Hs.55481	zinc finger protein 165	4.12
438176	AW138970	Hs.122113	ESTs	4.10
435532	AW291469	Hs.117363	Homo sapiens, clone IMAGE:3682908, mRNA	4.10
419505	AW294755	Hs.198529	ESTs	4.08
452824	W727643	Hs.73965	splicing factor, arginine/serine-rich 2	4.08
414152	NM_003248	Hs.75774	thrombospondin 4	4.08
419589	T85017	Hs.11192	KIAA0074 protein	4.07
404253			NA	4.06
421741	AK001879	Hs.107527	hypothetical protein FLJ11017	4.06
428218	AA424266	Hs.123642	EphA3	4.06
428858	AA438760		glnzmg7011.1 Scores_total_fuse_Nb2F8_	4.06
422336	AA303115	Hs.183752	microsome protein, beta	4.05
442875	BE023303	Hs.23625	Homo sapiens clone TCCC02A0142 mRNA sequ	4.04
421841	AA908197	Hs.108850	MAK-related kinase	4.04
451177	A1959719	Hs.13034	ESTs	4.04
425188	AK002852	Hs.155071	Hypothetical protein FLJ11150	4.04
417262	AA282746	Hs.5343	Homo sapiens cDNA FLJ14265 f5, clone PL	4.03
424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nu	4.02
438777	AA625487	Hs.142179	ESTs	4.02
423343	AA324543	Hs.246106	ESTs	4.02
425788	BE465417	Hs.231859	ESTs, Weakly similar to rab3 effector-4	4.02
409928	AL137163	Hs.57549	hypothetical protein dJ47364	4.01
406671	AA129547	Hs.285754	mei proto-oncogene (hepatocytic growth fa	4.01
442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23155 f5, clone L	4.00
433225	AW115515	Hs.173540	ATPase, Class V, type 10D	4.00
411765	H13346		glnzmg7011.1 Scores_broad_3NbH8at Homo	4.00
452022	AW072330	Hs.293875	ESTs	4.00
451805	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.99
423541	AA266922	Hs.125778	gastrointestinal peptide	3.99
414132	AB01128	Hs.48480	ESTs	3.99
452453	A902519		glnzmg7011.1 Scores_broad_3NbH8at Homo	3.98
418454	AA315308	Hs.195870	hypothetical protein FLJ141991	3.98
430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	3.98
453160	AJ283307	Hs.239884	H2B histone family, member L	3.97
417235	AA816278	Hs.24250	ESTs	3.95
425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	3.95
414135	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.94
436928	AK029880	Hs.152371	down syndrome critical region protein DS	3.94
431753	Y75029	Hs.2841	neurexin IV	3.94
453161	AA528608	Hs.61656	ESTs	3.94
454821	AW833504		glnzmg7011.1 Scores_broad_3NbH8at Homo	3.94
427951	AW263165	Hs.143134	ESTs	3.94
438453	BE284974	Hs.55566	thyroid hormone receptor interactor 13	3.93
409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	3.93
418396	A176805	Hs.26591	ESTs	3.92
451411	AA017492	Hs.135555	EST	3.92
445895	AJ734003	Hs.127699	KIAA1803 protein	3.92
407658	AA058900	Hs.32646	hypothetical protein FLJ21901	3.91
442896	R37725	Hs.251108	ESTs	3.90
433361	AW466373	Hs.300141	ribosomal protein L30	3.90
419926	AW808092	Hs.93795	DKFZP6602223 protein	3.89
413175	AA046934	Hs.75529	nuclear GTPase	3.89
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	3.86
428549	AA430064	Hs.220929	Homo sapiens cDNA FLJ14369 f5, clone HE	3.86
455120	AA535244	Hs.17935	RAB2, member RAS oncogene family	3.86
452164	A1694413	Hs.32549	olfactory receptor, family 2, subfamily	3.85
421247	BE319127	Hs.102910	general transcription factor IIIH, polype	3.85
417720	AA205625	Hs.208067	ESTs	3.85
418811	AK001407	Hs.88653	hypothetical protein FLJ10545	3.84

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430899	BE318217	Hs.183528	hypothetical protein FLJ14906	3.84
421246	AW562962	Hs.102897	CGI-47 protein	3.83
407366	AF026942	Hs.334838	glt.Homo sapiens cpg33 mRNA, partial sequ	3.83
428698	AA852773	Hs.334838	KIAA1866 protein	3.82
435202	A1971313	Hs.170204	KIAA0551 protein	3.82
454074	RS3531	Hs.28419	ESTs	3.82
448917	A1683598	Hs.201615	ESTs	3.82
410507	AA355288	Hs.40834	translational epithelia response protein	3.82
452971	W31918	Hs.34665	ESTs	3.82
454563	A1247343	Hs.149332	ESTs	3.82
450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fs, clone MA	3.80
423025	AA831267	Hs.12244	hypothetical protein FLJ20097	3.80
425656	AB018264	Hs.158688	KIAA0741 gene product	3.80
407168	RA6175	Hs.117183	ESTs	3.79
403422	NA		NA	3.79
425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.79
4327239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	3.79
461305	AA744550	Hs.136345	ESTs	3.78
433800	A024361	Hs.135150	lmp type-1 cell membrane-associated gly	3.77
428665	BE544095	Hs.164990	BarH-like homeobox 1	3.76
424188	AW594552	Hs.142634	zinc finger protein	3.75
424638	A1672106	Hs.49303	Homo sapiens cDNA FLJ11663 fs, clone HE	3.75
451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	3.75
448105	AW591433	Hs.298241	Transmembrane protease, serine 3	3.74
452785	AL359942	Hs.295434	erythroid differentiation and deacetylase	3.74
459000	AA903705	Hs.4190	Homo sapiens cDNA: FLJ23269 fs, clone C	3.74
432653	N62990	Hs.293185	ESTs, Weakly similar to Jc7328 amino aci	3.73
409632	W74021	Hs.55279	serine (or cysteine) proteinase inhibit	3.73
414883	AA526966	Hs.334983	CDC28 protein kinase 1	3.73
415064	AA159804	Hs.149305	hypothetical protein MGC2603	3.72
432188	AW75305	Hs.50458	ESTs	3.72
450194	AW338318	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	3.72
415263	AA948033	Hs.130853	ESTs	3.71
408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.71
408460	AA054726	Hs.285574	ESTs	3.71
431496	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFpZp547125 (fr	3.70
443486	NM_003428	Hs.9450	zinc finger protein B4 (HPF2)	3.68
432021	AA524470	Hs.58753	ESTs	3.68
420092	AA814043	Hs.88045	ESTs	3.68
414620	AW445008	Hs.77637	homolo box A4	3.68
429432	A1878059	Hs.20876	synaptosomal complex protein 2	3.68
435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-n	3.67
430544	AA481086	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.67
432542	AW083920	Hs.10658	clau-din 2	3.67
410782	AW504860	Hs.268638	hypothetical protein FLJ12573	3.66
421106	AA877124	Hs.172844	ESTs	3.64
439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.64
418735	NA8769	Hs.44609	ESTs	3.64
411598	BE339654	Hs.70337	H3 histone family, member A	3.63
424887	J55076	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.63
436411	AW616352		gltba6.3c07.y1 NH_MGC_12 Homo sapiens cD	3.63
429774	A1522215	Hs.50883	KIAA1804 protein	3.62
448844	A1581519	Hs.177164	ESTs	3.61
420473	AB030326	Hs.51965	KIAA1209 protein	3.61
441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fs, clone NT	3.61
429534	AW976987	Hs.163327	ESTs, Weakly similar to 2102950A B cell	3.60
414706	AW340125	Hs.76889	KIAA0097 gene product	3.60
435211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	3.59
422938	NM_001809	Hs.1594	centromere protein A (TACC)	3.59
451381	BE241831	Hs.172330	hypothetical protein MGC2705	3.58
428664	AK001666	Hs.180995	similar to SALL1 (sal (Drosophila)-like	3.58
424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT	3.58
440717	AA904527	Hs.42027	ESTs	3.58
450698	W31489	Hs.95044	ESTs, Weakly similar to 138022 hypetheti	3.58
423675	A1950509	Hs.131342	small inducible cytokine subfamily A (Cy	3.58
424582	A1379461	Hs.153636	for upstream element (FUSE) binding pro	3.57
410784	AW183201		glt.2.LUMO077-070508-085.FGS LUMO077 Homo	3.55
411096	UB0034	Hs.65853	mitochondrial intermembrane peptidase	3.55
430294	A1583226	Hs.32976	guanine nucleotide binding protein 4	3.54
439225	AA192669	Hs.45032	ESTs	3.54
429163	AB014603	Hs.191955	KIAA0704 protein	3.54
419948	AB041035	Hs.93847	NADPH oxidase 4	3.53
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.52
408556	UA9516	Hs.46362	5-hydroxytryptamine (serotonin) receptor	3.52
417048	AB088775	Hs.55438	per aryltransferyl diphosphate synthase 1	3.52
423101	A1919950	Hs.123642	EphA3	3.52
419216	AL067618	Hs.164021	small inducible cytokine subfamily B (Cy	3.51
444754	T83911	Hs.111881	transmembrane 4 superfamily member 4	3.51
422043	AF151852	Hs.111449	CD9-94 protein	3.50
424766	NA		NA	3.50
441513	AW014557	Hs.112420	ESTs	3.50
444301	AK000136	Hs.10760	asporin (LRR class 1)	3.50
417315	A1080042	Hs.336901	ribosomal protein S24	3.50

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	407182	AA312551	Hs.230157	ESTs	3.49
	443204	AW026878	Hs.29643	Homo sapiens cDNA FLJ13103 fls, clone NT	3.49
	432889	A860145	Hs.55118	ESTs	3.49
	453644	A813444	Hs.42197	ESTs	3.48
5	427886	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fls, clone H	3.48
	405466		NA		3.48
	410804	U64820	Hs.65521	Machado-Joseph disease (spinocerebellar	3.48
	430357	AW976789	Hs.165607	ESTs	3.46
10	419428	Y11490	Hs.85032	thyroid hormone receptor interactor 11	3.46
	422260	AA315993	Hs.105434	polymerizing gene type IV	3.46
	412828	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.46
	451403	AA855569	Hs.40919	Homo sapiens cDNA FLJ14511 fls, clone NT	3.46
	406117		NA		3.46
	458242	BE399588	Hs.28465	Homo sapiens cDNA: FLJ21869 fls, clone H	3.45
15	438552	AA43323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	3.45
	440105	AA694010	Hs.6932	Homo sapiens clone Z3809 mRNA sequence	3.45
	443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	3.45
	426320	W47395	Hs.165300	transforming growth factor, beta 2	3.45
	444478	W07318	Hs.240	N phase phosphoprotein 1	3.45
20	425904	A880590	Hs.82238	POP4 (processing of precursor, S. cerev	3.44
	416702	AA186428	Hs.85591	ESTs	3.44
	446868	A1560305	Hs.199852	ESTs	3.42
	410304	A259027	Hs.5057	carboxypeptidase D	3.42
25	428771	AB028992	Hs.193143	KIAA1063 protein	3.42
	446519	AU078643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.42
	429628	H03604	Hs.13268	ESTs	3.40
	448815	AB033352	Hs.22151	KIAA1226 protein	3.40
	456032	AW951448	Hs.301711	ESTs	3.39
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.39
30	414275	AW970254	Hs.889	Charot-Leyden crystal protein	3.38
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	3.38
	410507	A527282	Hs.29857	ESTs	3.38
	430704	AW813091	Hs.335799	ESTs	3.38
	423600	A8633599	Hs.310359	ESTs	3.38
35	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	3.38
	438178	AW148612	Hs.152475	ESTs	3.37
	417791	AW955339	Hs.111471	ESTs	3.37
	408867	AA437199	Hs.656	cell division cycle 25C	3.37
40	449802	AW901804	Hs.23584	hypothetical protein FLJ20147	3.37
	457003	S78234	Hs.172405	cell division cycle 27	3.36
	458076	BE2081	Hs.164478	hypothetical protein FLJ21539 similar to	3.36
	436203	BE384582	Hs.5076	Homo sapiens cDNA: FLJ22128 fls, clone H	3.36
	418782	A1792648	Hs.14665	ESTs	3.34
	449722	BE280074	Hs.23360	cyclin B1	3.34
45	447584	AA57263	Hs.37244	ESTs	3.34
	451103	RS2804	Hs.25556	DKFZP564D026 protein	3.34
	408812	BE397160	Hs.254763	ESTs, weakly similar to A42442 integrin	3.34
	448305	AA825207	Hs.264915	Homo sapiens cDNA FLJ12908 fls, clone NT	3.34
50	418849	AW474547	Hs.53355	Homo sapiens PIG-M mRNA for mannosyltran	3.33
	450531	AW201532	Hs.203800	ESTs	3.32
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associ	3.32
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zymen)	3.31
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acyl	3.30
55	421037	AU684608	Hs.159353	ESTs	3.30
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.30
	431312	AB020264	Hs.284425	hypothetical protein IMPACT	3.30
	447078	AW885727	Hs.301570	ESTs	3.30
	422408	NA			3.29
60	437044	AU038654	Hs.69517	cDNA for differentially expressed C016 g	3.29
	423126	AA322245	Hs.290165	ESTs	3.28
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.27
	451917	AW091351	Hs.50820	Homo sapiens unknown mRNA	3.27
	419335	AW090146	Hs.284137	hypothetical protein FLJ12988	3.26
65	411078	A220220	Hs.182364	CocosaCrip	3.26
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	3.26
	427119	AW880562	Hs.114574	ESTs	3.26
	409250	NA			3.25
	429044	AD61490	Hs.145527	ESTs	3.25
70	451050	AW537420	Hs.69662	ESTs	3.24
	447425	A1963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	3.24
	410389	AW054049	Hs.8177	ESTs, weakly similar to PRK8; salivary	3.23
	416565	AW002660	Hs.444979	endoplasmic reticulum resident protein 5	3.22
	442028	A239437	Hs.48945	ESTs	3.22
	409110	AA191493	Hs.48778	niban protein	3.22
75	418926	AA232658	Hs.165794	UDP-glucose glycoprotein glucosyltransfer	3.22
	403353	BE438838	Hs.414298	mitochondrial ribosomal protein 5-17	3.21
	445417	AW001058	Hs.12680	Homo sapiens cDNA FLJ10196 fls, clone HE	3.20
	442979	AW440782	Hs.174743	ESTs	3.20
	439292	AA090421	Hs.55555	hypothetical protein MG05347	3.20
80	440953	AB020326	Hs.124135	Homo sapiens cDNA FLJ13951 fls, clone NT	3.20
	447020	T27308	Hs.16908	hypothetical protein FLJ11046	3.20
	451181	AW96330	Hs.207461	ESTs	3.19
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.19

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	411573	AB029000	Hs.70823	KIAA1077 protein	3.19
	424639	U02911	Hs.150402	activin A receptor, type I	3.18
	443179	A926402	Hs.6933	hypothetical protein FLJ12694	3.18
	452545	N31940	Hs.14434	ESTs, Weakly similar to U8022 hypothesis	3.18
	433924	AA573547	Hs.26549	KIAA1708 protein	3.18
	414737	A160386	Hs.125087	ESTs	3.18
	444230	H65537	Hs.146067	ESTs	3.18
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.17
	428945	AJW19203	Hs.98974	ESTs, Weakly similar to S65824 reverse t	3.17
	424095	NM_002914	Hs.135226	replication factor C (activator 1) 2 (40	3.17
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.17
	443598	AJW49970	Hs.14822	ESTs, Weakly similar to 178885 scintoth	3.16
	413516	BE145907	Hs.61886	gp.MR0.H10208-221295-204-e12.H10208 Homo	3.16
	434369	AA871235	Hs.129098	ESTs	3.16
	431322	AW195222	gp.EST382704 MAGE resequencess, MAGK Homo	3.15	
	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransferase	3.15
	453331	A1240665	Hs.8895	ESTs	3.15
	410286	A1739159	Hs.61886	DKFZP586N2124 protein	3.14
	408637	A110280	Hs.301152	Homo sapiens mRNA: cDNA DKFZp434F053 (f	3.14
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.14
	419078	M93119	Hs.89584	insulinoma-associated 1	3.14
	414080	AA135257	Hs.47763	B aggressive lymphoma gene	3.14
	451525	AV001757	Hs.14005	ESTs	3.13
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.13
	433163	AF231338	Hs.222024	transcription factor BMAL2	3.12
	424783	AA913909	Hs.153089	TATA box binding protein (TBP)-associate	3.12
	431370	BE066819	gp.MR0.B10374-225300-001-603.B10374 Homo	3.12	
	437181	A1396015	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	3.12
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.11
	453867	A1929383	Hs.33032	hypothetical protein DKFZp434N185	3.11
	437641	AA811452	Hs.291911	ESTs	3.10
	428651	AF196478	Hs.189401	serpinin A10	3.09
	427927	A1879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.09
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.09
	414569	AF109298	Hs.118259	prostate cancer associated protein 1	3.09
	406633	AW963372	Hs.46677	PR02030 protein	3.09
	405381			NA	3.08
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	3.08
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.08
	434136	AA625004		gp.mR0.B10374-225300-001-603.B10374 Homo	3.07
	423322	US36330	Hs.155637	protein kinase, DNA-activated, catalytic	3.07
	433656	A1364997	Hs.7572	ESTs	3.07
	427043	AA397679	Hs.3991	ESTs	3.06
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.06
	419229	AB827237	Hs.283684	ESTs	3.05
	414718	H95348	Hs.107987	ESTs	3.05
	439737	A1751438	Hs.41271	Homo sapiens mRNA full length insert cDN	3.05
	448587	A1536552	Hs.28338	KIAA1545 protein	3.04
	448595	A3014544	Hs.21572	KIAA0644 gene product	3.04
	407201	H31998	Hs.164265	hypothetical protein FLJ20657	3.04
	423065	R95158	Hs.267130	Homo sapiens, clone MGC-5406, mRNA, comp	3.04
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	3.04
	416198	H27332	Hs.99598	hypothetical protein MGC3338	3.04
	429410	X98104	Hs.201676	H-phase phosphoprotein 10 (U3 small nud	3.04
	432140	AW000404	Hs.272688	hypothetical protein FLJ20297	3.03
	414031	A110684	Hs.7645	fibrinogen, B beta polypeptide	3.03
	446142	A1754993	Hs.145968	ESTs	3.02
	402167			NA	3.02
	402296			NA	3.02
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.02
	419910	AA662913	Hs.150173	ESTs, Weakly similar to A46010 X-linked	3.02
	424001	W67583	Hs.137476	paternally expressed 10	3.01
	413530	M86153	Hs.75818	RAS11K, member RAS oncogene family	3.01
	439924	A985897	Hs.125293	ESTs	3.01
	414343	AL036166	Hs.323378	coated vesicle membrane protein	3.01
	432201	A1338113	Hs.258241	Transmembrane protease, serine 3	3.00
	445845	A1281870	Hs.145555	ESTs	3.00
	402727	H75701	Hs.95866	complement component 4-binding protein,	3.00
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.00
	403637	NA		NA	3.00
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	3.00
	413430	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fls, clone NT	3.00
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fls, clone HE	2.99
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	2.99
	442204	AB335458	Hs.21914	ESTs	2.98
	429682	NM_006206	Hs.211602	SMC1 structural maintenance of chromoso	2.98
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.97
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	2.97
	441826	AW503603	Hs.129915	phosphonesterase related	2.97
	433404		Hs.102720	ESTs	2.96
	450508	NM_004460	Hs.418	(fibrinolytic activation protein, alpha	2.96
	423880	BE278111	Hs.134200	DKFZP564C186 protein	2.96
	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	2.96

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	408155	AB014528	Hs.43133	KIAA0629 gene product	2.96
	424131	AA33714	Hs.199685	ESTs	2.96
	451250	AA491275	Hs.236940	hypothetical protein FLJ12542	2.96
5	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.95
	447829	AA33029	Hs.164104	ESTs	2.95
	410651	BE540255	Hs.6594	Homo sapiens cDNA: FLJ20444 fs, clone H	2.95
	417873	BE266569	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	2.95
	452693	T79153	Hs.45689	zinc finger protein Z28	2.95
	407742	AF166252	Hs.30084	sulfotransferase family, cytosolic, 1C,	2.94
10	421430	AW297555	Hs.97083	Homo sapiens cDNA: FLJ23004 fs, clone L	2.94
	407995	A1094748	Hs.100134	hypothetical protein FLJ2787	2.94
	413281	AA661271	Hs.222024	transcription factor BMAL2	2.94
	452381	H23329	Hs.290980	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.94
	441020	W79283	Hs.35962	ESTs	2.94
15	452397	J04048	Hs.156346	topoisomerase (DNA) II alpha (170kD)	2.94
	420005	AW271106	Hs.133254	ESTs	2.93
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.93
	438602	AF217515	Hs.283532	uncharacterized bone marrow protein EM03	2.93
20	417247	AK060351	Hs.287955	Homo sapiens cDNA: FLJ13300 fs, clone NT	2.93
	443341	AW531480	Hs.8688	ESTs	2.92
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.92
	410144	W07189	Hs.68185	ESTs, Weakly similar to ALR3_HUMAN ADP-R	2.92
	434450	S78664	Hs.87	neuroblastoma-like 1 (p107)	2.92
	450402	BE218027	Hs.89969	ESTs	2.92
25	427026	U80736	Hs.110826	truncated repeat containing 9	2.92
	421562	AA530994	Hs.334471	ghrelin precursor	2.92
	419434	AF1051152	Hs.63668	cell-line receptor 2	2.92
	427655	AJ911812	Hs.119018	transcription factor NFE	2.91
30	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.90
	412416	A1628253	Hs.22580	alkylglycerone phosphate synthase	2.90
	446232	AJ281848	Hs.194691	retinoic acid induced 3	2.90
	454600	AW161001	gc-MRA:ST0124-270300-405-b11 ST0124 Homo	2.90	
	438018	AKC01160	Hs.5999	hypothetical protein FLJ10298	2.90
	433252	AB040957	Hs.151343	KIAA1524 protein	2.90
35	444385	BE363596	Hs.191621	ESTs, Moderately similar to ALU5_HUMAN A	2.89
	443654	A1745185	Hs.8359	yes-associated protein 65 kDa	2.89
	421308	AA680132	Hs.192843	leucine zipper protein FKSG14	2.89
	411643	A1924519	Hs.192570	hypothetical protein FLJ22028	2.89
	418559	Y07828	Hs.91096	ring finger protein	2.89
40	433527	AW235613	Hs.133020	ESTs	2.88
	432274	D35122	Hs.2007	tumor necrosis factor (ligand) superfamily	2.88
	406182	NA	NA	NA	2.88
	432731	R31178	Hs.287820	fibronectin 1	2.88
	429274	A379772	Hs.95006	ESTs	2.87
45	418216	AA862240	Hs.265929	AF15q14 protein	2.87
	410166	AK001376	Hs.59346	hypothetical protein FLJ110514	2.86
	452685	AW838026	Hs.330414	ESTs, Moderately similar to S65657 alpha	2.86
	424696	BE439547	Hs.151903	GriE-like protein cochaperone	2.86
	410174	AA306007	Hs.59451	DKFZP434C245 protein	2.85
	443640	A1872643	Hs.134218	ESTs	2.85
	432912	BE007371	Hs.200313	ESTs	2.85
	431611	U58766	Hs.264428	tissue specific transplantation antigen	2.85
	446955	D13757	Hs.1311	phosphoribosyl pyrophosphate amidotransf	2.85
50	424770	AA425562	Hs.11965	Homo sapiens HICME1IP mRNA, partial cds	2.84
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alpha	2.84
	403639	NA	NA	NA	2.84
	451110	A1955040	Hs.265398	ESTs, Weakly similar to transformation-e	2.84
	416185	A1997581	Hs.47367	KIAA1785 protein	2.84
60	446955	BE613126	Hs.47783	B aggressive lymphoma gene	2.83
	423441	R66649	Hs.278359	absent in melanoma 1 like	2.83
	450584	AA040403	Hs.60071	ESTs	2.83
	420191	AW003565	Hs.152323	Homo sapiens mRNA for FLJ00057 protein,	2.83
	425599	AW066745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83
65	424408	A1754813	Hs.146428	collagen, type V, alpha 1	2.83
	448769	N60037	Hs.38173	ESTs	2.82
	444946	AW119205	Hs.156457	hypothetical protein FLJ22408	2.82
	435347	AW014813	Hs.116963	ESTs	2.82
	438435	AA807142	Hs.42194	hypothetical protein FLJ22649 similar to	2.82
	427687	AW003867	Hs.1570	histamine receptor H1	2.82
	426951	AA393636	Hs.97454	ESTs	2.82
70	427670	AA418187	Hs.330515	ESTs	2.82
	442577	AA202998	Hs.163900	ESTs	2.82
	441016	AW138553	Hs.25845	ESTs	2.81
	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.81
75	417150	N76497	Hs.1787	proteolipid protein 1 (Ptd2:lec: Mezbac	2.81
	409346	A1162066	Hs.54320	hypothetical protein DKFZp762D2095	2.81
	410407	X66539	Hs.63287	carbonic anhydrase IX	2.81
	407137	T97307	Hs.1787	glycylserine(S)-Sarcosine feta liver spleen	2.81
80	435849	BE365242	Hs.160398	claudin 2	2.80
	426695	AW118118	Hs.112729	ESTs	2.80
	428301	AW528656	Hs.58440	ESTs, Weakly similar to 138022 hypophos	2.80
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fs, clone HE	2.80
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	2.80

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	419423	D26488	Hs.90315	KIAA0007 protein	2.78
	452355	N54596	Hs.75072	G protein-coupled receptor 34	2.79
	456266	U97698	Hs.155593	mucin 6, gastric	2.79
	457465	AW301344	Hs.122908	DNA replication factor	2.79
5	476472	BE246138	Hs.30863	ESTs	2.78
	474081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.78
	452851	NM_004450	Hs.159842	glucosaminyl (N-acetyl) transferase 1, c	2.78
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fs, clone HE	2.78
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of B	2.78
10	410001	A8102841	Hs.57856	PTFAIRE protein kinase 1	2.78
	453700	A8103426	Hs.560	acidophorin B mRNA, coding enzyme, ca	2.78
	431250	BE264549	Hs.251377	taxol resistance associated gene 3	2.77
	414043	A1521210	Hs.97977	ESTs	2.77
	418054	NM_002318	Hs.61354	lysyl oxidase-like 2	2.77
15	439223	AW23699	Hs.250618	UL16 binding protein 2	2.76
	425956	M60808	Hs.164568	fibroblast growth factor 7 (keratinocyte	2.76
	437612	AA827715	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	2.76
	428119	W54997	Hs.189917	ESTs	2.76
	455574	AT411122	Hs.101810	Homo sapiens cDNA FLJ14232 fs, clone NT	2.76
20	442339	BE259668	Hs.227591	ESTs, Weakly similar to 15011033a, Leu zip	2.76
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.76
	418217	A1910647	Hs.13442	ESTs	2.76
	420222	AA256253	Hs.120817	ESTs	2.76
	408243	Y00787	Hs.624	interleukin 8	2.75
25	421346	Z34277	Hs.103707	apomucin	2.75
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.75
	425773	N21279	Hs.237749	ESTs	2.75
	440511	A1970384	Hs.197075	ESTs	2.74
30	424827	A1057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fs, clone L	2.74
	448621	A1097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
	428523	AW674540	Hs.98626	ESTs	2.73
	410839	NM_006849	Hs.65261	protein disulfide isomerase	2.73
	437300	AL305777	Hs.112198	Homo sapiens mRNA; cDNA DKFZp547M073 (f	2.73
	424641	AB001106	Hs.151413	g/a maturation factor, beta	2.73
35	431708	A1698136	Hs.108673	ESTs	2.73
	436209	AW859417	Hs.254020	ESTs, Moderately similar to unnamed prot	2.73
	441790	AW294909	Hs.132208	ESTs	2.73
	428862	NM_003346	Hs.2316	SRY (sex determining region Y) box 9 (ca	2.73
40	409506	NM_006153	Hs.54589	NCK adaptor protein 1	2.73
	423482	BE280172	Hs.125258	galactokinase 2	2.72
	417015	M63772	Hs.80876	fibrin containing monooxygenase 3	2.72
	448165	NM_005591	Hs.202379	meiotic recombination (S. cerevisiae) 11	2.72
	448826	A1580252	Hs.293246	ESTs, Weakly similar to putative p150 (H	2.72
	447803	BE620578	Hs.30858	ESTs, Weakly similar to S65657 alpha-1C-	2.72
45	429703	193154	Hs.28705	ESTs	2.72
	447956	AA147829	Hs.301431	endothelial zinc finger protein induced	2.72
	410902	AW809665	Hs.152759	gb-MRA-STO124-261059-015-g07 ST0124 Homo	2.72
	424745	AA214618	Hs.152759	activator of S phase kinase	2.72
50	454469	AW792775	Hs.152759	gc-CMD-UM0001-010305-258-g10 UM0001 Homo	2.72
	458632	AF744445	Hs.167073	Homo sapiens cDNA FLJ13047 fs, clone NT	2.72
	450012	AA307703	Hs.279766	kinesin family member 4A	2.72
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.72
	438006	AA775026	Hs.203802	ESTs	2.72
55	425552	AA902462	Hs.98806	hypothetical protein	2.71
	427038	NM_014533	Hs.173268	KIAA155 gene product	2.71
	402939	AA704875	Hs.44307	ESTs, Moderately similar to 138022 hypot	2.71
	425371	D45441	Hs.155981	mesothelin	2.71
	439857	AA847194	Hs.232002	ESTs	2.71
	455309	AW840117	Hs.232002	gc-ICA-NN0077-150400-012-g04 NN0077 Homo	2.71
60	439580	AF068401	Hs.293847	ESTs, Moderately similar to S65657 alpha	2.70
	437257	A1283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.70
	435039	AW043621	Hs.130526	ESTs	2.70
	438796	V67821	Hs.109550	genehormin 1	2.70
65	407013	U39537	Hs.109550	chitinase nebulin mRNA, partial cds	2.70
	445413	AA151342	Hs.12677	CGI-147 protein	2.70
	419416	U11700	Hs.84499	ATPase, Cu++ transporting, beta polypept	2.70
	441362	BE614410	Hs.23344	RAD51 (S. cerevisiae) homolog (E coli R	2.69
	448045	A1297435	Hs.20165	prostate stem cell antigen	2.69
70	441868	AA400276	Hs.183485	ESTs	2.69
	449076	AE627826	Hs.209109	ESTs	2.69
	427528	AJ077143	Hs.179585	minichromosome maintenance deficient (S.	2.69
	427617	DA2063	Hs.199179	RAV binding protein 2	2.69
	414618	A204600	Hs.96978	hypothetical protein MG3L10764	2.69
75	441350	A8020690	Hs.7782	paraneoplastic antigen MA2	2.68
	419310	AA236233	Hs.188716	ESTs	2.68
	445279	RA1900	Hs.22745	ESTs	2.68
	423741	BE379846	Hs.6904	Homo sapiens mRNA full length insert cDN	2.68
	446692	Z44514	Hs.156829	Homo sapiens mRNA for KIAA1763 protein,	2.68
80	449300	A856959	Hs.227165	ESTs	2.68
	444585	AW170015	Hs.6594	ESTs	2.68
	444384	BE114527	Hs.11065	Homo sapiens HDJME13P mRNA, partial cds	2.68
	448104	AE674818	Hs.316433	Homo sapiens cDNA FLJ11375 fs, clone HE	2.67
	446639	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.67

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	428361	NM_018505	Hs.183858	transcriptional intermediary factor 1	2.57
	418971	AA360392	Hs.87113	ESTs	2.66
	446152	A129036	Hs.150028	ESTs	2.66
	441553	AA281219	Hs.121296	ESTs	2.66
5	403548			NA	2.66
	452699	AW295390	Hs.213062	ESTs	2.66
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-actin	2.66
	453085	NA4545	Hs.251865	ESTs	2.65
	409595	AW103364	Hs.727	inhibin, beta A (activin A, activin Ab a	2.65
10	409446	A551173	Hs.47688	ESTs	2.65
	422094	AF125535	Hs.772027	F-box only protein 5	2.65
	445462	AA378776	Hs.286649	hypothetical protein MGC3077	2.64
	432670	AA806536	Hs.291841	ESTs	2.64
	418634	AK000064	Hs.86995	ATPase, H ⁺ -transporting, lysosomal (vacu	2.64
15	453528	AW243307	Hs.83307	hypothetical protein	2.64
	442171	AW654954	Hs.128899	ESTs	2.64
	416248	H93169	Hs.23450	mitochondrial ribosomal protein S25	2.64
	414631	AW970130	Hs.65406	ESTs	2.64
	422358	BE358949	Hs.131162	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.64
20	413597	AW302885	Hs.117183	ESTs	2.63
	446031	A1271704	Hs.18987	Homo sapiens BAC clone RP11-505D17 from	2.63
	450142	AW207469	Hs.24485	chondroin sulfate proteoglycan 5 (beta	2.63
	436304	AA339622	Hs.108867	ESTs	2.63
	436632	T91829	Hs.14870	Homo sapiens, Similar to hact domain and	2.63
25	449207	AL044222	Hs.23255	nucleoporin 155kD	2.62
	416111	AA033813	Hs.75018	chromatin assembly factor 1, subunit A (2.62
	414747	U35872	Hs.77224	centromere protein P (350kDa), nucleos	2.62
	423811	AW295598	Hs.58095	homeo box CA	2.62
	439474	A1824060	Hs.211501	ESTs	2.62
30	417218	AA005247	Hs.285754	met proto-oncogene (hepatocytic growth fa	2.62
	408031	AA081355	Hs.42173	Homo sapiens cDNA FL10366 fs, clone NT	2.62
	442821	BE391928	Hs.8732	transmembrane protein 4	2.62
	416245	AA088757	Hs.83883	transmembrane, prostatic androgen induc	2.62
35	447917	AL048037	Hs.164588	ESTs, Moderately similar to neuronal th	2.61
	442840	D75987	Hs.153479	extra spindle poles, S. cerevisiae, homo	2.61
	424968	AB060271	Hs.125445	hypothetical protein FLJ12495	2.61
	423055	RS8624	Hs.2186	eukaryotic translation elongation factor	2.61
	433037	NM_014158	Hs.279638	HSPC607 protein	2.61
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.60
40	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.60
	414653	U31116	Hs.77551	carotynogen, beta (43kD dystrophin-associ	2.60
	457233	A1355005	Hs.221698	ESTs	2.60
	418049	A1970536	Hs.16603	hypothetical protein FLJ13163	2.60
	418946	A1958441	Hs.164526	ESTs	2.60
45	441681	AW125145	Hs.126678	ESTs	2.60
	443742	AW627805	Hs.145421	ESTs	2.60
	433668	AA612960	Hs.337300	ESTs	2.60
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.59
	444542	A1617293	Hs.280380	aminopeptidase	2.59
50	452940	AA022722	Hs.2173	acyltransferase 4 (alpha (1,3) glucosy	2.59
	452170	NM_001394	Hs.2339	dual specificity phosphatase 4	2.59
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.59
	401458			NA	2.58
	438016	AA806465	Hs.121538	Human DNA sequence from clone RP11-472E5	2.58
55	403980	AW971504	Hs.122164	diaphanous (Drosophila, homolog) 3	2.58
	441581	BE551408	Hs.127196	ESTs	2.58
	435693	A033134	Hs.119887	ESTs	2.58
	431814	BE256242	Hs.270847	delta-tubulin	2.58
60	446269	AW281355	Hs.14559	hypothetical protein FLJ10540	2.58
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (pur	2.58
	456999	AA319758	Hs.253581	eukaryotic translation elongation factor	2.58
	425234	AW152225	Hs.105699	ESTs, Weakly similar to t38022 hypotheti	2.58
	434423	NM_050769	Hs.3844	UIM domain only 4	2.57
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	2.57
65	433929	A1375499	Hs.273739	ESTs	2.57
	414907	X90725	Hs.77597	pole (Drosophila)-like kinase	2.57
	411789	A7-245525	Hs.72157	DNY-ZP5641922 protein	2.57
	435627	W88774	Hs.118370	ESTs	2.57
70	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	2.57
	432375	BE533609	Hs.2962	S100 calcium-binding protein P	2.57
	424057	A1338974	Hs.126593	ESTs	2.57
	420315	AW114850	Hs.183384	putative 28 kDa protein	2.57
	435663	A023707	Hs.134273	ESTs	2.56
	435277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	2.56
75	427747	AW411425	Hs.180955	serine/threonine kinase 12	2.56
	438182	AW242140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.56
	421102	AA470993	Hs.283805	procalcitonin beta 6	2.56
	445725	AK000956	Hs.13209	hypothetical protein FLJ10094	2.56
	448243	AW369771	Hs.25620	Integrin, beta 8	2.56
80	442881	A0223175	Hs.167022	ESTs	2.56
	422165	AL041159	Hs.1461	histidine decarboxylase	2.56
	425843	BE313280	Hs.159627	death associated protein 3	2.56
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.55

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5	416806	NM_000288	Hs.79953	peroxisomal biogenesis factor 7	2.55
	438113	AA67908	Hs.8882	ESTs	2.55
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	2.55
	448275	BE514434	Hs.20830	kinesin-like 2	2.55
	419987	NM_005014	Hs.94070	osteonectonin	2.55
	439529	ST026	Hs.94070	gh-intein activator factor (human, panc	2.55
	452240	AI991147	Hs.61232	ESTs	2.55
	417806	AI867277	Hs.183733	ESTs	2.55
10	421482	AL135462	Hs.104715	inversion	2.55
	455884	AA054678	Hs.155150	fibronectinase P (14kD)	2.55
	429561	BE614474	Hs.289074	F-box only protein 22	2.55
	411274	NM_002776	Hs.69423	kallikrein 10	2.55
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.54
	446666	NM_014953	Hs.323346	KIAA1008 protein	2.54
15	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 #	2.54
	452778	RT1338	Hs.5921	Homo sapiens cDNA: FLJ121592 lis, clone C	2.54
	430733	AW979920	Hs.283361	ESTs	2.54
	421184	NM_003616	Hs.102436	survival of motor neuron protein intrac	2.54
	435361	AI168596	Hs.111117	ESTs	2.54
20	452833	BE599681	Hs.30736	KIAA0124 protein	2.54
	422330	D30783	Hs.115263	epigruin	2.54
	424962	NM_012288	Hs.153954	TRAM-like protein	2.54
	432654	AA470519	Hs.192417	ghnctH10.5.1 NCG_CGAP_Pr1 Homo sapiens	2.53
25	447178	AW594641	Hs.192417	ESTs	2.53
	411773	NM_006799	Hs.72026	protease, serine, 21 (testis)	2.53
	433671	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.53
	419449	H18417	Hs.57483	Homo sapiens cDNA: FLJ14294 lit, clone PL	2.53
	448019	AW947164	Hs.155641	ESTs, Moderately similar to 138022 hypot	2.52
30	409435	AI810721	Hs.95424	ESTs	2.52
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	2.52
	431386	BE178536	Hs.111930	membrane-spanning 4-domains, subfamily A	2.52
	422314	K01900	Hs.734950	interferon, alpha 6	2.52
	441343	AI970348	Hs.132230	ESTs	2.52
	417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	2.52
35	401747			NA	2.52
	448626	AB020946	Hs.21351	KIAA1023 protein	2.52
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	2.52
	413627	BE182082	Hs.246973	ESTs	2.51
40	441286	NM_002374	Hs.167	microtubule-associated protein 2	2.51
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	2.51
	423537	AA778725	Hs.164549	ESTs	2.51
	443171	BE281128	Hs.9030	TONDU	2.50
	446536	AC002563	Hs.15767	citron (pho-interacting, serine/threonin	2.50
45	420795	AA323037	Hs.128645	sorting nexin 16	2.50
	444582	AS38880	Hs.94812	ESTs	2.50
	445459	AI478629	Hs.158465	healy ortholog of mouse putative ROK re	2.50
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	2.50
	414315	Z24878	Hs.62699	gh:H5865D052 STRATAGENE Human skeletal m	2.50
50	407586	AA740564	Hs.62699	ESTs	2.50
	403911	AW503857	Hs.4007	Sarcotominal-associated protein	2.50
	431571	AW503496	Hs.180610	splicing factor prime/altamine rich (2.50
	433843	AW021423	Hs.112810	ESTs	2.50
	456254	T19844		gh:B711F Heart Homo sapiens cDNA clone B	2.50
55	403137			NA	2.50
	425895	AI269484	Hs.161427	zinc finger protein 215	2.50
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	2.50

TABLE 45B

60	Proy:	Unique Eos probe identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Proy	CAT Number	Accessions
65	410784	1221005_1	AW803201 BE079700 BE062940
	410902	1226078_1	AW809565 AW810108 AW809781 AW809844
	411765	125780_1	H43346 AA248302 AA095182
	413170	1351040_1	BE068819 BE068821 BE068825
	413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145852 BE145856
70	414315	143512_1	Z24878 AA94098 F13654 AA94040 AA143127
	428858	266453_1	AA436780 AW237453 BE327496 N47347 NS6967
	430264	315006_1	AA470516 BE303010 BE302564 BE394120
	431322	331543_1	AW576022 AA503009 AA502098 AA502805 AA502809 T32168
	431438	380572_1	AA625804 AW418787 AW074833 AI675642 AA393368
75	436411	419334_1	AW674352 AA715374 Z25205
	438159	45106_-2	Z83947
	439529	46059_-1	ST3205
	451105	859083_1	AJ761324 AW880941 AW880937
	452453	918300_1	AJ902519 AJ902518 AJ902516
80	454669	1213727_1	AW792775 BE072508 AW792958
	454690	1260077_1	AW810091 AW810052 AW810110 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006
	454821	1236365_1	AW803574 AW809594 AA196522 AW810345 AW810432 AW809960
	455309	1278153_1	AA625804 AW418787 AW074833 AI675642 AA393368
	455309	1278153_1	AW894017 AW893956 AW894032

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409062	AL157498	Hs.59159	Homo sapiens mRNA: cDNA DKFZp564B182 (fr	15.30
402895	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	15.20
415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	15.20
428820	AA436187	Hs.172631	integrin, alpha M (complement component	15.19
410763	AF279145	Hs.8968	hypothetical protein FLJ21776	15.19
436539	A027360	Hs.31409	ESTs	15.10
458997	AW537420	Hs.69662	ESTs	15.00
432731	R31178	Hs.287820	fibronectin 1	14.90
459247	H46243	Hs.110373	ESTs, Highly similar to T42626 secreted	14.70
451909	RS2795	Hs.25854	interleukin 13 receptor, alpha 2	14.70
452242	RS0956	Hs.155993	glycocytoconscience	14.70
428427	M86699	Hs.169840	TTK protein kinase	14.50
439524	A1985897	Hs.125293	ESTs	14.45
414869	AA157291	Hs.21479	ubiquitin 1	14.40
411571	A029000	Hs.70823	KIAA1077 protein	14.40
418693	A1750876	Hs.87409	thrombospondin 1	14.37
421823	N40850	Hs.28625	ESTs	14.30
423903	M57765	Hs.1721	interleukin 11	14.20
419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	14.10
447417	AW732858	Hs.143067	KIAA1602 protein	13.96
416406	D68961	Hs.79299	lipoma HMGIC fusion partner-like 2	13.90
446392	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain	13.90
412863	AA121673	Hs.59757	zinc finger protein 281	13.80
453509	AA001616	Hs.84591	ESTs	13.80
440953	A1683036	Hs.124135	Homo sapiens cDNA FLJ13051 fs, clone NT	13.80
432415	T16971	Hs.283014	ESTs, Weakly similar to A05332 mucin 2 p	13.60
428769	AW207175	Hs.106771	ESTs	13.60
415292	AA179233	Hs.42290	nasopharyngeal carcinoma susceptibility	13.60
424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	13.41
438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fs, clone PL	13.40
431958	X83629	Hs.2877	cothrinin 3, type 1, P-cadherin (placenta	13.30
430972	M32063	Hs.1718	ab-Human H19 RNA gene, complete cds.	13.26
432368	AW970244	Hs.162188	ESTs	13.19
424806	AA382523	Hs.105689	MSTP031 protein	13.16
440351	AF330833	Hs.7179	RAD1 (S. pombe) homolog	13.08
437789	AI581344	Hs.12782	ESTs, Weakly similar to T17330 hypotheti	12.98
447164	AF208541	Hs.17518	Homo sapiens cys5 mRNA, partial sequence	12.90
417412	X16896	Hs.82112	interleukin 1 receptor, type I	12.80
402363	NA	NA	NA	12.78
444301	AK000136	Hs.10760	asporin (LRR class 1)	12.75
416783	AA205186	Hs.79889	monocyte to macrophage differentiation-a	12.65
435706	W31254	Hs.7045	GLD4 protein	12.50
414618	A104600	Hs.96078	hypothetical protein MG010764	12.50
439737	A1751438	Hs.41271	Homo sapiens mRNA full length insert cDN	12.49
405770	NA	NA	NA	12.46
419879	NM_001327	Hs.167370	carcinoembryon antigen	12.45
414132	A1801235	Hs.48480	ESTs	12.40
410434	AF061152	Hs.63668	tol-like receptor 2	12.30
451082	A1027268	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	12.26
407891	AA488620	Hs.41135	endomucin-2	12.20
450506	NM_004460	Hs.418	lipotelectin activation protein, alpha	12.01
411213	AA679930	Hs.69285	neuropilin 1	12.00
436476	AA326108	Hs.33829	bHLH protein DEC2	12.00
413382	AW295647	Hs.71331	hypothetical protein MG05350	11.90
449318	AW228021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	11.90
401747	NA	NA	NA	11.88
409619	AK001015	Hs.55220	BCL2-associated athanogene 2	11.84
432696	AJ224741	Hs.278451	myosin 3	11.80
402298	AK032279	Hs.61635	six transmembrane epithelial antigen of	11.73
425668	U48361	Hs.159223	NGF-A binding protein 2 (ERG1 binding p	11.72
407938	AA905007	Hs.85050	phospholamban	11.70
419948	AB041035	Hs.93847	NADPH oxidase 4	11.70
459645	AA074346	Hs.200715	ESTs	11.51
438462	A624122	Hs.89578	general transcription factor TFIH, polytype	11.50
434851	AA806164	Hs.116502	ESTs	11.50
418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	11.47
413453	AA128640	Hs.128065	ESTs	11.40
440228	A0239437	Hs.48495	ESTs	11.40
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	11.39
453313	BE005771	Hs.153746	hypothetical protein FLJ2499	11.20
421633	AF121680	Hs.106280	sorting nexin 10	11.20
410339	AW19449	Hs.294268	ESTs	11.20
448111	AA053486	Hs.20315	interferon-induced protein with tetratri	11.15
453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.15
430217	N47863	Hs.336901	ribosomal protein S24	11.10
452823	AB012124	Hs.38696	transcription factor-like S (basic helix	11.10
416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	11.06
415854	H40164	Hs.80296	Purkinje cell protein 4	10.90
447072	BE1594	Hs.17279	tyrosin (protein sulfotransferase 1	10.90
424882	A337945	Hs.153626	for upstream element (PUS2) binding prot	10.80
444693	AW004654	Hs.208320	hypothetical protein FLJ23537	10.80
408750	BE294069	Hs.93561	hypothetical protein FLJ10512	10.80
450221	AA328102	Hs.24641	cytochrome associated protein 2	10.80

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5	436411	AW574352		gb.baf3c97.y1 NH ₂ MGC_12 Homo sapiens cD	10.80
	441693	AA304673	Hs.7943	RFPS-mediating protein	10.80
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	10.80
	441801	AW424799	Hs.86366	ESTs	10.80
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentin)	10.80
	415727	BE501389	Hs.20348	ESTs, Weakly similar to APAF_HUMAN APOPT	10.80
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14408 fs, clone HE	10.80
	421650	AA781795	Hs.122587	ESTs	10.80
10	436999	AA115911	Hs.65339	ras homology gene family, member E	10.70
	421814	L12230	Hs.108623	thrombospondin 2	10.69
	415060	L1223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	10.67
	421462	AF016495	Hs.104624	aquaporin 9	10.66
	104444	W73484		gb.z054604.s1 Sources_filed heart_NH419W	10.61
	420743	N46721	Hs.183506	hypothetical protein FLJ14213	10.60
15	446142	AT754693	Hs.145968	ESTs	10.60
	444114	TS8003	Hs.10323	Homo sapiens mRNA from chromosome 5q31-3	10.60
	422020	AA383092	Hs.1600	replication protein A3 (144D)	10.55
	433891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	10.50
20	417352	AA195919		gb.z059009.s1 Stratiopae muscle 937209 H	10.46
	417666	AW067903	Hs.82772	collagen, type X, alpha 1	10.42
	427718	AT796680	Hs.25933	ESTs	10.40
	412689	P26660	Hs.24305	ESTs	10.40
	433322	A3567347	Hs.44698	Homo sapiens clone TCCTCA00151 mRNA sequ	10.40
25	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.30
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.30
	409044	A1129586	Hs.33033	hypothetical protein FLJ14623	10.30
	423600	AB533559	Hs.310359	ESTs	10.30
	433819	AW511097	Hs.112765	ESTs	10.18
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	10.10
30	410503	AW975746	Hs.189862	KIAA1702 protein	10.10
	433800	A034361	Hs.135150	lung, type I cell membrane-associated gly	10.10
	429357	AA779725	Hs.164689	ESTs	10.00
	452638	U65011	Hs.30743	preferentially expressed antigen in meta	10.00
35	414117	W88559	Hs.1787	proteolipid protein 1 (Pellicaeus-Merzbac	10.00
	410198	H27332	Hs.95958	hypothetical protein MGC5338	10.00
	413918	AW015698	Hs.71245	ESTs	10.00
	400570	NA		NA	10.00
40	439333	AW384710	Hs.125258	Homo sapiens cDNA FLJ17395 fs, clone TH	9.97
	444963	AW384082	Hs.104679	serine (or cysteine) proteinase inhibit	9.93
	450101	AV649980	Hs.24305	Human hsc407 mRNA sequence	9.90
	434352	AF129505	Hs.86492	small muscle protein, X-linked	9.90
	453160	AI263307	Hs.239884	H2B histone family, member L	9.90
	433929	AJ375499	Hs.27379	ESTs	9.89
45	413273	U75679	Hs.75257	stem-loop (histone) binding protein	9.81
	437536	X01221	Hs.144448	ESTs	9.80
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	9.80
	452291	AF015592	Hs.28853	CDCT (cell division cycle 7, S. cerevisi	9.80
	438913	AI380429	Hs.172445	ESTs	9.80
50	417849	AW201587	Hs.82713	nuclein 2	9.76
	424086	AI351010	Hs.102257	lysyl oxidase	9.72
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	9.70
	414422	AA147224	Hs.337232	ESTs	9.70
	419197	N49921	Hs.27441	KIAA1615 protein	9.70
55	427690	AT141320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone C	9.70
	449347	AV649748	Hs.295901	KIAA0493 protein	9.70
	409643	AW450866	Hs.257359	ESTs	9.70
	435209	AW850417	Hs.254020	ESTs, Moderately similar to unnamed prot	9.70
	439616	AW664696	Hs.301732	hypothetical protein MGC5336	9.60
60	430290	AT734110	Hs.138356	ESTs	9.60
	447124	AW976438	Hs.17428	BDP1-like protein	9.60
	413879	AA139661	Hs.212533	Homo sapiens cDNA: FLJ22572 fs, clone H	9.60
	426101	AW968034	Hs.125073	CDCT-related protein kinase 7	9.58
	418067	AT127958	Hs.83393	cystatin EM	9.54
	424001	W67883	Hs.137476	paternally expressed 10	9.50
65	443037	AW503035	Hs.299166	synaptin 7	9.50
	426483	AK001745	Hs.184626	hypothetical protein FLJ10883	9.50
	420170	U43374	Hs.98531	Human normal keratinocyte mRNA	9.50
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	9.50
	443162	T49951	Hs.9029	DKF ZP4346032 protein	9.45
70	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	9.43
	424076	AT786255	Hs.137676	ribosomal protein L34 pseudogene 1	9.40
	440052	AT633744	Hs.195648	ESTs, Weakly similar to C80222 hypothe	9.40
	403137	NA		NA	9.37
75	418051	AW192536	Hs.19479	ESTs	9.35
	416701	AA814948	Hs.96243	ESTs, Weakly similar to ALUC_HUMAN III	9.30
	430291	AW660345	Hs.238126	CGI-49 protein	9.30
	426137	AL040683	Hs.167031	DKF ZP566D133 protein	9.30
	400195	NA		NA	9.30
80	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fs, clone NI	9.20
	423936	U77629	Hs.135539	achalae-sculle complex (Drosophila) homol	9.20
	414259	W44633	Hs.301296	Homo sapiens cDNA FLJ23131 fs, clone L	9.20
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	9.20
	405543	NA		NA	9.20

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	420900	AL046533	Hs. 41269	ESTs	9.11
	450757	BE081050	Hs. 31370	ESTs, Weakly similar to KIAA1324 protein	9.10
	410929	HA1723	Hs. 30543	ESTs	9.10
5	427319	AW631495	Hs. 27135	B-cell receptor associated protein BAP29	9.10
	432745	AB039670	Hs. 9728	ALEX1 protein	9.10
	436574	AK253537	Hs. 126465	ESTs	9.10
	407192	AA692000	gb:af12602.1 Soares_testis_NHT Homo sap	9.08	
	426075	AW513691	Hs. 270149	ESTs, Weakly similar to 2109260A B cell	9.07
10	408778	A500519	Hs. 63382	hypothetical protein PR02714	9.00
	434542	AA769310	Hs. 61760	hypothetical protein FLJ13164	9.00
	404440		NA	NA	9.00
	407168	RS4575	Hs. 117183	ESTs	9.00
	451678	AA374181	Hs. 26799	DKFZP564D074 protein	9.00
	431946	A018336	Hs. 131730	ESTs	9.92
	408075	NM_015424	Hs. 41684	DKFZP43M168 protein	8.90
	409928	AL137163	Hs. 57549	hypothetical protein dJ47304	8.90
	430254	A1538226	Hs. 32976	guanine nucleotide binding protein 4	8.89
	454929	AF196481	Hs. 12256	midline 2	8.86
20	442717	RB3362	Hs. 160591	ESTs, Weakly similar to T23975 hypothe	8.80
	400909	NM_014781	Hs. 59421	KIAA0203 gene product	8.80
	419261	X07875	Hs. 89791	wingless-type MMTV integration site fami	8.80
	416190	NS4000		gh:yy9402.1 Soares_multiple sclerosis_	8.77
	444783	AK001468	Hs. 62180	anilin (Drosophila Scaps homology), act	8.60
25	415440	AB22912	Hs. 79335	Homo sapiens, similar to SWI5H-related	8.76
	421262	AA206746	Hs. 5343	Homo sapiens cDNA FLJ14265 fs, clone PL	8.70
	441031	A110584	Hs. 7645	fibronectin, B beta polypeptide	8.70
	452234	AW084176	Hs. 223296	ESTs, Weakly similar to 138022 hypothe	8.70
	452822	XB5589	Hs. 238617	hypothetical protein FLJ22521	8.70
	430462	AS584156	Hs. 105640	Homo sapiens, clone IMAGE:4139775, mRNA,	8.65
30	426457	AW894667	Hs. 169965	chimerin (chimerin) 1	8.65
	412054	W87482	Hs. 302209	ESTs	8.64
	450235	AW162998	Hs. 24664	KIAA1375 protein	8.63
	419782	A1792648	Hs. 14865	ESTs	8.60
	452631	A1188658	Hs. 87496	ESTs	8.60
35	425258	AB07883	Hs. 180059	Homo sapiens cDNA FLJ20653 fs, clone KA	8.60
	432014	H86741	Hs. 38540	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.60
	440270	NM_015986	Hs. 7120	cystine receptor-like molecule 9	8.60
	414784	NM_000344	Hs. 288966	survival of motor neuron 1, telomeric	8.60
40	426809	BE313114	Hs. 29706	ESTs	8.60
	419704	AA429104	Hs. 45057	ESTs	8.60
	452095	NM_015308	Hs. 30585	porexin 1	8.60
	432639	AW973785		gb:EST385886 MAGE sequences. MAGM Homo	8.60
	430418	R98852	Hs. 36029	heart and neural crest derivatives expre	8.58
45	450480	XB2125	Hs. 25040	zinc finger protein 239	8.58
	444984	H15474	Hs. 132898	fatty acid desaturase 1	8.58
	419086	NM_000216	Hs. 85591	Katmann syndrome 1 sequence	8.57
	430518	AW363687	Hs. 82916	chaperonin containing TCP1, subunit 6A (8.50
	424735	U31875	Hs. 272499	short-chain alcohol dehydrogenase family	8.50
50	414061	NM_000399	Hs. 300280	amylase, alpha 2A; pancreatic	8.50
	407894	AJ278313	Hs. 41143	phosphoserine-specific phosphatase	8.50
	441079	AW150697	Hs. 107418	ESTs	8.50
	419354	M62839	Hs. 1252	apolipoprotein H (beta-2-glycoprotein I)	8.50
	418618	U66097	Hs. 86724	GTP cyclohydrolase 1 (dopa-responsive dy	8.50
55	415555	AW002090	Hs. 180398	endoplasmic reticulum resident protein 5	8.50
	441540	C03467	Hs. 127128	ESTs	8.50
	415434	AW163045	Hs. 79334	nuclear factor, interleukin 3 regulated	8.50
	417801	AA417383	Hs. 82582	integrin, beta like 1 (with EGF-like rep	8.50
	420885	AL117427	Hs. 172778	Homo sapiens mRNA, cDNA DKFZp566P013 (fr	8.48
	430515	AJ278111	Hs. 195262	putative tumor antigen	8.43
60	416315	AA1179483	Hs. 73605	ESTs	8.42
	408432	AW195262		gb:u67b05.x1 NCL_GCAP_CM.1 Homo sapiens	8.40
	410094	BF147897	Hs. 58953	general transcription factor IIF, polype	8.40
	415198	AA234938	Hs. 97364	ESTs	8.36
65	448920	AWA08009	Hs. 22580	alkylglycerone phosphate synthase	8.36
	410305	AF030409	Hs. 62185	solute carrier family 9 (sodium/hydrogen	8.31
	408687	AL110280	Hs. 301152	Homo sapiens mRNA, cDNA DKFZp434F053 (fr	8.30
	427707	NM_065578	Hs. 180398	UIM domain containing preformed transloc	8.30
	450660	H89244	Hs. 303227	heterogeneous nuclear ribonucleoprotein	8.30
70	451957	AF196320	Hs. 10299	Homo sapiens cDNA FLJ13545 fs, clone PL	8.30
	443677	AL120986	Hs. 150627	ESTs, Weakly similar to 138022 hypothe	8.30
	457997	AA806616	Hs. 205523	ESTs	8.30
	451934	AI540642	Hs. 61082	ESTs	8.30
	404335		NA	NA	8.30
	445073	AW291389	Hs. 13055	hypothetical protein FLJ13520	8.30
75	431566	AF176012	Hs. 206720	UIM domain containing protein 1	8.29
	446307	T50053	Hs. 9094	ESTs	8.28
	423928	AA332680		gb:EST35768 Embryo, 8 week.1 Homo sapien	8.26
	436420	AA443966	Hs. 31595	ESTs	8.25
	426110	NM_002913	Hs. 165663	replication factor C (activator 1) 1 (14	8.25
80	442988	A0026130	Hs. 131683	ESTs	8.25
	402408		NA	NA	8.24
	438707	U08239	Hs. 5326	amino acid system N transporter 2, porcu	8.23
	425770	NM_014363	Hs. 155492	spastic ataxia of Charlevoix-Saguenay (s	8.22

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	448704	AW080932	Hs.243247	heterogeneous nuclear protein similar to progesterone membrane binding protein	8.71
	452582	AA456193	Hs.5071	signal transducer and activator of trans	8.20
	411984	NM_005419	Hs.72988	proprotein convertase subtilisin/tin	8.20
5	420018	U56387	Hs.94316	proprotein convertase subtilisin/tin	8.20
	437548	AA743240	Hs.11582	ESTs	8.20
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.20
	447066	BE167667	Hs.32163	ESTs	8.20
	425932	M81650	Hs.1968	semenogelin I	8.20
10	431819	AA515995	Hs.152304	kinesin-like 5 mitotic kinesin-like pro	8.20
	431810	HS1155	Hs.270845	gb.am0303.x1 Striatum schizo brain S1	8.20
	459702	A1204995	Hs.272620	pregnancy specific beta-1-glycoprotein 9	8.18
	408687	M31126	Hs.110855	ESTs	8.17
	413109	AW398445	Hs.152252	SW/SNF related, matrix associated, acti	8.16
15	424720	M89907	Hs.281070	ESTs	8.10
	424335	AW021508	Hs.11325	ESTs	8.10
	453096	AW294631	Hs.180612	peroxisomal membrane protein 3 (350D, Zs	8.10
	427738	NM_000318	Hs.126931	ESTs	8.10
	457796	AA513369	Hs.159429	Homo sapiens mRNA; cDNA DKFZp434M0216 (f	8.10
20	425340	N35538	Hs.168950	Homo sapiens mRNA; cDNA DKFZp434M046 (f	8.10
	445165	AV652831	Hs.56044	ESTs	8.06
	418046	W49670	Hs.188554	Heterochromatin-like protein 1	8.04
	426269	H15302	Hs.188554	ESTs	8.04
	439451	AF066270	Hs.188554	ESTs	8.02
	419559	Y07829	Hs.188554	ESTs	8.00
25	405268	AA625304	Hs.17731	hypothetical protein FLJ12892	8.00
	447207	AA442233	Hs.17731	ESTs	8.00
	446077	AW063613	Hs.156798	ESTs	8.00
	424685	AW107223	Hs.75295	guanylate cyclase 1, soluble, alpha 3	8.00
	407013	U35637	Hs.75295	gb:Human nebulin mRNA, partial cds	7.99
30	414523	AL076633	Hs.76353	serine (or cysteine) proteinase inhibito	7.98
	440637	AW900115	Hs.7309	Homo sapiens clone Z3741 mRNA sequence	7.96
	410776	AW673454	Hs.63286	ESTs, Moderately similar to ALU1_HUMAN A	7.95
	425821	NM_007231	Hs.162211	scute carrier family 6 (neurotransmitte	7.94
	415565	RS9946	Hs.184852	KIAA1553 protein	7.92
35	453331	A1240665	Hs.8895	ESTs	7.92
	446527	W36694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	7.90
	417316	AW063937	Hs.12891	ESTs	7.90
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	7.90
	444769	AI191650	Hs.221436	ESTs	7.90
40	444772	A1138596	Hs.154619	ESTs	7.90
	425264	AA353953	Hs.20269	ESTs, Weakly similar to gonadotropin ind	7.90
	412642	BE244598	Hs.805	hepatocyte growth factor (hepatopietin A	7.90
	453765	BE799901	Hs.35091	hypothetical protein FLJ10775	7.90
45	421568	AB011125	Hs.105749	KIAA0553 protein	7.90
	446444	AI143737	Hs.24370	ESTs	7.90
	420000	AB036083	Hs.54282	pc3-inducible ribonucleotide reductase s	7.86
	473237	BE513073	gb:s01171435F1 NIH_MGC_15 Homo sapiens c	7.86	
	408582	R27430	Hs.271565	ESTs	7.84
50	419235	AW470411	Hs.288453	neuritin	7.83
	435620	AA438727	Hs.124045	ESTs, Weakly similar to A46010 X-linked	7.82
	441690	R81733	Hs.33106	ESTs	7.80
	417735	AA188175	Hs.82506	KIAA1254 protein	7.80
	441795	N58115	Hs.21137	AD024 protein	7.80
55	442992	A1014659	Hs.13287	ESTs	7.80
	422554	AA312219	Hs.296338	ESTs	7.80
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	7.80
	428627	BE002593	Hs.187660	putative Rab6 GDP/GTP exchange factor ho	7.80
	422228	A153533	Hs.337138	ESTs	7.80
60	429399	AA452244	Hs.16727	ESTs	7.80
	436396	A1683487	Hs.152213	wingless-type MMTV integration site fami	7.77
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hypercalcaemia	7.76
	429396	AW954958	Hs.201626	Homo sapiens clone Z2015 mRNA sequence	7.75
	453439	A1574138	Hs.23076	guanine nucleotide binding protein 4	7.75
65	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 ts, clone H	7.71
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	7.71
	428655	H05769	Hs.188757	Homo sapiens, clone MGC-5564, mRNA, comp	7.70
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	7.70
	404696		NA	NA	7.70
70	418947	W52990	Hs.22860	ESTs	7.70
	427401	U20582	Hs.2149	actin like protein	7.70
	410748	BE363816	Hs.12532	chromosome 1 open reading frame 21	7.70
	425782	AI92141	Hs.196270	kinase transposon carrier	7.70
	446955	AW613138	Hs.156747	ESTs	7.70
75	449199	AG90122	Hs.196988	ESTs	7.70
	443212	AW769515	Hs.102500	hypothetical protein FLJ20481	7.70
	446155	AS53695	Hs.159422	Homo sapiens cDNA FLJ13997 ts, clone Y7	7.70
	427164	AB037721	Hs.173671	KIAA1300 protein	7.70
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	7.70
	452588	AA889120	Hs.110637	homeo box A10	7.70
80	451838	AW005866	Hs.193990	ESTs	7.67
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	7.66
	451227	R84429	Hs.151944	ESTs, Weakly similar to high-risk human	7.66
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ1280 ts, clone MA	7.65

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	425202	AW962282	Hs.152049	ESTs, Weakly similar to 380222 hypoteti	7.20
	433764			NA	7.20
	416896	A152862	Hs.5638	KIAA1572 protein	7.20
	416636	N32536	Hs.42545	ESTs	7.20
5	428071	AF212848	Hs.182339	etc homologous factor	7.20
	450742	AF070459	Hs.24485	chromatin sulfate proteoglycan 5 (hama	7.18
	451017	BE091847	Hs.181173	hypothetical protein MGC10771	7.17
	409759	N40285	Hs.81182	histamine N-methyltransferase	7.16
10	452448	AW182440	Hs.61369	ESTs, Weakly similar to unnamed protein	7.16
	437951	AB29125	Hs.43545	ESTs	7.16
	407938	AF05508	Hs.312078	ESTs, Weakly similar to A9019 dynein lbc	7.15
	419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	7.12
	411759	AB94575	Hs.27207	KIAA0982 protein	7.11
15	430355	NM_006219	Hs.239818	phosphoinositide-3-kinase, catalytic, bc	7.10
	415511	AA429750	Hs.75113	general transcription factor IIA	7.10
	409032	AW301807	Hs.297280	ESTs	7.10
	424539	L02911	Hs.150402	activin A receptor, type I	7.10
	439221	AA737106	Hs.32250	ESTs, Moderately similar to 178855 serin	7.10
20	430719	AA48988	Hs.293795	ESTs	7.10
	430020	AA127940	Hs.57811	ESTs	7.10
	420218	AW958037	Hs.286	ribosomal protein L4	7.10
	443487	A1073491	Hs.259887	ESTs, Highly similar to KPBB_HUMAN PHOSP	7.10
	414855	AA157155	Hs.274414	hypothetical protein FLJ14457	7.10
25	428724	AL250128	Hs.191268	KIAA1530 protein	7.10
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	7.10
	419125	AB101444	Hs.135276	ESTs	7.09
	430744	AL038564	Hs.59517	cDNA for differentially expressed CO15 g	7.09
	433730	AK092135	Hs.3542	hypothetical protein FLJ11270	7.07
30	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	7.07
	457019	AA421844	Hs.12830	hypothetical protein	7.07
	405997	AB018348	Hs.55947	KIAA0805 protein	7.06
	400977	NA		NA	7.06
	430968	AA831857	Hs.209071	ESTs	7.03
35	451684	AF216751	Hs.25813	CDA14	7.03
	404029			NA	7.02
	448719	AA033527	Hs.21858	truncotide repeat containing 3	7.02
	445577	NA0696	Hs.137064	cytosplasmic polyadenylation element bind	7.00
	419647	AA348947	Hs.59186	hypothetical protein	7.00
40	440705	AW136928		gb.UH-H-B1-asp-0-08-0-U1.s1 NCL-CGAP_Su	7.00
	429598	AA811257	Hs.259710	ESTs	7.00
	450332	AW970602	Hs.126421	ESTs	7.00
	427389	AA531291	Hs.101054	Homo sapiens cDNA FLJ12777 fs, clone NT	7.00
	453931	AL121278	Hs.25144	ESTs	7.00
45	432343	NM_002960	Hs.2961	S100 calcium binding protein A3	7.00
	452679	AW167599	Hs.232282	ESTs	7.00
	431695	AA259684	Hs.257819	protein phosphatase 1, regulatory (inhib	7.00
	413583	AL120806	Hs.5888	ESTs	7.00
	436758	AW977167	Hs.155272	ESTs	7.00
50	455944	BE160543		gpPw1-IT0422-291299-002-03 HT0422 Homo	6.98
	433332	AL137502	Hs.238679	Rag D protein	6.96
	437613	R19892	Hs.10267	MIL I protein	6.95
	440524	R71254	Hs.16798	ESTs	6.95
	451047	AB022317	Hs.25887	sama domain, immunoglobulin domain (lg),	6.93
55	453377	AB003091	Hs.74313	KIAA1265 protein	6.93
	457396	Z22964	Hs.320817	DKFZ2047E1010 protein	6.87
	417393	R10484	Hs.82071	Cbp/p300-interacting transactivator, wit	6.92
	414417	BE299433	Hs.68533	KIAA1679 protein	6.92
	412246	AF150873	Hs.69233	zinc finger protein	6.90
	411003	AA181018	Hs.133056	hypothetical protein FLJ13920	6.90
60	413833	Z15005	Hs.75573	centromere protein E (312x0)	6.90
	405595	NA		NA	6.90
	431589	AA305688	Hs.267955	UDP-GalNAc4GlcNAc beta 1,3-galactosyltr	6.90
	414429	RS1494	Hs.71818	ESTs	6.90
65	424541	AB001106	Hs.151413	glia maturation factor, beta	6.90
	418895	AA894638	Hs.14600	ESTs	6.90
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	6.90
	446006	NM_064403	Hs.13530	deathness, autosomal dominant 5	6.90
	432038	AA524746	Hs.152110	ESTs	6.87
70	446510	AV559433	Hs.282594	ESTs, Weakly similar to 380222 hypoteti	6.86
	451285	AW139789	Hs.15370	Homo sapiens cDNA FLJ11652 fs, clone HE	6.85
	408915	NM_016951	Hs.48950	hepatocellular carcinoma novel gene-3 pro	6.85
	416934	TE3846	Hs.191115	ESTs	6.82
	435143	R12375	Hs.194600	ESTs	6.82
	442660	AW138174	Hs.130651	ESTs	6.81
75	432729	AK000292	Hs.278732	hypothetical protein FLJ20895	6.82
	435990	AD11562	Hs.131793	ESTs	6.80
	449832	AL272268	Hs.22958	calcium channel, voltage-dependent, alph	6.80
	453688	AW381270	Hs.194110	hypothetical protein PRO2730	6.80
80	421475	AW953805	Hs.21887	ESTs	6.80
	430510	AW152915	Hs.241575	hypothetical protein PRO2577	6.80
	405945	AA153582	Hs.50094	Homo sapiens mRNA, cDNA DKFZ343A0851 f	6.80
	410298	AB593821	Hs.182185	ESTs	6.80
	402660	AW207748	Hs.59115	ESTs	6.80

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	427752	AA470687	Hs.104772	ESTs	6.80
	414080	AA133257	Hs.47783	B aggressive lymphoma gene	6.80
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	6.80
5	416913	AW534714		gb.RC1-DT0001-031259-011 DT0001 Homo	6.80
	426990	AA393167	Hs.41294	ESTs	6.80
	411773	NM_006799	Hs.72026	proteasome, some, 21 (testis)	6.80
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.79
	437619	AW351491	Hs.534853	hypothetical protein FLJ23544	6.79
	434267	AJ206589	Hs.116243	ESTs	6.79
10	419358	T78763	Hs.90063	neurocalcin delta	6.79
	433854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	6.78
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	6.77
	443184	AI639728	Hs.131973	ESTs	6.77
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	6.77
	429483	AA574532	Hs.728708	ESTs	6.76
	425605	BE54C300	Hs.7076	KIAA1705 protein	6.76
	429045	AW553186	Hs.92400	ESTs	6.76
	438776	AW245243	Hs.334368	hypothetical protein MGC11257	6.75
20	458174	AA781530	Hs.127236	hypothetical protein FLJ12879	6.74
	445129	R38876	Hs.21394	ESTs	6.74
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE3682908, mRNA	6.73
	444442	AI149234	Hs.256423	ESTs, Moderately similar to IS4374 gene	6.73
	431240	AA496790	Hs.179481	ESTs	6.72
	427109	S73265	Hs.1473	gastrin-releasing peptide	6.70
25	416555	AW968613	Hs.79428	BCL2adenovirus E1B 19kD-interacting pro	6.70
	423811	AW295958	Hs.50895	homo box CA	6.70
	443995	AW204099	Hs.337720	ESTs, Weakly similar to AF126780 1 retin	6.70
	426586	AI590399	Hs.40762	ESTs	6.70
	419574	AK001989	Hs.91165	hypothetical protein	6.70
	418269	AA806113	Hs.189025	ESTs	6.70
	434184	AW207019	Hs.148135	sarcomothrombin kinase 33	6.70
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4269 lent	6.70
	433370	AK701923	Hs.139336	ATP-binding cassette, sub-family C (CFTR	6.70
	409506	NM_006153	Hs.54589	NCK adaptor protein 1	6.70
30	454029	W05150	Hs.37304	homo box A5	6.70
	413365	AW205188	Hs.124304	Homo sapiens cDNA FLJ14635 fs, clone NT	6.70
	447247	AW365351	Hs.297355	Homo sapiens cDNA FLJ13090 fs, clone NT	6.70
	426566	AF131536	Hs.170453	tropomodulin	6.70
	446261	AA313893	Hs.306219	hypothetical protein FLJ12615 similar to	6.70
40	408547	AA574291	Hs.57837	ESTs	6.70
	430456	AA783300	Hs.225768	ESTs, Weakly similar to I38022 hypotheti	6.70
	419527	BE162802	Hs.246973	ESTs	6.70
	410498	AA355749	gb.ES164459 Jurkat T-cells V1 Homo sapie	6.70	
	434015	AA844518	Hs.300676	hypothetical protein FLJ13386	6.70
45	453691	HI12235	Hs.276505	ESTs	6.68
	415928	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.68
	415885	DT9983	Hs.78894	KIAA0161 gene product	6.68
	406529	AW410458	Hs.5258	chromosome 11 open reading frame2	6.68
50	438242	AW241910	Hs.122554	ESTs, Weakly similar to JX0369 collagen	6.68
	442643	UB2756	Hs.5551	PRP4/ATKWD splicing factor	6.67
	424802	X79201	Hs.153221	synovial sarcoma, translocated to X chro	6.67
	415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	6.67
	456714	R20916	Hs.202501	ESTs	6.66
	414891	AF608833	Hs.55992	ESTs, Weakly similar to ALU8_HUMAN ALU S	6.65
55	433960	AB040866	Hs.83975	KIAA1533 protein	6.65
	406268	NA		NA	6.63
	453180	NA6243	Hs.110373	ESTs, Highly similar to T42626 secreted	6.62
	403973	NA		NA	6.60
	436862	AB21940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	6.60
60	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypoth	6.60
	453387	AF990741	Hs.252809	ESTs	6.60
	424084	AF640675	Hs.20914	hypothetical protein FLJ23056	6.60
	418444	AF802889	Hs.85155	butyrate response factor 1 (EGF-response	6.60
	448172	N75276	Hs.135804	ESTs	6.60
65	409571	AA504249	Hs.187565	ESTs	6.60
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	6.60
	430701	AF168833	Hs.293971	ESTs	6.60
	430373	AB151780	Hs.337282	ESTs	6.60
	415384	AA490866	Hs.39429	ESTs	6.60
70	429828	AB019494	Hs.225767	IDN3 protein	6.60
	441761	AF228880		gb.np4c06.x1 NCL_CGAP_CoII Homo sapiens	6.60
	411046	AF001742	Hs.67991	hypothetical protein DKF2p4430522	6.60
	421111	AF295047	Hs.43532	ESTs, Weakly similar to T20177 hypotheti	6.60
75	407424	AF120493		gb.Homo sapiens elastase 1 precursor (EL	6.59
	412396	AW947995	Hs.79078	gb.FM1-MT0010-200300-001-110 MT0010 Homo	6.57
	416209	AA236776	Hs.79078	MAO2 (mitotic arrest deficient, yeast, h	6.57
	405674	AA332152	Hs.288036	tRNA isopentenylpyrophosphate transferas	6.57
	400600			NA	6.56
80	457893	AA744292	gb.m51d05.x1 NCL_CGAP_Py18 Homo sapiens	6.55	
	426108	AA822037	Hs.165468	programmed cell death 5	6.54
	422133	AA9612779	Hs.333151	Homo sapiens lymphatic carcinoma relat	6.54
	421044	AF061971	Hs.311736	Human DNA sequence from clone RP1-238D15	6.54
	414136	AA812434	Hs.115023	SMC2 (structural maintenance of chromoso	6.53

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5	400351	AF060169	Hs.272369	Homo sapiens AS11 protein mRNA, partial	6.52
	413670	AB000115	Hs.75470	hypothetical protein, expressed in vitro	6.52
	410416	BE410072	Hs.63304	protein phosphatase methyltransferase-1	6.50
	419852	AW503756	Hs.286184	hypothetical protein dJ5102.5	6.50
	419677	N77342	Hs.21851	Homo sapiens cDNA FLJ12900 fs, clone NT	6.50
10	413306	AF186114	Hs.270237	tumor necrosis factor (ligand) superfamily	6.50
	429774	AB22215	Hs.50993	KIAA1804 protein	6.50
	428228	AA424352	Hs.210586	ESTs	6.50
	418134	AA397769	Hs.86617	ESTs	6.50
	403855	NA		NA	6.50
15	422704	AA972147	Hs.132275	ESTs	6.50
	416737	AF154335	Hs.79691	LIM domain protein	6.50
	429854	RS5508	Hs.99472	ESTs	6.50
	422572	X12784	Hs.119129	collagen, type IV, alpha 1	6.49
	435000	BE24211	Hs.119120	ubiquitin ligase SMURF1	6.48
20	454835	AW833763		gb:QV4-TT0006-130100-077-410 TT0008 Homo	6.48
	434603	AF147384		gb:Homo sapiens full length insert cDNA	6.48
	408243	Y00787	Hs.624	interleukin 8	6.48
	423177	AA831552	Hs.269016	Homo sapiens cDNA: FLJ21243 fs, clone C	6.47
	451316	AT770011	Hs.206310	ESTs	6.46
25	448339	AL035920	Hs.20538	RNA binding motif, single stranded inter	6.46
	433423	BE407127	Hs.8997	heat shock 70KD protein 1A	6.44
	410338	AW075168	Hs.133337	ESTs, Weakly similar to unnamed protein	6.44
	434025	AF114264	Hs.216381	Homo sapiens clone H44025 unknown mRNA	6.42
	440526	AB32243	Hs.214711	ESTs	6.42
30	432727	AA305233	Hs.278712	eukaryotic translation initiation factor	6.41
	433009	AA761668		gln2c24c08.x1 NC2_CGAP_GCE1 Homo sapiens	6.40
	433762	NW453	Hs.285737	Homo sapiens cDNA: FLJ20096 fs, clone A	6.40
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fs, clone PL	6.40
	407162	N6385	Hs.142634	zinc finger protein	6.40
35	446152	AL292036	Hs.150528	ESTs	6.40
	422828	AL133396	Hs.121281	p10n protein 2 (nucle)	6.40
	418966	TE8754		gb:U1507.x1 Stratagene lung (G37210) H	6.40
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	6.40
	429039	AI524793	Hs.301897	ESTs	6.40
40	447254	NM_004153	Hs.173808	origin recognition complex, subunit 1 (y	6.40
	431159	AA688879	Hs.118648	ESTs	6.40
	429625	AA455568	Hs.193614	ESTs	6.40
	430180	AA331406	Hs.75456	A kinase (PRKA) anchor protein 10	6.40
	408420	NM_006915	Hs.44766	reitinins pigmenica 2 (x-linked recessi	6.40
45	426572	AB003763	Hs.178623	hypothetical protein FLJ11183	6.40
	449811	AI262106	Hs.12653	ESTs	6.40
	440105	AA694010	Hs.6932	Homo sapiens clone Z3809 mRNA sequence	6.40
	440395	AA884412	Hs.216342	ESTs	6.37
	429100	X78565	Hs.289114	hexabrachion (hexascin C, cytolactin)	6.37
50	417771	AA804698	Hs.82547	retinoic acid receptor responder flazaro	6.36
	417092	H97508	Hs.181165	eukaryotic translation elongation factor	6.36
	412227	AW902282		gb:QV3-NN1023-260400-169-g10 NN1023 Homo	6.36
	408845			NA	6.36
	403546	NA		NA	6.36
55	412345	AW938386		gb:FM4-DT0057-201299-002-G10 DT0057 Homo	6.35
	422186	AW962364	Hs.129051	ESTs	6.34
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	6.34
	417687	AB285596	Hs.250691	ESTs	6.33
	426223	AW077812	Hs.130391	ESTs	6.32
60	417588	Z44510		gb:U5C220091 normalized infant brain cDN	6.32
	432629	AW860548	Hs.280658	ESTs	6.31
	440495	AA887212	Hs.14161	hypothetical protein DKFZp4341930	6.31
	407711	AL138272	Hs.62713	ESTs	6.31
	417517	AF001176	Hs.82738	POP4 (processing of precursor, S. cerev	6.30
65	431041	AA490967	Hs.195955	KIAA0704 protein	6.30
	445571	A0378000	Hs.158489	Weakly similar to Z184_HUMAN ZINC	6.30
	433309	AA807080	Hs.126568	ESTs	6.30
	415659	W27214	Hs.78547	zinc finger protein (clone 647)	6.30
	420771	AI954365	Hs.42892	ESTs	6.30
70	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.30
	400950	NA		NA	6.30
	428652	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypophos	6.30
	439813	AA646321	Hs.124501	ESTs	6.30
	449444	AW818436	Hs.233590	solute carrier family 16 (monocarboxylic	6.30
75	453596	AA441038	Hs.62905	hypothetical protein FLJ14834	6.30
	446047	TS1454	Hs.62945	Homo sapiens cDNA: FLJ21930 fs, clone H	6.30
	435820	AA700580	Hs.189000	ESTs	6.30
	452576	AB023177	Hs.29900	KIAA0960 protein	6.30
	448924	AW450669	Hs.186399	ESTs	6.30
80	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	6.30
	412591	BE217736	Hs.252653	ESTs, Weakly similar to T28845 hypophos	6.30
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	6.30
	419088	AI538323	Hs.52620	integrin, beta 8	6.30
	401424			NA	6.30
	412189	RS0982	Hs.22581	ESTs	6.30
	435501	AW051819	Hs.129908	KIAA0501 protein	6.30
	408221	AA912183	Hs.47447	ESTs	6.28

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413943	AW054416	Hs.144687	Homo sapiens cDNA FLJ12581 fs, clone NT	6.28
416845	H55279	Hs.144687	gbyd2062.s1 Soares fetal liver spleen	6.27
402732	NA	NA	NA	6.26
413224	A1732470	Hs.191157	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.24
415642	U19878	Hs.336224	transmembrane protein with EGF-like and	6.24
440284	BE502240	Hs.35552	hypothetical protein FLJ23343	6.24
419548	AW978142	Hs.376248	Homo sapiens cDNA: FLJ22071 fs, clone H	6.23
453880	A803166	Hs.28462	ESTs, Weakly similar to U80222 hypothetical	6.22
422675	BE018517	Hs.119140	eukaryotic translation initiation factor	6.22
413384	NM_00401	Hs.753334	exonuclease (multipipe) 2	6.21
445584	AF217158	Hs.6360	PTD012 protein	6.21
461065	AW25132	Hs.222231	ESTs, Weakly similar to granule cell m	6.21
420807	AA280627	Hs.67846	ESTs	6.20
421155	H87879	Hs.102257	lysozyme	6.20
414121	AA358752	Hs.334624	hypothetical protein FLJ14825	6.20
440209	H05049	Hs.22769	neurexin 3	6.20
408170	AW204516	Hs.31835	ESTs	6.20
433590	N98410	Hs.48354	Homo sapiens regulator of G-protein sign	6.20
442906	AK57814	Hs.270272	ESTs	6.20
420617	AK001652	Hs.59423	ATP-dependent RNA helicase	6.20
402343		NA	NA	6.20
432682	A1376400	Hs.159580	ESTs	6.20
452109	A1525873	Hs.61164	hypothetical protein FLJ14909	6.20
429564	A018130	Hs.21374	ESTs	6.20
417256	U84332	Hs.81791	tumor necrosis factor receptor superfam	6.20
435525	A1831297	Hs.123310	ESTs	6.20
413604	R51767	Hs.119140	gbyd3y311.1 Soares infant brain 11B H	6.20
425305	AA363025	Hs.155572	Human clone Z3801 mRNA sequence	6.20
443285	A1301918	Hs.334264	ESTs	6.20
446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	6.20
451027	AW512924	Hs.40808	ESTs	6.20
452243	AL355715	Hs.28555	programmed cell death 9	6.19
429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	6.17
424060	XG2108	Hs.138629	H.sapiens mRNA for subtelomeric repeat s	6.17
432494	AA551060	Hs.4024	gbyd4/402.s1 NC_CGAP_Sch1 Homo sapiens	6.16
448186	AA262105	Hs.91747	Homo sapiens cDNA FLJ14205 fs, clone NT	6.16
419538	W4504	Hs.15474	profilin 2	6.14
445596	W25950	Hs.14512	D1P8 protein	6.13
433036	AA574091	Hs.105964	ESTs	6.13
457155	AL110243	Hs.187991	DNF2P554A122 protein	6.13
443715	A1583187	Hs.3700	gbyd1 E1	6.13
422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	6.12
453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fs, clone NT	6.11
424897	D63216	Hs.153584	fizzled-related protein	6.11
429180	A3011171	Hs.198037	KIAA0559 protein	6.11
434084	AW977850	Hs.23856	hypothetical protein MGCS297	6.10
413339	A1818080	Hs.194290	ESTs	6.10
453685	AL110309	Hs.194290	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.10
421195	BE444650	Hs.130017	ESTs	6.10
453296	AA034413	Hs.62560	ESTs	6.10
444985	A1677737	Hs.28329	hypothetical protein FLJ14005	6.10
423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	6.10
419841	BE005848	Hs.7328	ESTs	6.10
429190	H10850	Hs.328602	ESTs	6.10
426116	AA868729	Hs.144694	ESTs	6.10
451441	AA017601	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	6.10
401740		NA	NA	6.10
441953	H11695	Hs.322290	disruptor of plating 10	6.10
401464	AF039241	Hs.3028	histone deacetylase 5	6.10
405033		NA	NA	6.10
410743	AA089474	Hs.272153	ESTs	6.10
454758	AW845266	Hs.24790	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.10
417728	AW133437	Hs.24790	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.10
418553	T88954	Hs.24790	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.09
431617	AK000738	Hs.24790	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.08
455608	BE011437	Hs.24790	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.08
450755	AA010384	Hs.159464	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.07
455217	AW867534	Hs.159464	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.07
437179	AA393508	Hs.300642	serologically defined colon cancer anti	6.06
408622	AA056080	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	6.06
415308	F05251	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	6.06
428417	AK001659	Hs.184227	F-box only protein 21	6.05
425501	AW043782	Hs.293616	ESTs	6.03
431077	AF69133	Hs.115560	hypothetical protein FLJ12810	6.03
403040		NA	NA	6.02
445704	AA93742	Hs.165210	ESTs, Moderately similar to U80222 hypot	6.02
415637	R25517	Hs.165210	gbyd4/402.s1 16699-003-B08 C10031 Homo	6.02
427925	N51323	Hs.255925	Homo sapiens, clone IMAGE:3448993, mRNA	6.02
404702	NA	NA	NA	6.02
433183	AF231338	Hs.222024	transcription factor BMAL2	6.01
437782	T78028	Hs.154679	synaptotagmin 1	6.01
443633	AJ64108	Hs.135125	ESTs	6.01
422253	AA307639	Hs.129908	KIAA0591 protein	6.00

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420609	AI640551	Hs.88878	Homo sapiens cDNA: FLJ23536 fls, clone L	6.00
407612	U95403	Hs.37142	eglin-A5	6.00
450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	6.00
453853	AL040600	Hs.188083	ESTs	6.00
444188	AI393165	Hs.6599	poplhy/psyl/ isoverase B (cyclophilin	6.00
451813	NM_016117	Hs.27182	phospholipase A2 activating protein	6.00
422505	AL120862	Hs.124165	ESTs	6.00
420734	AW972872	Hs.293736	ESTs	6.00
452082	BE148180		gb:RC4-IT0232-211059-011-e04 HT0232 Homo	6.00
444200	AA327113	Hs.140957	ESTs	6.00
447432	AW958473	Hs.301957	nucle (nucleoside diphosphate linked mol	6.00
419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	6.00
428412	AA428240	Hs.126983	ESTs	6.00
407790	AI027274	Hs.288941	Homo sapiens cDNA: FLJ14966 fls, clone PL	6.00
428545	AW152803	Hs.109074	ESTs, Weakly similar to S55924 reverse 1	6.00
431878	AA521707	Hs.270022	ESTs, Weakly similar to ALU4_HUMANALU S	6.00
425282	AW163518	Hs.155455	huntingtin interacting protein 2	6.00
401053			NA	6.00
411561	AW667875		gb:NR0-SN0040-050500-003-011 SN0040 Homo	6.00
411800	N39342	Hs.103042	microtubule-associated protein 1B	5.99
446925	AW974605	Hs.175699	ESTs	5.98
401708	NA		NA	5.98
445894	AF001578	Hs.24129	CLL7 protein	5.98
403278	NA		NA	5.96
455212	AW666330		gb:QV4-SN0024-080406-157-e01 SN0024 Homo	5.95
410116	AW630671	Hs.59636	squamous cell carcinoma antigen recogniz	5.96
441271	AA927290	Hs.130462	ESTs	5.95
404072			NA	5.95
431596	T34708	Hs.272927	Set23 (G. cerevisiae) homolog A	5.94
421622	AB037748	Hs.106204	KIAA1327 protein	5.93
441300	R35083	Hs.181535	ESTs	5.92
455117	AF208555	Hs.13830	hypothetical protein	5.91
428659	AB955345	Hs.25425	ESTs	5.91
443767	BE562136	Hs.9736	proteasome (prosome, macropain) 26S subu	5.91
440510	H08427	Hs.309155	ESTs, Weakly similar to ISHUS protein d	5.90
414777	BE466904		gb:h2803.x1 NCL_GGAP_GG6 Homo sapiens	5.90
451686	AA052246	Hs.110293	ESTs	5.90
438032	BE045624	Hs.152992	ESTs	5.90
450470	Z75330	Hs.286148	stromal antigen 1	5.90
430533	AA480886	Hs.201552	ESTs, Weakly similar to T17289 hypotheti	5.90
423562	AL048314	Hs.260709	ESTs	5.90
451742	T77609	Hs.117970	arkynin 2, neuronal	5.90
431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	5.90
412537	AL031778	Hs.7397	nuclear transcription factor Y, alpha	5.90
447233	AF746333	Hs.17801	Homo sapiens, clone IMAGE3307015, mRNA,	5.90
410804	U64870	Hs.66521	Nachtscho-Joseph disease (spino-cellular	5.90
452519	AW298597	Hs.61884	Homo sapiens, clone IMAGE428025, mRNA,	5.90
433885	N29882	Hs.44104	ESTs	5.90
453403	BE486639	Hs.61779	Homo sapiens cDNA: FLJ13591 fls, clone PL	5.90
448743	AB032952	Hs.21095	KIAA1135 protein	5.90
447153	AA805202	Hs.315582	ESTs	5.90
457593	AA363946	Hs.20969	ESTs	5.90
404632			NA	5.90
443354	AB008524	Hs.14912	KIAA2085 protein	5.90
452240	AI591147	Hs.61732	ESTs	5.90
410424	AA084984		gb:zn11a08.r1 Stratigene hNT neuron (837	5.90
404170			NA	5.89
458390	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN HII	5.89
408296	AL117452	Hs.44155	DNFZP58651517 protein	5.88
444406	AI147237	Hs.300697	immunoglobulin heavy constant gamma 3 (G	5.87
413894	BE177983		gb:RC3-HT0600-230300-021-g to HT0600 Homo	5.87
453922	AF053306	Hs.360708	bedding uninhibited by benzimidazoles 1	5.86
446700	AW206257	Hs.156325	Human DNA sequence from clone RP11.145L2	5.86
443377	AF792547	Hs.133292	ESTs	5.86
419162	AA234591	Hs.304123	ESTs	5.85
429508	AA628980	Hs.152731	down syndrome critical region protein DS	5.84
428650	AI560456	Hs.107319	ESTs	5.84
437410	AW023340	Hs.14880	ESTs	5.84
428303	AW974476	Hs.183601	regulator of G-protein signaling 16	5.84
401004			NA	5.83
414504	AW059181	Hs.115175	sterile alpha motif and leucine zipper c	5.83
410379	BE151480		gb:RCB-HT0295-071199-011-e01 HT0295 Homo	5.82
404576	BE154142	Hs.96833	ESTs	5.82
438352	BE614347	Hs.169615	hypothetical protein FLJ20089	5.81
423057	AW961597	Hs.130816	ESTs, Moderately similar to 138022 hypot	5.80
423250	HS6585	Hs.198308	lysophosphatidic acid protein	5.80
413048	M63221	Hs.75182	mammalian receptor, C type 1	5.80
451367	AA923729	Hs.26322	cell cycle related kinase	5.80
418647	AA226198		gb:nc25a07.1 NCL_GGAP_P11 Homo sapiens	5.80
421589	AW954177	Hs.82919	cdh5	5.80
427969	NM_001963	Hs.2230	epidermal growth factor (beta-oncogen	5.80
451406	AI694320	Hs.6795	ESTs, Weakly similar to T17248 hypotheti	5.80
436095	H55931	Hs.269582	ESTs	5.80

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	443363	AA02659	Hs.133255	ESTs	5.80
	457244	AA581385	Hs.152473	ESTs, Weakly similar to 1380222 hypothetical	5.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.80
5	440688	AA040591	Hs.147440	ESTs, Weakly similar to Z192, HUMAN ZINC	5.80
	445745	AB007924	Hs.13245	KIAA0455 gene product	5.80
	405637	NA		NA	5.80
	415293	RA9462	Hs.106541	ESTs	5.80
	440404	AJ015881	Hs.324527	mitochondrial ribosomal protein S5	5.80
10	427227	AW771958	Hs.175437	ESTs, Moderately similar to PCA2591	5.80
	423395	AA205613	Hs.175437	gb:EST25922 Cerebellum II Homo sapiens c	5.80
	410555	U92549	Hs.64311	a disintegrin and metalloproteinase domain	5.80
	416900	RB2342	Hs.79856	ESTs, Weakly similar to Z55657 alpha-1C-	5.80
	422108	AA297914	Hs.111749	postmeiotic segregation increased [S. ce	5.80
15	430618	AJ311928	Hs.111749	gb:gb0904x1 NC1_CGAP_K05 Homo sapiens	5.80
	444749	AJ190672	Hs.65926	ESTs	5.80
	417515	LA2403	Hs.82237	ataxia-telomerase group D-associated	5.79
	456192	D64109	Hs.80248	RNA-binding protein gene with multiple s	5.78
	411253	AW833897	Hs.220538	gb:OVO-TT0009-111595-055-067 TT0009 Homo	5.78
20	417219	AW973473	Hs.220538	ESTs	5.78
	409450	AW628650	Hs.517500	hypothetical protein FLJ13164	5.76
	412013	AA400753	Hs.43761	ESTs, Weakly similar to A46010 X-linked	5.76
	425566	AW162943	Hs.250618	UL 16 binding protein 2	5.75
	417877	AJ025829	Hs.86120	ESTs	5.75
	437114	AA536441	Hs.153085	ESTs	5.75
25	421238	AB033101	Hs.102795	Homo sapiens cDNA FLJ10708 fl, clone NT	5.74
	428959	AF100779	Hs.194680	WNT11 inducible signaling pathway protein	5.73
	415209	F00183	Hs.172004	bin	5.73
	429522	Z91530	Hs.226117	H1 histone family, member 0	5.72
30	429022	AA256283	Hs.120817	ESTs	5.71
	431485	BE621320	Hs.257486	hypothetical protein FLJ20062	5.71
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	5.71
	434276	AF123659	Hs.53905	leucine zipper, putative tumor suppressor	5.71
	436085	RS2518	Hs.7987	ESTs	5.70
35	444379	N99035	Hs.222657	ESTs	5.70
	401348	NA		NA	5.70
	428678	AA435864	Hs.48926	ESTs	5.70
	422564	A114806	Hs.221120	ESTs	5.70
	425650	BE077084	Hs.335432	ESTs	5.70
40	408384	BE144344	Hs.7589	ESTs, Weakly similar to A46010 X-linked	5.70
	404948	AA078643	gb:7P08B01 Chromosome 7 Placental cDNA L	5.70	
	421165	AA355407	Hs.102206	potassium inwardly-rectifying channel, s	5.70
	432931	AW581935	Hs.141440	Homo sapiens mRNA, cDNA DKFZ4341079 (fr	5.70
	432903	AA448530	Hs.8453	KIAA1587 protein	5.70
45	442029	AW556698	Hs.144556	neural precursor cell expressed, develop	5.70
	451922	BE463995	Hs.211633	ESTs	5.70
	407808	AA632559	Hs.279789	histone deacetylase 3	5.70
	428161	M99954	Hs.162741	TLA1 cytotoxic granule-associated RNA-bi	5.70
	413430	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fl, clone NT	5.70
50	428223	AA424313	Hs.98402	ESTs	5.70
	427972	AA504870	Hs.181304	putative gene product	5.70
	412963	NM_005429	Hs.79141	vascular endothelial growth factor C	5.70
	416319	AJ815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	5.70
	458044	AW679114	Hs.326135	ESTs	5.70
55	422911	AW807634	Hs.279739	putative zinc finger protein NY-REN-34 a	5.70
	411543	A124519	Hs.192570	hypothetical protein FLJ22028	5.70
	408867	AA437199	Hs.656	cell division cycle 25C	5.70
	428679	AA431765	gb:zbw80c03.s1 Soares_testis_NHT Homo sap	5.70	
	428827	W68418	Hs.30715	potassium voltage-gated channel, Isk-rel	5.70
60	420570	AA148720	Hs.161263	ESTs	5.70
	457441	BE467737	Hs.146125	ESTs	5.70
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	5.70
	420192	AA256281	Hs.105040	ESTs	5.69
	423642	BE000831	Hs.23637	Homo sapiens cDNA FLJ11812 fl, clone HE	5.69
65	454511	AW648146	gb:RCD-MT0013-280300-031-e02 MT0013 Homo	5.68	
	419586	AB084885	Hs.144759	ESTs, Weakly similar to 1380222 hypothetical	5.67
	416777	AF146760	Hs.79344	DKFZP564M1416 protein	5.67
	435849	BE335242	Hs.16098	claudin 2	5.67
	451882	AA744389	gb:gb1et10.s1 NC1_CGAP_P18 Homo sapiens	5.66	
70	450191	AW137243	Hs.222446	ESTs	5.66
	438553	AW188099	Hs.131813	ESTs	5.65
	422910	AJ265058	Hs.121591	Human DNA sequence from PAC 257A7 on chr	5.66
	453504	AW504168	Hs.252706	Homo sapiens, clone MGC:15605, mRNA, com	5.66
75	445302	AK001537	Hs.12468	hypothetical protein FLJ10675	5.65
	446080	AJ221741	Hs.117777	ESTs	5.65
	425474	Z48054	Hs.158084	peroxisome receptor 1	5.65
	423542	AW083920	Hs.16098	claudin 2	5.65
	446983	AA157484	Hs.97199	complement component C1q receptor	5.65
	420898	AB002379	Hs.100113	KIAA0381 protein	5.65
80	401372		NA	NA	5.64
	428541	AJ925270	Hs.299214	Homo sapiens, clone IMAGE:282225, mRNA	5.63
	425249	A05422	Hs.158352	nucleophorin protein 1	5.63
	459705	BE062764	Hs.270252	ESTs, Weakly similar to androgen recepto	5.63
	451863	AL120634	Hs.305923	ATPase, Ca++ transporting, plasma membra	5.62

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	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	5.62
	401183		NA	NA	5.62
	426029	AW294138	Hs.255277	ESTs	5.61
5	443462	AW064690	Hs.171176	ESTs	5.61
	447102	BE163434	Hs.98471	ESTs, Weakly similar to 118712 hypothel	5.60
	419159	122819	Hs.48940	TEK tyrosine kinase, endothelial (venous	5.60
	444577	A1207721	Hs.11393	RAD51 (S. cerevisiae) homolog C	5.60
	423605	AF047826	Hs.126887	cadherin 19, type 2	5.60
10	413447	AW969388	Hs.10450	Homo sapiens cDNA: FLJ22063 fls, clone H	5.60
	442597	A1949562	Hs.43387	ESTs	5.60
	424295	A1631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	5.60
	430679	RA4428	Hs.22801	ESTs	5.60
	449358	AA001229	Hs.131436	ESTs	5.60
	418348	A1537167	Hs.95322	hypothetical protein FLJ23560	5.60
15	433133	AB127249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.60
	444059	RE6743	Hs.116774	Integrin, alpha 1	5.60
	438157	AW137011	Hs.49576	ESTs	5.60
	428233	A358831	Hs.20578	ESTs	5.60
	434265	AA494511	Hs.130554	Homo sapiens cDNA: FLJ23089 fls, clone L	5.60
20	451652	AA018968	Hs.133536	ESTs	5.59
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.59
	447591	A1875417	Hs.282655	ESTs	5.58
	411958	AA767382	Hs.193417	ESTs	5.57
	438146	Z39847	Hs.67948	ESTs	5.57
25	413595	AW236215	Hs.16145	ESTs	5.57
	422406	AF025441	Hs.116206	Opa-interacting protein 5	5.56
	426529	D25259	Hs.319844	ESTs, Moderately similar to 154374 gene	5.56
	439582	WY9161	Hs.118327	Homo sapiens cDNA FLJ115122 fls, clone HE	5.56
	408744	AW806177		gb:MR1-UM0108-130400-003-d04 UM0108 Homo	5.56
30	447230	AW972147	Hs.101395	hypothetical protein MGC11352	5.54
	428956	AA436735	Hs.183171	hypothetical protein FLJ22002	5.54
	446813	AA971436	Hs.162118	KIAA0503 protein	5.53
	451424	A1862026	Hs.302810	Novel human gene mapping to chromosome 20	5.53
35	410516	BE337917	Hs.90034	hypothetical protein FLJ21916	5.53
	453994	BE180564	Hs.165590	ribosomal protein S13	5.53
	435583	AA767714	Hs.291627	ESTs	5.52
	431585	BE242803	Hs.262923	hypothetical protein FLJ10326	5.51
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	5.51
	427966	R97130	Hs.189969	ESTs	5.51
40	433811	AK0327692	Hs.3446	mitogen-activated protein kinase kinase	5.51
	401244		NA	NA	5.50
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	5.50
	434006	AF113688		gb:Homo sapiens clone FLB4630	5.50
45	426650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.50
	427507	AF244637	Hs.178152	toll-like receptor 7	5.50
	425868	BE386898	Hs.131152	ESTs, Weakly similar to ALU5_HUMAN ALU S	5.50
	405065	NA	NA	NA	5.50
	444302	AI140115	Hs.225130	ESTs	5.50
50	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	5.50
	435866	AJ291132	Hs.151498	ESTs	5.50
	438279	AA806166	Hs.154762	HIV-1 rev binding protein 2	5.50
	427189	H82453	Hs.5635	ESTs	5.50
	415283	AA548033	Hs.130853	ESTs	5.50
55	441818	A1530451	Hs.7976	KIAA0232 protein	5.50
	407834	AW084991	Hs.26100	ESTs	5.50
	404012	NA	NA	NA	5.50
	449532	AB754444	Hs.263024	ESTs	5.50
	423760	AA775891	Hs.191980	ESTs	5.50
60	431578	BE16655	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	5.50
	423172	R15652		gb:HH503-F Adult heart, Coriell Hsomo sa	5.50
	422295	AF051151	Hs.114408	toll-like receptor 5	5.50
	429044	A261490	Hs.126527	ESTs	5.50
	435280	AA581404	Hs.280032	Homo sapiens cDNA FLJ14135 fls, clone MA	5.50
65	414323	NM_014759	Hs.334688	KIAA0273 gene product	5.50
	405511	NA	NA	NA	5.49
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	5.48
	434434	AA532516	Hs.157201	ESTs	5.48
	421987	R66740	Hs.110613	KIAA0220 protein	5.48
	410276	A1554545	Hs.68301	ESTs	5.47
70	435867	AA594229	Hs.114052	ESTs	5.47
	453837	AL136387		Incubated viral AP repeat-containing 7 (liv	5.47
	409617	BE003760	Hs.552095	Homo sapiens mRNA, cDNA DKFZp434K0514 f	5.47
	430387	AWG72884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.47
	401629	NA	NA	NA	5.46
75	433071	BE150229	Hs.281954	retinal outer segment membrane protein 1	5.46
	426247	R14426	Hs.286194	ESTs	5.46
	418049	AA211467	Hs.190488	Homo sapiens, Similar to nuclear localiz	5.45
	418247	R55174		gb:y87h04.1 Soares infant brain 1N18 H	5.45
80	453716	AA037675	Hs.152675	ESTs	5.44
	431157	AB239691	Hs.126768	ESTs	5.44
	426873	AI190540	Hs.131092	ESTs	5.43
	437092	AA744252		gb:ny51d05.s1 NCL_CGAP_P118 Homo sapiens	5.42
	445782	AAW407672	Hs.315367	Homo sapiens, Similar to hypothetical pr	5.42

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	447393	A137458	Ha.158831	EST	5.42
	425283	AA354338	Ha.131100	ESTs	5.42
	401208	NA	NA	NA	5.42
	430536	A809163	Ha.9908	nitrogen fixation cluster like	5.42
5	405523			NA	5.42
	409012	AL117435	Ha.49725	DKFZP434B216 protein	5.41
	429803	W81489	Ha.223025	RAB31, member RAS oncogene family	5.41
	436982	AB015305	Ha.5378	spondin 1, (I-spondin) extracellular mat	5.40
	422892	AA988176	Ha.121553	hypothetical protein FLJ120641	5.40
10	456027	BE127387	Ha.13913	NAA1577 protein	5.40
	411897	AW579566	Ha.326876	Homo sapiens SDOX mRNA, complete cds	5.40
	449689	AF286421	Ha.23889	DKFZP554A032 protein	5.40
	423865	A1753709	Ha.152484	ESTs, Weakly similar to 138022 hypochel	5.40
	402248	AW854832		gb:CV2.CT2061-201069.011.405 C16261 Homo	5.40
15	418516	NM_205218	Ha.85701	phosphorocollase-3-kinase, catalytic, al	5.40
	423289	N17774		gh:yz53e01.r1 Soares_multiple_sclerosis_	5.40
	453365	AA035211	Ha.17404	ESTs	5.40
	406485			NA	5.40
	441558	AW173339	Ha.135665	ESTs	5.40
20	432907	BE319103	Ha.324667	ESTs	5.40
	440570	A1205712	Ha.126998	ESTs	5.40
	445062	A1339915	Ha.44324	ESTs	5.40
	421639	NM_012032	Ha.106309	Fkcd of GATA2	5.40
	419408	A156703	Ha.1456	glycerol kinase	5.40
25	419539	AW530803	Ha.89497	lamin B1	5.40
	426010	AA135663	Ha.1975	hypothetical protein FLJ121007	5.40
	400750	NA	NA	NA	5.40
	424550	AJW578156	Ha.250824	Homo sapiens cDNA: FLJ23435 fs, clone H	5.40
30	414998	NM_002543	Ha.77729	oxidized low density lipoprotein [lecin	5.39
	433384	A1021992	Ha.124244	ESTs	5.38
	428781	AF154759	Ha.153364	putative 28 kDa protein	5.38
	438150	AA037534	Ha.79059	transforming growth factor, beta recepto	5.38
	408639			NA	5.38
	425485	NM_006207	Ha.170040	platelet-derived growth factor receptor-	5.37
	424205	AA335925		gb:EST.A11732 Endometrial tumor Homo sapie	5.36
	459596	H20954	Ha.113871	ESTs	5.36
	402534	AW993556	Ha.205914	spoxy (Drosophila) homolog 4	5.36
	414547	T47770	Ha.191463	ESTs	5.35
	419551	AA287987	Ha.13477	ESTs, Weakly similar to 1207285A reverse	5.35
40	411945	AL033527	Ha.92137	v-myc avian myelocytomatosis viral oncog	5.34
	425764	AW999509	Ha.112572	Homo sapiens cDNA: FLJ14130 fs, clone MA	5.34
	405552			NA	5.33
	448030	N30714	Ha.325950	membrane-spanning 4-domains, subfamily A	5.32
	424284	BE541008	Ha.6193	hypothetical protein FLJ14590	5.32
	427141	AW753185	Ha.160528	dynamitin 1-like	5.31
45	426021	AW770997	Ha.34392	ESTs, Weakly similar to 138022 hypochel	5.31
	442186	AJ984083	Ha.269746	ESTs, Weakly similar to T03306 PSD-95/SA	5.30
	437319	BE410598	Ha.56405	Homo sapiens cDNA: FLJ13545 fs, clone PL	5.30
	405287	NA		NA	5.30
50	427032	AF012023	Ha.173274	integrin cytoplasmic domain-associated p	5.30
	415371	R15239		gb:Y81802.r1 Soares infant brain 118B H	5.30
	420024	AA252905	Ha.194477	E3 ubiquitin ligase SMURF2	5.30
	434408	AA011771	Ha.132506	ESTs	5.30
	434739	AA804487	Ha.144130	ESTs	5.30
55	421327	AA537255	Ha.188802	ESTs	5.30
	453058	AW6112293	Ha.288664	Homo sapiens cDNA: FLJ11750 fs, clone HE	5.30
	448776	BE302464	Ha.30057	MRS2 (S. cerevisiae)-like, magnesium hom	5.30
	417845	AL117461	Ha.82719	Homo sapiens mRNA: cDNA DKFZp589F1822 (f	5.30
	424264	AA405519		gh:11710.1 NC1_CGAP_P11 Homo sapiens	5.30
60	411402	BE209785	Ha.69805	NRAS-related gene	5.30
	415220	AA811938	Ha.291759	ESTs	5.30
	407995	A094748	Ha.100134	hypothetical protein FLJ12787	5.30
	459266	AW907468	Ha.998271	hypothetical protein FLJ14547	5.30
65	452449	AW058658	Ha.20943	ESTs	5.30
	430366	A1057368	Ha.105575	ESTs	5.30
	434360	AW015415	Ha.127780	ESTs	5.29
	422560	F11469	Ha.113281	zinc finger protein 266	5.29
	441704	AA65766	Ha.201688	ESTs	5.29
	413635	AW080230	Ha.134244	ESTs	5.29
70	434342	AJ761138	Ha.116768	ESTs	5.29
	423409	NM_004466	Ha.125207	polymerase (RNA) II (DNA directed) (39k	5.29
	419500	U01960	Ha.3626	hatch-lip protein C3P1	5.29
	452381	H23329	Ha.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.29
	409068	AW226991	Ha.102495	ESTs, Moderately similar to 138022 hypochel	5.29
75	434890	AA932386	Ha.292667	ESTs	5.28
	408096	BE226162	Ha.83755	glyoxylate reductase	5.28
	418036	Z27916	Ha.83337	latent transforming growth factor beta b	5.28
	435443	AJ248674	Ha.14295	ESTs	5.26
	414269	AA298489	Ha.303171	olfactory receptor, family S1, subfamily	5.26
80	408371	AF161545	Ha.279883	hypothetical protein	5.26
	401285	NA		NA	5.26
	450904	R07118	Ha.189924	ESTs	5.26
	416351	H49704	Ha.173522	ESTs	5.26

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465524	AA390611	Hs.163841	ESTs	5.25
472601	A127359	Hs.289868	head shock 90kD protein 1, alpha	5.25
452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13320 fls, clone OV	5.24
444825	AW167813	Hs.248	mitogen-activated protein kinase kinase	5.24
412953	Z45794	Hs.238809	ESTs	5.24
404117	NA		NA	5.22
427986	AL046175	Hs.108169	Homo sapiens mRNA; cDNA DKFZp86C1619 f1	5.22
421787	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, m	5.22
432255	RS8970	Hs.5887	ESTs	5.22
424697	AL136189	Hs.250708	CAXA box 1	5.20
449771	AB68702	Hs.54916	ESTs	5.20
432193	AA372264	Hs.273193	hypothetical protein FLJ10706	5.20
438885	AB66558	Hs.184987	ESTs	5.20
407182	AA312551	Hs.230157	ESTs	5.20
452150	H42490	Hs.260844	ESTs	5.20
419680	AA249720	Hs.69335	ESTs	5.20
438940	AF075045	Hs.271609	ESTs	5.20
405362	NA		NA	5.20
448370	AK002114	Hs.23495	hypothetical protein FLJ11252	5.20
442353	BE795534	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	5.20
409331	M36634	Hs.53973	vasoactive intestinal peptide	5.20
415397	H10818		gbym0410.1.1 Scores infant brain 1NB H	5.20
406735	AA603092		gbrnp37a91a1 NC_024971.1 Homo sapiens	5.20
418485	U79421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	5.20
431480	AA532274	Hs.257005	hypothetical protein FLJ20837	5.20
425523	AB007948	Hs.158244	KIAA0479 protein	5.20
429673	R70318	Hs.339730	ESTs	5.20
432527	AA287747	Hs.173012	ESTs, Weakly similar to A46010 X-linked	5.20
457030	A1301740	Hs.173381	dihydroxyiminoase-like 2	5.20
424638	AI472106	Hs.49303	Homo sapiens cDNA FLJ11663 fls, clone HE	5.20
454434	AA083558	Hs.261286	ESTs	5.20
448336	RS3848	Hs.44676	ESTs	5.20
429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	5.20
434803	AW974640	Hs.303413	ESTs	5.20
403195	NA		NA	5.20
435226	AI021912	Hs.167963	ESTs	5.20
451654	AA889881	Hs.152952	5 nucleotidase (CD73)	5.19
440385	AA884283	Hs.192136	ESTs	5.20
432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	5.20
400484			ph-EST72995 Ovary II Homo sapiens cDNA 5	5.19
425757	AA363171		ESTs	5.19
448841	AI671902	Hs.199602	ESTs	5.19
420303	AA258282	Hs.278436	KIAA1474 protein	5.19
429887	AI675749	Hs.211608	nucleoporin 153D	5.19
453345	AA302862	Hs.90063	neurocalcin delta	5.18
447499	AW252580	Hs.147674	procalcitonin beta 16	5.18
404913			NA	5.18
405114	NA		NA	5.18
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	5.18
411925	W46701	Hs.29657	ESTs	5.17
401735	NA		NA	5.17
425250	AA353495	Hs.269762	ESTs, Weakly similar to A47582 B-cell gr	5.16
454388	AA630905	Hs.333300	hypothetical protein FLJ14026	5.16
449532	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-li	5.16
443646	A085198	Hs.164226	ESTs	5.15
438032	AA150797	Hs.109276	latexin protein	5.15
456896	M67639	Hs.155685	receptor tyrosine kinase-like orphan rec	5.15
433672	BE791165	Hs.288038	TLS-associated serine-arginine protein 1	5.15
432626	X75383	Hs.250770	ACO for serine protease homologue	5.14
439441	WS7993	Hs.323135	ESTs	5.14
400205	NA		NA	5.14
430854	AW440369	Hs.47026	ESTs	5.14
408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	5.14
456804	AI421645	Hs.139851	caveolin 2	5.14
424690	BE538356	Hs.151777	eukaryotic translation initiation factor	5.13
449210	AK635363	Hs.197636	ESTs	5.12
419013	T90378	Hs.144653	ESTs	5.12
425843	BE313280	Hs.159627	death associated protein 3	5.12
422545	X02761	Hs.287820	fibronectin 1	5.12
424785	R23519	Hs.6126	hypothetical protein dJ1141E15.2	5.11
447633	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	5.10
422411	AW749443	Hs.22511	ESTs	5.10
457565	BE794029	Hs.279903	Ras homology enriched in brain 2	5.10
437722	AW292947	Hs.122872	ESTs, Weakly similar to J00033 hypothetical	5.10
446893	AI610818	Hs.71110	ESTs	5.10
401581			NA	5.10
417511	AL049176	Hs.82223	chordin-like	5.10
427336	AI761322	Hs.115285	dihydrolyamide S-acetyltransferase (E2	5.10
437662	AA765387	Hs.145096	ESTs	5.10
429526	AA454182	Hs.99350	ESTs	5.10
447332	AW445012	Hs.100918	ESTs	5.10
436207	AA334774	Hs.12945	hypothetical protein MGCI3159	5.10
428155	H17012	Hs.146033	ESTs	5.10

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	420185	AL044056	Hs.158047	ESTs	5.10
	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	5.10
	440913	A287481	Hs.160593	ESTs	5.10
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	5.10
5	428603	BE241619	Hs.24641	cytochrome oxidase associated protein 2	5.10
	436577	W84774	Hs.17643	ESTs	5.10
	430241	NA	NA	NA	5.10
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	5.10
	41674253	AI674253	Hs.15828	ESTs	5.10
	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fls, clone HE	5.10
	430849	AI940727	Hs.270556	ESTs, Highly similar to AF156779.1 ASD-4	5.10
	425205	AW969557	Hs.90012	hypothetical protein FLJ23441	5.10
	440381	AA917808	Hs.190405	ESTs	5.10
	441033	BE562555	gb:601335867.1 NH_MGC_44	Homo sapiens c	5.10
	402229	R16717	Hs.6929	hypothetical protein FLJ11562	5.10
	447197	R30575	gb:yl66051.1	Soares placenta Nb2HP Homo	5.10
	442150	A3368158	Hs.70983	PTPL1-associated RhoGAP 1	5.10
	415651	A207162	Hs.3815	statmin like-protein RIB3	5.10
	435655	AW960427	Hs.79039	transforming growth factor, beta recepto	5.09
20	434442	AA373415	Hs.152826	ESTs	5.09
	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ111079 fls, clone PL	5.09
	435419	A281066	Hs.152635	ESTs	5.09
	427620	NM_003705	Hs.179866	solute carrier family 25 (mitochondrial	5.09
	445705	AA305320	Hs.108812	hypothetical protein FLJ22004	5.08
25	424071	R71340	Hs.12876	ESTs	5.08
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.08
	426400	M78361	Hs.169743	Homo sapiens clone 25121 neuronal octet	5.08
	429626	AA443385	Hs.221993	ESTs	5.08
	455847	BE146775	gb:QV4-110222-181099-013-e04	HT0222 Homo	5.08
	416110	Z42262	Hs.322644	hypothetical protein DKFZ5644A.176	5.08
	436854	AA749167	Hs.173911	ESTs	5.08
	421799	AW972292	Hs.292998	ESTs	5.08
	452154	AW952265	Hs.302746	MYSTP028 protein	5.08
	444944	AW139205	Hs.158457	hypothetical protein FLJ22408	5.08
35	445950	AJ267957	Hs.145706	ESTs	5.08
	443124	A033500	Hs.132895	ESTs	5.06
	440696	AJ384455	Hs.147492	Homo sapiens cDNA FLJ11777 fls, clone HE	5.06
40	444713	AW612074	Hs.167331	Homo sapiens cDNA: FLJ22141 fls, clone H	5.06
	447970	AW066109	Hs.20135	chromosome X open reading frame 6	5.06
	419307	AW953190	Hs.23160	ESTs	5.06
	421954	AA410245	Hs.40323	BUB3 (budding uninhibited by benzimidazo	5.06
	451607	WS3264	Hs.27089	hypothetical protein FLJ22291 similar to	5.05
	421762	AB023820	Hs.105258	actin binding protein; macrophilin (microf	5.05
	407976	AI633875	Hs.7823	hypothetical protein FLJ21343	5.05
45	406669		NA	NA	5.04
	416153	R13894	gb:Y52a06.1	Soares infant brain 1MB H	5.04
	422442	H55709	Hs.2250	levamisole inhibitory factor (cholenergic	5.04
	406038	Y14443	Hs.86219	zinc finger protein 200	5.03
	440659	AF134160	Hs.7327	claudin 1	5.03
50	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.02
	446051	BE540951	Hs.37054	gprh-A3	5.02
	443387	BE139135	Hs.254629	ESTs	5.02
	414407	AA147026	Hs.76704	ESTs	5.02
	408349	BE548947	Hs.44276	homeo box C10	5.01
55	452510	Z33566	Hs.30491	ESTs	5.01
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	5.00
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	5.00
	447857	AA081218	Hs.58008	Homo sapiens cDNA FLJ14206 fls, clone NT	5.00
	423648	AK000495	Hs.130546	hypothetical protein FLJ20449	5.00
60	412997	BE346600	gb:U41485.1	f1 NCL_CGAP_RDF2 Homo sapiens	5.00
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	5.00
	411636	AW855001	gb:PM3-CT0263-091299-007-05	CT0263 Homo	5.00
	418111	R42003	Hs.106513	ESTs	5.00
	422709	NA	NA	NA	5.00
65	408677	AJ275892	Hs.46801	sorting nexin 14	5.00
	411350	AW877011	gb:QV2-PT0010-250300-056-b05	PT0010 Homo	5.00
	453832	AA709285	Hs.5907	hypothetical protein FLJ13078	5.00
	450800	A282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.00
70	408512	AW920013	Hs.265937	ESTs	5.00
	453240	AI969564	Hs.166254	hypothetical protein DKFZp5661133	5.00
	440491	R35252	Hs.24944	ESTs, Weakly similar to Z109260A B cell	5.00
	423696	AA332216	Hs.130594	ESTs	5.00
	423001	AA933608	Hs.187039	ESTs	5.00
75	410968	AA199907	Hs.67397	homeo box A1	5.00
	436859	AA732081	Hs.270053	ESTs	5.00
	425198	A097560	Hs.61210	ESTs, Weakly similar to I38022 hypothell	5.00
	424511	BE300512	Hs.153657	ESTs, Moderately similar to ALUT_HUMAN A	5.00
	414831	AW970130	Hs.65406	ESTs	5.00
	405481		NA	NA	5.00
80	431118	BE264001	Hs.250502	carbonic anhydrase VIII	5.00
	421373	AA868229	Hs.167771	ESTs	5.00
	424916	AW857440	Hs.270261	ESTs	5.00
	433106	AB902443	Hs.184418	ESTs	5.00

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445165	63181_1	AV62831 AA191140 AA329706 AI267893 AI79686 AW675672 AW195369 BE002835 BE003284 AA190592 AA769594 AW275548 R56781 AA807313
447197	711623_1	AW696985 K31806
453685	977734_1	R30275 A336646 R36167
454511	1205533_1	AL110309 AW088119 IZ22881
454758	1233743_1	AW948146 AW948135 AW802578
454835	1235607_1	AW845266 AW845254 AW819440 AW819430 AW819425 AW819423
455082	1252687_1	AW63783 AW633704 AW653816
455208	1260551_1	BE148180 AW855210 AW855243
455212	1260676_1	BE180276 AW866156 BE180165
455217	1261652_1	AW863320 AW866410 AW865332 AW866411 AW866327 AW866326 AW866335 AW866334 AW865331 AW866333 AW866328 AW866329
455608	1337369_1	AW876734 AW876733 AW876732
455847	1373358_1	BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
455944	1385568_1	BE146775 BE146789 BE146792 BE147010 BE146941 BE146801 BE146998 BE147011 BE146903 BE146901
457892	432526_1	BE160643 BE160585
457893	432536_1	AA744389 AA744278 AA744284 AA744299 AA745380 AA745433 AA846905 AA847698
458279	975649_1	AA744292 AA745577 AW748517 AW748564 AW748511 AW748513 AW748530 AW748574 BE062923
		AW814996 ALD47199 AW850979

20	TABLE 46C:	
	Play:	Unique number corresponding to an Eos probelet
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402 489-496.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400484	8569067	Minus	52725-52912
400570	984797	Minus	156767-158682,178082-178208,186819-186957
400639	9887597	Plus	23155-23980
400845	9189605	Plus	34428-34612
400880	9757499	Minus	151830-152104,152549-152744
400889	9636306	Plus	29152-30102
400950	7858461	Minus	157020-159554
400977	8072510	Plus	73950-74364
401004	7229882	Plus	62580-62772
401093	8516137	Minus	22335-23166
401183	7670214	Minus	33921-40601
401205	9743388	Plus	167373-167433,167936-168031
401208	7712287	Plus	163145-163281
401244	4627300	Minus	56359-56376
401348	9930781	Minus	9365-9490
401372	9941181	Plus	127056-127196
401424	8176894	Plus	24223-24428
401581	9502454	Plus	9440-10165
401628	8575965	Minus	165336-169788
401708	2951946	Plus	154511-155258
401736	3219338	Plus	1771-1894
401740	2982189	Plus	148357-148484,148591-148690
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130953,131097-131258,131866-131932,132451-132575,133560-134011
401961	4581193	Minus	124054-124209
402343	8099256	Plus	4677-6084
402363	9454515	Plus	25693-25991
402408	9796239	Minus	110326-110491
402524	9790518	Minus	20329-21096
402709	8901246	Minus	56647-57065
402732	9211639	Minus	147904-148107
403040	3133144	Minus	91632-91788,97918-98115
403137	9211494	Minus	92349-92572,929258-93084,93579-93712,93949-94072,94591-94748,95214-95337
403199	8941963	Minus	58885-59036,66518-66789
403278	8072597	Plus	146823-146986
403546	8078400	Plus	94703-94849
403764	7717105	Minus	118562-118653
403776	7770611	Plus	1414-1513,1624-1756
403859	7708954	Plus	113738-113858
403973	8575876	Plus	93873-94384
404012	8655948	Plus	851356-852233
404028	7671252	Plus	108719-111112
404072	9631705	Plus	49546-50499
404117	9796029	Plus	149723-149920
404170	9930793	Plus	168836-169248
404335	9838027	Minus	21030-21145,26504-26692
404440	7528051	Plus	80430-81581
404632	9796668	Plus	45096-45229
404702	7630798	Plus	78043-78880
404913	7341740	Plus	97717-97976
404986	6070890	Plus	37999-38146,38652-38998,39727-39872,40557-40674,42351-42450
405033	7107731	Minus	142358-142546
405065	7684500	Minus	13855-14027
405114	8096838	Minus	97013-97560
405287	7928229	Plus	89802-89999
405362	2821462	Minus	97253-97742
405362	2337862	Minus	103008-105142,105980-106091,140445-140556,142519-142641

405481	3688109	Plus	5719-5837, 8719-8818
405511	9454623	Plus	573731-57852
405523	9454643	Plus	1145501-14688, 117265-117407, 119490-119599, 123237-123395, 131140-131217
405543	9857582	Minus	104338-104449
405545	1057480	Plus	118677-118807, 119091-119296, 121626-121823
405637	6289259	Plus	189852-189979
405696	4399523	Minus	1865-2013, 72126
405770	2735037	Plus	61067-62075
405993	9795559	Plus	94502-94714, 96776-96914, 98795-98928, 102423-102576, 105087-105191, 107023-107122, 108652-108992

TABLE 47A: ABOUT 370 GENES SIGNIFICANTLY DOWN-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH

Table 47A lists about 370 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 46A, except that the numerator and denominator were switched and the ratio was equal to or less than 0.33.

denominator were switched and the ratio was equal to or less than 0.55.

Play: Unique Ecos probe/est identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

[illegible]

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	401685	NA	NA	0.17	
	441519	AA972740	Hs.127092	ESTs	0.17
	438327	H87407	Hs.172944	chorionic gonadotropin, beta polypeptide	0.17
	402761	BE387621	Hs.108809	chaperonin containing TCP1, subunit 7 (c	0.17
5	424268	AA357653	Hs.307438	Human DNA sequence from clone 495010 on	0.18
	414507	AW102637	Hs.13349	Homo sapiens cDNA FLJ14647 fs, clone NT	0.18
	413808	J00287	Hs.182183	Homo sapiens mRNA for cathepsin, 3' UTR	0.18
	401132	NA	NA	NA	0.18
	412374	X01388	Hs.73849	apolipoprotein C-III	0.18
	423417	AA000365	Hs.128342	potassium large conductance calcium-acti	0.18
	416777	AI191235	Hs.98321	gb E21d12.x1 NCI_CGAP_Bin23 Homo sapien	0.18
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	0.18
	424122	AA335593	Hs.116147	ESTs	0.18
15	417332	AW972717	Hs.288462	hypothetical protein FLJ25111	0.18
	434597	AW574668	Hs.193376	gb E3186757 IMAGE: ressequencs, MAGM Homo	0.19
	428804	AA000713	Hs.193376	hypothetical protein FLJ20705	0.19
	410280	AA083558	Hs.261286	ESTs	0.19
	405982	AA071244	Hs.98321	gb nm73g03.x1 Stratagene neuroepithelium	0.19
20	429062	AA420683	Hs.98321	hypothetical protein FLJ14103	0.19
	426069	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fs, clone HE	0.19
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	0.19
	414802	AJ793107	Hs.27018	Ris	0.19
	457432	NM_005136	Hs.268538	potassium voltage-gated channel, Isk-rel	0.19
	446909	AA004885	Hs.30982	ESTs	0.19
25	435447	AI872032	Hs.30982	gb wm72e03.x1 NCI_CGAP_U02 Homo sapiens	0.19
	408611	NM_004367	Hs.46468	chemokine (C-C motif) receptor 6	0.20
	423577	AW810107	Hs.58633	Homo sapiens cDNA: FLJ21245 fs, clone H	0.20
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	0.20
30	436741	AA860163	Hs.291319	ESTs	0.20
	426635	BE395109	Hs.129327	hypothetical protein MGC13067	0.20
	418277	AW135221	Hs.130812	ESTs	0.20
	446871	BE107076	Hs.159265	kupfer-related zinc finger protein hckr	0.20
	459370	AA899982	Hs.271826	ESTs, Weakly similar to D80222 hypothetical	0.21
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	0.21
	432887	AJ926047	Hs.126859	ESTs	0.21
	421296	NM_002666	Hs.162523	perlepin	0.21
	449216	AW255417	Hs.224616	ESTs	0.21
	414835	AA156720	Hs.185342	ESTs	0.21
40	459233	AJ39966	Hs.210015	gb MR0-CT0015-160795-002-b05 CT0015 Homo	0.21
	439756	AL359651	Hs.263652	Homo sapiens mRNA full length insert cDN	0.21
	427167	AJ239607	Hs.59196	hypothetical protein hGC11324	0.21
	400410	AF154915	Hs.283958	homeo box D12	0.22
	409826	AW501137	Hs.184507	gb UHF-BP0p-ai-e-12-0-U1 NIH_MGC_5	0.22
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.22
45	455988	BE168828	Hs.184507	gb GY1-HT0517-020400-145-64 HT0517 Homo	0.22
	404145	NA	NA	NA	0.22
	454011	M31008	Hs.37009	alkaline phosphatase, intestinal	0.22
	430588	AI741461	Hs.161904	ESTs	0.22
	403652	NA	NA	NA	0.22
50	440410	AW204436	Hs.128715	ESTs	0.22
	453871	BE300380	Hs.69476	Homo sapiens cDNA FLJ12758 fs, clone NT	0.22
	458667	AJ222075	Hs.147831	ESTs	0.22
	438004	AA703332	Hs.196270	klome transporter/carrier	0.22
55	417408	F17211	Hs.86592	Homo sapiens cDNA FLJ14647 fs, clone NT	0.22
	448643	AI557531	Hs.86592	gb p21-1.06.D05.s tumor2 Homo sapiens cD	0.22
	404401	NA	NA	NA	0.22
	428088	AA421130	Hs.112640	EST	0.22
	427074	AA527435	Hs.178589	hepatocellular carcinoma antigen gene S2	0.22
	421972	W18185	Hs.1454	osonic inhibitory polypeptides	0.22
60	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.22
	441155	AW161008	Hs.7719	GAB(A) receptor-associated protein	0.22
	402750	NA	NA	NA	0.22
	438587	AA811450	Hs.136994	ESTs	0.22
	404848	NA	NA	NA	0.22
	427833	AA416615	Hs.98242	ESTs	0.23
	439907	AA853978	Hs.124577	ESTs	0.23
	414373	AW162907	Hs.178989	proline-rich protein with nuclear target	0.23
	446817	AJ700684	Hs.134156	ESTs	0.23
	437333	AA748898	Hs.134156	gb ny76h10.s1 NCI_CGAP_GCB1 Homo sapiens	0.23
	404097	NA	NA	NA	0.23
70	444393	AA014174	Hs.301956	zinc finger protein	0.23
	463208	T41366	Hs.301956	gb p11d11.191TV Outward Aa-primed IncDN	0.23
	401042	NA	NA	NA	0.23
	458441	AW842283	Hs.79933	cyclin I	0.23
75	435547	AW117431	Hs.191906	ESTs	0.23
	429060	AW139155	Hs.194995	hypothetical protein DKF1pK40C0320	0.23
	425158	AW954631	Hs.266940	1-complex-associated-testis-expressed 1-	0.23
	448758	AD018311	Hs.21917	KIAA0758 protein	0.23
	441240	AA623749	Hs.133442	ESTs	0.23
	435622	H71937	Hs.322894	ESTs, Weakly similar to D80222 hypotheti	0.23
	424104	AA669515	Hs.144950	ESTs	0.23
80	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.23
	444515	AW204908	Hs.165979	ESTs	0.23

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5	432684	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.24
	430650	NA		NA	0.24
	432108	N09127	Hs.332557	ESTs, Weakly similar to A4610 X-linked	0.24
	456699	BE068121		gb:CM1-8T0368-061299-060-a02 BT0368 Homo	0.24
	435979	MR8895	Hs.76800	alcohol dehydrogenase 6 (class V)	0.24
10	439657	W05349		gb:U95555.s1 Soares, Jentel, Jentel, NBR+H9W	0.24
	407512	X15874		gb:Human pTRES mRNA for repetitive sequen	0.24
	440875	AW138036	Hs.201788	ESTs	0.24
	404753			NA	0.24
	411119	M03627	Hs.753	hormyl peptide receptor 1	0.24
15	418922	A0002058	Hs.87383	hypothetical protein	0.24
	415327	H22769		gb:ym64c02.r1 Soares infant brain T1B1 H	0.24
	429446	A1547111		gb:PM2.1_A01_G12.r myonin Homo sapiens c	0.24
	455391	BE156230		gb:QV0-HT0367-310100-102-c11 HT0367 Homo	0.25
	422818	AA04290	Hs.97848	ESTs	0.25
20	435338	AA678071	Hs.194300	ESTs, Weakly similar to C80227 hypotheti	0.25
	414203	BE262170	Hs.78629	ATPase, Na+/K+- transporting, beta 1 poly	0.25
	403941	NA		NA	0.25
	414332	BE779406		gb:501157981F1 NIH_MGC_21 Homo sapiens c	0.25
	412908	MM_001841	Hs.73037	carbamoyl receptor 2 (macrophage)	0.25
25	424985	A0507236	Hs.279935	Homo sapiens cDNA FLJ11780 fs, clone HE	0.25
	450736	AW970060		gb:EST382140 MAGE resequences, MAGK Homo	0.25
	431166	H02761		ESTs	0.25
	455306	AW839449		gb:RC4-NN00227-060400-011-009 NN00227 Homo	0.25
	435464	BE548300	Hs.192999	ESTs, Moderately similar to K0AA0961 pro	0.25
30	418525	AW450369	Hs.86937	ESTs	0.25
	407790			NA	0.25
	411869	H20027	Hs.24309	ESTs	0.25
	400337	S66407	Hs.748032	FLT4	0.25
	424884	AW299437	Hs.725717	ESTs	0.25
35	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7kd protein [0.25
	439780	AL109698		gb:Homo sapiens mRNA full length insert	0.25
	408947	AL080993	Hs.49117	Homo sapiens mRNA, cDNA DKFZp564N1662 (I	0.25
	404900	NA		NA	0.25
	411918	A1733373	Hs.128119	ESTs	0.25
40	441639	A153267	Hs.303953	ESTs	0.25
	455296	A0507236	Hs.100869	ESTs	0.25
	452755	AW138537	Hs.213436	ESTs, Weakly similar to A34067 hypotheti	0.25
	427183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	0.25
	415186	AA162945		Homo sapiens cDNA FLJ14199 fs, clone NT	0.26
45	428450	AA24451		hypothetical protein FLJ23311	0.26
	454615	BE045344		ESTs, Moderately similar to unnamed prot	0.26
	454633	AW811380		gb:IL3-ST0143-290999-019-005 ST0143 Homo	0.26
	424853	BE549737	Hs.132967	Human EST clone 122687 manner transposo	0.26
	455802	BE141491		gb:MRD-HT0680-011099-002-h06 HT0680 Homo	0.26
50	414003	AA134172		gb:ro13c1.s1 Syntrophin colon (537204)	0.26
	436363	AA643926	Hs.124434	ESTs	0.26
	456074	BE405525	Hs.902	neurotrophin 2 (bilateral acoustic neur	0.26
	430569	AF241254	Hs.178098	angiotensin I converting enzyme (proxid	0.26
	445635	AF769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.26
55	405953	NA		NA	0.26
	411021	F00055	Hs.172004	IGH	0.26
	428443	BE518106	Hs.184376	CDC10 (cell division cycle 10, S. cerevi	0.26
	434345	AF127772		gb:Homo sapiens cell-line EB-CASS clone E	0.26
	453743	BE072754		gb:ROD-HT0561-210100-032-a07 BT0561 Homo	0.26
60	451138	W02287	Hs.40268	ESTs	0.26
	443528	H63337	Hs.38178	hypothetical protein FLJ23468	0.26
	441040	AW449782	Hs.178983	ESTs	0.26
	453830	AW501248	Hs.258624	Homo sapiens cDNA: FLJ23435 fs, clone H	0.26
	428861	AW352224	Hs.265365	ESTs, Weakly similar to ALUS_HUMAN ALU S	0.26
65	435469	AW388237	Hs.191204	ESTs	0.27
	427562	R64274	Hs.26534	ESTs	0.27
	434779	AF153815	Hs.50151	potassium inwardly rectifying channel, s	0.27
	423528	AB011137	Hs.308538	K0AA065 gene product	0.27
	406589			NA	0.27
70	450059	BE220223	Hs.279626	ESTs	0.27
	417266	L36196	Hs.81804	acidtransferase family, cytosolic, 2A,	0.27
	454007	AW015870	Hs.232081	ESTs	0.27
	425062	N57014	Hs.75874	pregnancy-associated plasma protein A	0.27
	441665	AD01355	Hs.151285	ESTs	0.27
75	405037	NA		NA	0.27
	446920	AW269037	Hs.254986	ESTs	0.27
	448487	AI523720	Hs.177567	ESTs	0.27
	447567	AW474513	Hs.224397	ESTs, Weakly similar to 108531 Wskott-A	0.27
	408540	L13220	Hs.639	calbindin 3, (vitamin D-dependent calciu	0.27
80	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.27
	432501	BE546532	Hs.25982	Homo sapiens mRNA for K0A1863 protein,	0.27
	401350	NA		NA	0.27
	417569	R00271	Hs.144651	ESTs	0.27
	443342	A527065	Hs.146480	ESTs	0.27
	427105	AA744584	Hs.222127	ESTs	0.27
	432119	T80289	Hs.320241	Homo sapiens clone 24762 mRNA sequence	0.27
	419056	MR8957	Hs.89575	CD79B antigen (immunoglobulin-associated	0.28

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	427812	AA770424	Hs.58162	ESTs	0.28
	423557	AB011176	Hs.123901	KIAA0694 gene product	0.28
	445311	AW027556	Hs.156286	ESTs	0.28
5	402758	NA		NA	0.28
	448240	AA478345	Hs.191834	ESTs	0.28
	401333	NA		NA	0.28
	444107	T46539	Hs.10319	UDP glycosyltransferase 2 family, polype	0.28
	454738	BE072139		gb.PM1-810533-291259-002-b05.B10533 Homo	0.28
10	442896	R37725	Hs.261108	ESTs	0.28
	447949	AA48820	Hs.155339	EST	0.28
	435625	H50654	Hs.113999	ESTs	0.28
	415817	U88957	Hs.78867	protein tyrosine phosphatase, receptor-t	0.28
	438380	T05430	Hs.6194	chondroitin sulfate proteoglycan BEHAVBb	0.28
	442967	AB02460	Hs.228977	ESTs	0.28
15	448062	AW255923	Hs.255472	KIAA1843 protein	0.28
	425860	L29339	Hs.1954	solute carrier family 5 (sodium/glucose	0.28
	451839	AB20516	Hs.16857	ESTs	0.28
	446000	AV659032	Hs.1534	homoposin	0.28
	443506	H11061	Hs.153124	ESTs. Weakly similar to I38022 hypophel	0.28
20	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibit	0.28
	445461	AW661846	Hs.148836	ESTs	0.28
	409337	H71289	Hs.228535	ESTs	0.28
	411414	AW872236		gb.CM0-NM0057-150400-335-c06.NM0057 Homo	0.28
	427642	R40761	Hs.9834	ESTs	0.28
25	456392	V28766		gb.51d3 Human retina cDNA randomly prime	0.28
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	0.28
	410285	AA023609		gb.zm53005.r1 Stratagene fibroblast (937	0.28
	442466	RS5073	Hs.124130	ESTs	0.28
	423770	AW976766	Hs.132776	Homo sapiens cDNA FLJ10077.f1, clone HE	0.28
30	423467	AK000214	Hs.129014	hypothetical protein FLJ20207	0.29
	458716	N59013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (l	0.29
	422335	AW1418648	Hs.105917	neurobin II	0.29
	431087	H12723	Hs.290791	ESTs	0.29
	459106	AW589793	Hs.224713	ESTs	0.29
35	414870	N72264	Hs.300670	KIAA1204 protein	0.29
	402243	NA		NA	0.29
	432628	R02394	Hs.269436	ESTs. Moderately similar to PCA259 lemi	0.29
	404364	NA		NA	0.29
	400480	NA		NA	0.29
40	456083	U46522	Hs.77252	fragile histidine triad gene	0.29
	446508	AW250546		gb.Z021774.Spinn NH4.MGC_7 Homo sapiens	0.29
	422201	NM_001505	Hs.113207	G protein-coupled receptor 30	0.29
	443919	AI051284	Hs.135224	ESTs. Weakly similar to A47582 B-cell gr	0.29
	453948	AI970797	Hs.64869	ESTs	0.29
45	402792	NA		NA	0.29
	418957	AT92615	Hs.188712	ESTs	0.29
	457960	AA771181	Hs.258149	ESTs	0.29
	404269			NA	0.29
	435388	AF090697	Hs.6524	Homo sapiens clone IMAGE 25997	0.29
50	458239	BE433877	Hs.283389	ESTs	0.30
	414941	C14865	Hs.332341	ESTs	0.30
	404954			NA	0.30
	441609	AA946754	Hs.133460	ESTs	0.30
55	426915	AA416880	Hs.223738	ESTs	0.30
	403182	NA		NA	0.30
	402319			NA	0.30
	429699	AI383469	Hs.159300	ESTs	0.30
	406569	NA		NA	0.30
60	455312	AF107457	Hs.37005	homoeo box HB9	0.30
	431853	AA521034	Hs.70834	ESTs	0.30
	449768	AB972746	Hs.102945	ESTs. Weakly similar to I78885 serin/th	0.30
	443609	AV650231	Hs.282941	ESTs. Highly similar to A Chain A. Human	0.30
	454293	H69739	Hs.134013	ESTs. Moderately similar to H1651_HUMAN H	0.30
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.30
65	400128	NA		NA	0.30
	423208	AA323191	Hs.137064	cytoplasmic polyadenylation element bind	0.30
	434227	AF119893	Hs.63382	hypothetical protein PR02714	0.30
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.30
	401165	NA		NA	0.30
70	415394	R19249	Hs.22654	sodium channel, voltage-gated, type I, a	0.30
	443110	AW352243	Hs.132665	ESTs	0.30
	428724	AA383623	Hs.293616	ESTs	0.30
	416035	H42314		gb.y00902.z1 Scores adult brain N265HE5	0.30
	409753	AA234847		gb.zs37b10.r1 Scores_NHMFU_S1 Homo sapi	0.31
75	459221	BE246522	Hs.306121	leukocyte receptor cluster (LRC) encoded	0.31
	408895	AA501730	Hs.191464	ESTs	0.31
	405110	NA		NA	0.31
	432430	AW079984	Hs.262480	ESTs. Weakly similar to PIHL66 salivary	0.31
	428442	AA378656	Hs.106510	ESTs. Moderately similar to ALU2_HUMAN A	0.31
80	411765	H43346		gb.y0504H.r1 Scores bread 3NHHEst Homo	0.31
	431854	AA383550	Hs.271699	polymerase (DNA directed) iso	0.31
	457553	AI061866	Hs.304505	ESTs	0.31
	412301	AW936328		gb.QM4-DT0021-281299-070 DT0021 Homo	0.31

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5	418626	AW295508	Hs.135230	ESTs	0.31
	416158	Z41922		gb:HS0036101 normalized infant brain cDNA	0.31
	416275	H42823	Hs.155742	glyoxylate reductase/hydroxypruvate red	0.31
	419091	T85332	Hs.176294	ESTs	0.31
	420118	AW295297	Hs.182685	KIAA1276 protein	0.31
10	451094	A1949825	Hs.260395	ESTs	0.31
	403214	NA		NA	0.31
	412717	W00973	Hs.334728	ESTs	0.31
	427872	X17830	Hs.193400	interleukin 6 receptor	0.31
	455202	AW205154	Hs.255398	ESTs	0.31
15	433138	AJ002946	Hs.59729	semaphorin sem2	0.31
	436602	A1793222	Hs.156817	ESTs	0.31
	424844	D61524		gbrHUM13E07B Clontech human fetal brain	0.32
	435253	W51684		gb:AF1708.1 Sources_fetal_liver_spleen	0.32
	455350	AW501809		gb:OW-NH1020-170400-155462 NH1020 Homo	0.32
20	416320	H47867	Hs.34024	ESTs	0.32
	406333			NA	0.32
	443652	A080692	Hs.134229	ESTs, Weakly similar to I54401 hypertens	0.32
	457103	AA21187	Hs.169192	ESTs, Weakly similar to T COMPLEX TESTIS	0.32
	423593	AA328144		gb:EST31752 Embryo, 12 week 1 Homo sapie	0.32
25	453242	T98327	Hs.18343	ESTs	0.32
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	0.32
	403847	NA		NA	0.32
	458711	AL036877	Hs.282878	ESTs	0.32
	406242	NA		NA	0.32
30	433493	AA594915	Hs.155087	ESTs	0.32
	458147	AW752597		gb:IL3-CT02 14-161299-045-B06 CT0214 Homo	0.32
	437403	AZ06149	Hs.121196	ESTs	0.32
	407823	D44744	Hs.247447	ESTs	0.32
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fls. clone C	0.32
35	430089	AA004957	Hs.119840	ESTs	0.32
	457463	AW877031	Hs.272321	hypothetical protein FLJ12571	0.32
	433370	A084343	Hs.122310	ESTs	0.32
	436298	AW293496	Hs.180138	ESTs	0.32
	419768	T72104	Hs.93194	apodoprotein A-I	0.33
40	448428	A051280	Hs.195685	ESTs	0.33
	405291	NA		NA	0.33
	409699	BE154650		gb:PM3-HT0344-07 1299-003-c06 HT0344 Homo	0.33
	418162	T11958		gb:A0202R Heart Homo sapiens cDNA clone A	0.33
	408316	AW807771		gb:MR4-ST0098-090300-003-c05 ST0098 Homo	0.33
45	404187	NA		Homo sapiens clone 23832 mRNA sequence	0.33
	452992	A1792376	Hs.31290	ESTs	0.33
	448356	A1493734	Hs.329374	ESTs	0.33
	442423	BE326264	Hs.246842	ESTs	0.33
	439474	A0824060	Hs.211501	ESTs	0.33
50	457149	A4426575	Hs.207493	ESTs	0.33
	448623	BE613468	Hs.107515	ESTs, Weakly similar to T00329 hypothei	0.33
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	0.33
	415372	W28781		gb:SLH3 Human retina cDNA randomly prime	0.33
	405293	NA		NA	0.33
55	422933	AF073831	Hs.122359	calcium channel, voltage-dependent, alpb	0.33
	451818	A1819018	Hs.339668	ESTs	0.33
	441912	AA971484	Hs.159838	ESTs	0.33
	428013	AJ012590	Hs.194728	hexose-6-phosphate dehydrogenase (glucos	0.33
	422304	AK002016	Hs.114727	Homo sapiens, clone MGC-16327, mRNA, com	0.33
60	457394	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	0.33
	406597			NA	0.33
	451636	AW173270	Hs.140444	ESTs	0.33
	424226	M94153	Hs.19155	ESTs	0.33

TABLE 47B:

Play: Unique Exa probaset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

65	Play	CAT number	Accession
	408316	1051210_1	AW179260 AW1807851 AW179240 AW845951 AW807693 BE141176 AW807594 AW807772 AW846063 AW845963 AW179239
	409382	112508_1	AA071244 AA071477
	409699	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154667
	409753	115305_1	AA234847 AA077472
70	409828	1150571_1	AW501137 AW501295 AW501212
	410265	119128_1	AA083069 AA083790 AA112048
	411414	1245024_1	AW897236 AW845406
	411765	125700_1	H43346 AA248302 AA095182
	412301	1288123_1	AW536328 AW936539
75	412783	1327836_1	AW997986
	413382	1365954_1	BE090689 BE000068 BE090697 BE090880 BE090691 BE090696 BE090698 BE090696
	414003	140888_1	AA134472 RT6288 AW750262
	414383	1440279_1	BE79406 BE280100
	415327	1534137_1	H27769 R35182 Z43645 F06783 N92089 H71928
80	416035	1667294_1	H42314 H43080 H45217 H15384
	416156	1753980_1	Z41922 H23072 T73222
	418182	1725383_1	T11958 T11756 T11816 T20135 T19720 RA48874

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5	419372	1842942_1	V028781 W26588 W06377
	422731	220507_1	AL138411 AL138412 AA315860
	433593	229955_1	AA328144 AW962385 N30457
	424844	244291_1	D61524 AA347654 AW961758
	429446	304683_1	A5471111 VAW973749 AA559007
	430350	315401_1	BE169639 AA475976
	434345	38411_1	AF127772 AF062358 AF060217 AA652270 F23288
	434597	389383_1	AW974668 AA661959 AA649572 AA640401 AA640402
	435253	403476_1	V51884 W95119 AA471041
10	435447	405400_1	AB72932 AA682305 BE220163 WB8685 T81307 H91447
	437333	436167_1	AA748898 AW9597701 AA5997703
	439657	47499_1	W53589 W93487 AF086493
	439780	407673_1	AL109688 R23655 R26576
	446598	68463_1	AW250546 BE257108 BE251006 BE255957 BE259528 BE13012 AV689318
15	447677	732252_1	AA15235 AW055016 BE027490 BE1550241
	448643	773566_1	A1557531
	450736	844552_1	AW970050 A1732365 A1792313 AW839644
	454282	1091035_1	AW205422 H72616 H83825
	454633	1227504_1	AW811380 AW811385
20	454738	1234449_1	BE072139 BE157977 BE157974 AW857974 AW817778
	454790	1234752_1	AW820652 AW820773 AW821088
	455071	1252281_1	BE145826 BE145815 BE145822 AW854707 BE145912
	455308	1278147_1	AW835949 AW835950 AW835966
	455350	1283853_1	AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798
25	455391	1288067_1	BE156230 BE156239 AW536250
	455699	1351258_1	BE068121 BE068090 BE068153 BE068128 BE068197 BE068136 BE068140 BE068185 BE068105
	455743	1354978_1	BE073754 BE073765 BE073755 BE073756 BE073752 BE073795 BE073796 BE073704 BE073791 BE073733 BE073695
	455802	1370826_1	BE141491 BE141016 BE141479
	455826	1373392_1	BE144228 BE144291
30	455968	1391117_1	BE168828 BE168830 BE168823 BE168828 BE168828 BE168820 BE168826
	456328	1789791_1	T41368 T41369 T41294
	456392	1843069_1	W02786 W02600
	458147	480021_1	AW752597 AW848781 AW849052 AW848490 AW752699 AW752594 AW752700
35	459233	944881_1	A1939966 A1939988 A1939951 A1939981 A1939976 A1939959

TABLE 47C:

Play: Unique number corresponding to an Ems probelet
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Play	Ref	Strand	NL_position
40	400480	8439796	Minus 110653-111119
	401015	8117441	Plus 72260-72369
	401042	8117611	Plus 151364-151606
	401132	8705350	Minus 85679-85795
	401165	9436376	Minus 168244-168423
50	401333	9884881	Plus 13852-14061
	401350	9931226	Plus 14471-14623
	401623	8575907	Plus 163249-163623
	401683	7689961	Plus 2934-3446
	401685	7689961	Minus 8038-8319
55	402015	7417802	Plus 40791-40943,50038-50205,51530-51672,54448-54565,55933-56073
	402243	7690137	Minus 196521-196721
	402319	7582559	Plus 116689-117549
	402750	7210067	Plus 69466-69676,71139-71284,71572-71865
	402758	9213869	Plus 67638-67924
60	402760	9213869	Plus 136829-136952,137336-137521
	402790	4835258	Minus 147744-147861
	403182	9638273	Plus 102163-102345,102545-102725
	403214	7630945	Minus 76723-77027,79317-79484
	403652	6705848	Minus 42951-50129
	403670	7259739	Minus 83377-88537
65	403697	3962501	Minus 102965-103174
	403792	7230192	Minus 149707-149873
	403847	7718844	Plus 317240-317391,317913-318032
	403941	7454203	Plus 114876-115342
	404097	7770701	Plus 55512-55781
70	404145	9853643	Plus 30507-31206
	404187	4481839	Plus 764-7991
	404289	9711443	Plus 70261-70404,72944-73063
	404364	9964977	Minus 32986-33022
	404401	7259738	Plus 71066-71326
75	404753	7637341	Plus 14770-14831
	404844	8248547	Minus 23955-24034,25143-25264
	404900	7331453	Plus 22032-22219
	404954	7387327	Plus 131720-132042
	405037	7543748	Minus 127374-127578
80	405110	8096588	Minus 118540-119100
	405650	4926905	Minus 71743-72291
	405669	4508140	Plus 14130-14270
	405953	7960374	Minus 85101-85574

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406242	7417725	Minus	36736-36951		
406291	5686274	Plus	9562-9867		
406293	5686274	Minus	17664-17953		
406333	9213235	Plus	64689-64758		
406560	7711569	Minus	35 812-35292		
406569	8224211	Plus	38066-38695		
406597	8248613	Minus	132738-132985,134266-134425,135034-135192,135471-135608,137345-137478,138768-138912		
10	TABLE 48A: ABOUT 426 GENES UPREGULATED IN MELANOMA RELATIVE TO NORMAL BODY TISSUES				
	Table 48A lists about 426 genes upregulated in melanoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eca/AFlymelia Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.				
15	Phy:	Unique Eca probe set identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenelD:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Mean of melanoma AIs divided by the mean of normal tissue AIs, where the minimum value for the numerator and denominator was set to 1.0			
20	Phy	ExAccn	UnigenelD	Unigene Title	R1
	426555	NM 000372	Hs.2053	tyrosinase (oculocutaneous albinism IA)	376.61
	426655	H05769	Hs.188757	Homo sapiens, clone MGC.5564, mRNA, comp	324.36
	433377	NM 001522	Hs.201655	dopachrome tautomerase (dopachrome delta	231.30
	453344	BE349075	Hs.444571	ESTs	180.67
25	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	107.36
	417166	AA431323	Hs.421146	ESTs	97.76
	425234	AW152225	Hs.165959	ESTs, Weakly similar to I30822 hypochlorite	96.76
	344826	AF155661	Hs.222565	pyruvate dehydrogenase phosphatase	94.52
	427528	AW077143	Hs.179565	minichromosome maintenance deficient (S,	90.88
	432809	AL120669	Hs.6111	aryl-hydrocarbon receptor nuclear trans	87.91
	443983	H04482	Hs.163724	ESTs	85.55
	428513	BE220806	Hs.184697	Homo sapiens clone 23785 mRNA sequence	85.03
	419596	AL137535	Hs.40056	cadherin 15, type 2	84.27
	423605	AF047826	Hs.129887	cadherin 15, type 2	80.88
35	430540	AW245422		Homo sapiens cDNA: FLJ22105 ts, clone H	80.64
	115975	NM 004131	Hs.1051	granzyme B (granzyme Z, cytotoxic T-lym	75.09
	421633	AF121660	Hs.106260	sorbing nexin 10	71.52
	442064	AI422867	Hs.88594	ESTs	69.88
	418310	AA814100	Hs.86693	ESTs	67.94
40	423799	AW026500	Hs.125505	ISA24 protein	67.64
	432866	BE154829	Hs.279704	chromatin accessibility complex 1	63.24
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	63.18
	432862	NM 013257	Hs.279598	serum/glucocorticoid regulated kinase-1	62.33
	454038	AW052425		gb:CMG-CT0042-650899-018-01 CT0042 Homo	61.62
45	430338	IA6664	Hs.165935	hypothetical protein FLJ12015	60.52
	422363	T55979	Hs.115474	replication factor C (pactivator 1) 3 (28	56.73
	407748	AL075409	Hs.38176	KIAA606 protein; SCN Circadian Oscillator	56.33
	456800	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,	56.00
	441224	AL078584	Hs.7753	calpain	55.27
50	406418	AW953857	Hs.44743	KIAA1435 protein	56.79
	428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	56.45
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	56.29
	426274	NM 000055	Hs.1327	bulky/nucleohistonease	56.15
	407866	AA243261	Hs.266175	phosphoprotein associated with GEMs	55.82
55	420552	AA000492	Hs.58806	hypothetical protein	55.39
	442355	AA456339	Hs.8262	lysosomal-associated membrane protein 2	54.97
	429747	MR7507	Hs.2490	caspace 1, apoptosis-related cysteine pr	52.85
	410174	AA330607	Hs.59461	DKF ZP342C245 protein	52.00
	437396	BE140396	Hs.21621	hypothetical protein DKF Zp7620076	51.57
60	409557	BE182896	Hs.3686	ESTs	51.64
	424301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	51.42
	414403	AA706551	Hs.76064	ribosomal protein L27a	50.58
	452959	AA887829	Hs.40527	ESTs	50.21
	458997	AW937420		ESTs	49.97
65	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	49.85
	435905	AA959484	Hs.5003	KIAA0456 protein	49.76
	424900	AL735586	Hs.153203	MyoD family inhibitor	49.33
	426827	AA067805	Hs.172665	methyltetrahydrofolate dehydrogenase	47.91
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC, HUMAN III	47.45
70	420000	AB030603	Hs.94262	p53-inducible ribonucleotide reductase s	46.52
	419485	AA489023	Hs.59807	ESTs, Weakly similar to unnamed protein	46.79
	451134	AA318315	Hs.25699	hypothetical protein FLJ22155	45.52
	430066	AI929659	Hs.237825	signal recognition particle 72D	45.45
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattract	44.58
75	405447	AF121223	Hs.25010	hypothetical protein P15-2	43.36
	446019	AI362520		histone deacetylase 3	43.03
	430015	AW762399		ESTs	42.45
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14534 fs, clone PL	42.36
	405927	L41162	Hs.53563	collagen, type IX, alpha 3	42.30
80	425390	AI026334	Hs.156114	protein tyrosine phosphatase, non-recept	41.42
	411088	BE247593	Hs.145053	ESTs	41.21
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE360551, mRNA,	40.94
	441590	AI623207	Hs.190537	ESTs	40.66

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	457465	AW301344	Hs.122908	DNA replication factor	35.91
	430280	AA361258	Hs.237868	interleukin 7 receptor	36.91
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	38.70
5	421782	AA206914	Hs.40782	ESTs	38.55
	448275	BE514434	Hs.70030	kinesin-like 2	36.00
	453912	AL172131		SWI5NF related, matrix associated, act	37.94
	414644	AA298874	Hs.77494	deoxyguanosine kinase	37.85
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	37.70
10	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	37.64
	409078	AW327515		ESTs	37.30
	449845	AW871103	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	37.27
	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	37.21
	456819	A1767472	Hs.146290	ESTs, Weakly similar to putative p150 [H	37.21
15	451418	BE387790	Hs.26349	hypothetical protein FLJ20287	37.00
	433276	AW503733	Hs.3414	KIAA1488 protein	36.50
	445784	A1953155	Hs.146065	ESTs	35.36
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	33.09
	407755	AA116021	Hs.38260	ubiquitin specific protease 18	32.05
20	447337	AL109716	Hs.70034	Homo sapiens mRNA full length insert cDN	31.00
	438549	BE368601	Hs.21850	intracellular repeat containing 3	30.76
	429083	Y09397	Hs.227817	BCL2 related protein A1	30.73
	444670	H58373	Hs.332938	hypothetical protein MGCS370	28.45
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	27.62
	433576	BE000715	Hs.161091	ESTs	27.42
25	427173	BE395828	Hs.250619	protholin-like protein MD5019 (CEM15)	27.36
	408962	BE366436	Hs.44317	SRV (sex determining region Y)-box 10	26.66
	427257	A1739528	Hs.28345	ESTs	25.94
	414646	AA553776	Hs.301	CD48 antigen (B-cell membrane protein)	25.39
30	438765	AW871653	Hs.75319	ribonucleotide reductase M2 polypeptide	24.55
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	22.40
	427581	NM 014788	Hs.179703	KIAA0129 gene product	22.15
	435756	AF193766	Hs.13072	cytokine-like protein C17	20.61
	429988	N27639	Hs.334334	transcription factor AP-2 alpha (activat	19.79
	444853	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	18.73
35	417404	NM 007350	BE42101	pleckstrin homology-like domain, family	19.27
	450080	BE550224		metallothionein 1E (functional)	18.09
	417018	MI15038	Hs.80887	v-ras-1 Yamaguchi sarcoma viral related	17.97
	446054	AB014537	Hs.13904	KIAA0637 gene product	15.67
40	437656	NM 002104	Hs.3066	granzyme K (panine protease, granzyme 3;	15.54
	414896	AF002020	Hs.76918	Niemann-Pick disease, type C1	15.06
	457211	AW072665	Hs.32399	ESTs, Weakly similar to SS1797 vesiculol	14.83
	414821	ME3035	Hs.77424	Fc fragment of IgG, high affinity Ia re	14.84
	422465	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	14.61
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S	14.12
45	421334	BE297279	gb.60117562SF1 NIH_MGC_17 Homo sapiens c	13.94	
	424223	AF283777	Hs.116481	CD72 antigen	13.17
	406996	A1979168	Hs.344096	glycoprotein (transmembrane) emb	13.33
	416406	D89661	Hs.79299	lipoma HMGC fusion partner-like 2	12.76
	427536	BE277141	Hs.115803	gb.60117066SF1 NIH_MGC_20 Homo sapiens c	12.76
50	423188	MI01533	Hs.1634	cell division cycle 25A	12.56
	430770	AA765694	Hs.123296	ESTs	12.50
	407833	AW955637	Hs.66666	ESTs, Weakly similar to S19590 proline-r	12.09
	430822	AJ005371	Hs.248017	glyceralddehyde-3-phosphate dehydrogenase	11.46
55	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	10.57
	446950	AA350600	Hs.16672	hypothetical protein AF140225	10.04
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	9.98
	440356	AL120837	Hs.20993	high-glucose-regulated protein 8	9.88
	426799	AH478619	Hs.104677	ESTs	9.36
	437271	AL137445	Hs.26846	Homo sapiens mRNA; cDNA DKF Zp5660134 (f	9.03
60	447769	AW693704	Hs.320631	Homo sapiens cDNA FLJ14597 fs, clone NT	9.01
	408083	AW015310	Hs.23165	ESTs	8.99
	407966	AA295052	Hs.30516	Homo sapiens, clone MGC:15887, mRNA, com	8.99
	456524	A1510169	Hs.25132	KAR4070 gene product	8.91
	410101	A1338045	Hs.203559	hypothetical protein FLJ17201	8.90
65	417129	A1381800	Hs.300684	calicottin gene-related peptide-receptor	8.86
	453507	AF083217	Hs.33005	WD repeat domain 3	8.68
	447239	NM 007774	Hs.8579	cytosolic acyl coenzyme A thioester hydr	8.46
	456249	A2061144	Hs.82508	histone H2C06 protein	8.38
70	437796	BE140581	Hs.155573	polymerase (DNA directed), eta	8.35
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	8.20
	442711	AF151073	Hs.8545	hypothetical protein	8.14
	406405	AK001332	Hs.44672	hypothetical protein FLJ10470	7.96
	420208	BE279625	Hs.55572	sliver (mouse homolog) like	7.88
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	7.79
	449217	AA278336	Hs.23762	ribonucleotidyl transferase A family, 16	7.66
	451239	H24302	Hs.23127	ESTs	7.50
	442926	A1733982	Hs.333938	hypothetical protein MGCS370	7.40
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	7.39
	439574	AH469780		ESTs	7.13
80	431360	NM 090427	Hs.251680	tricin	7.12
	412430	AB087628	Hs.110741	ESTs	6.96
	452882	AW972990	Hs.196270	biolate transporter/chan	6.87
	436581	AA725726	Hs.180213	ESTs	6.64

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5	431317	AA502882		glbng23d91.s1 NG_CGAP_Ov2 Homo sapiens	6.53
	432364	BE221477	Hs.132137	ESTs, Moderately similar to A47552 6-ct	6.58
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22526 fs, clone H	6.53
	408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3	6.52
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	6.50
10	453878	AW964468	Hs.19025	DC37	6.48
	424148	BE242274	Hs.17411	integrin, beta 7	6.44
	407876	NM 004519	Hs.40866	potassium voltage-gated channel, KQT-4k	6.39
	409512	AW919187	Hs.283591	melanoma differentiation associated prot	6.39
	427951	AI826125	Hs.43546	ESTs	6.32
15	448664	AI973117	Hs.334591	splicing factor 3a, subunit 1, T20K	6.03
	416640	BE262478	Hs.79404	neuron-specific protein	6.01
	446830	BE175030		Human DNA sequence from clone RPS-1174N9	5.98
	452629	W02772	Hs.180178	Homo sapiens, clone IMAGE:3947276, mRNA,	5.93
	427390	AA32163	Hs.268231	Homo sapiens cDNA: FLJ23111 fs, clone L	5.73
20	427853	AI587098	Hs.58260	ESTs	5.55
	434398	AA121098	Hs.3638	serum-inducible kinase (SNIK)	5.54
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-etc	5.54
	428524	AA429772		ESTs	5.53
	431797	BE165641	Hs.270134	hypothetical protein FLJ20280	5.50
25	418403	DE6978	Hs.84790	KIAA0225 protein	5.50
	411524	AW850303		gbril.3-CT219-191199-030-F09 CT0219 Homo	5.47
	426158	NM 001982	Hs.195067	v-erb-b3 avian erythroblastic leukemia v	5.40
	443086	AW971725		size oculis homoeous (Drosophila) homolog	5.38
	447735	AA175266	Hs.6127	Homo sapiens cDNA: FLJ23020 fs, clone L	5.38
30	406843	AIW198333	Hs.119598	ribosomal protein L3	5.36
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	5.25
	447674	BE270640	Hs.19152	cyclin-dependent kinase 2	5.23
	410291	AA481131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	5.23
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17338, mRNA, com	5.09
35	420264	NM 014537	Hs.52463	KIAA0596 protein	5.03
	414734	AA151712	Hs.82572	ESTs	5.01
	426789	AI990401	Hs.21213	ESTs	4.99
	426793	X85887	Hs.172350	HIR (histone cell cycle regulation defect	4.98
	428612	AA770001		ESTs	4.57
40	411950	W03011	Hs.306881	MSTP043 protein	4.52
	447349	AI378546		gbric3604.r1 Scores_total_tetns_Nb2HF8_	4.46
	433328			Target Exon	4.85
	452840	AI059793	Hs.43481	hypothetical protein DKFZp564K152	4.83
	438310	AF086120	Hs.102793	ESTs	4.82
45	451281	AF068565	Hs.252708	ESTs	4.81
	431183	NM 008655	Hs.258936	KCEL (Lys-Asp-Glu-Leu) endoplasmic retic	4.82
	427871	AW956205	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	4.74
	435963	AF271212	Hs.322901	disruptor of silencing 10	4.67
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.66
50	414770	BE257224		Homo sapiens, clone IMAGE:3813720, mRNA	4.66
	419628	HE7546	Hs.46758	ESTs	4.64
	420258	AA477514	Hs.96247	transin-associated factor X	4.63
	448341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	4.58
	420267	N07030	Hs.175337	ESTs	4.57
55	412228	AW503785	Hs.73792	complement component (3dE)protein Barr vi	4.55
	432888	T86623		gbrdy1a08.s1 Scores fetal liver spleen	4.55
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	4.53
	418340	NM 013286	Hs.84162	chromosome 3p21.1 gene sequence	4.50
	409838	T97449	Hs.50032	small inducible cytokine subfamily A (Cy)	4.44
60	447454	AA464839	Hs.252966	hypothetical protein FLJ14697	4.42
	452036	NM 003500	Hs.27621	semA domain, seven thrombospondin repeat	4.41
	405903	K03121		glc-Human glyceroldehyde-3-phosphate dehy	4.40
	454541			glyoxysymidase-like 3	4.34
	434203	BE202677	Hs.283558	hypothetical protein PRO1855	4.33
65	450988	AW292933	Hs.254110	ESTs	4.31
	421535	AB002389	Hs.105478	phosphoribosylformylglycyltranslase synth	4.31
	415912	H08855	Hs.205493	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.30
	451259	NM 005052	Hs.26146	Down syndrome critical region gene 3	4.29
	452548	AL050321	Hs.301532	CRP2 binding protein	4.28
70	432195	AJ243669	Hs.8127	KIAA0144 gene product	4.24
	445101	T75202	Hs.12314	Homo sapiens mRNA, cDNA DKFZp566C1019 if	4.22
	423913	AA365789	Hs.26146	SECF2, vesicle trafficking protein (S c	4.19
	423454	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	4.18
	442092	AW578669		hypothetical protein FLJ12439	4.16
75	424954	NM 000546	Hs.1846	homo protein p53 (Li-Fraumeni syndrome)	4.05
	427719	AI331122	Hs.134726	ESTs	4.04
	415310	PI6113		gbrE3H05.r1 Scores infant brain 1N18 H	4.04
	416058	L08895	Hs.78995	MADS box transcription enhancer factor 2	4.03
	427828	AI024471	Hs.98232	ESTs	3.93
80	410079	U94362	Hs.58589	glycogenin 2	3.92
	420655	AA766289	Hs.86887	ESTs	3.92
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	3.90
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	3.89
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.88
	422159	AI867118		cathepsin	3.87
	429238	NM 002849	Hs.198288	protein lysine phosphatase, receptor t	3.86
	418827	BE327311	Hs.47166	HT021	3.84

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426050	BE391854	Hs. 7970	gb:501265394F1 NIH_MGC_44 Homo sapiens c	3.82
442271	AF000652	Hs. 8180	synectan binding protein (tyrosine)	3.81
410235	AA082977	Hs. 8180	gb:zn07010.r1 Stratagene hNT neuron (S37	3.79
408636	BE294925	Hs. 45580	CGI-12 protein	3.78
424624	AB032947	Hs. 151301	Ca2-dependent activator protein for secr	3.76
411400	AA311919	Hs. 59851	nuclear protein family A, member 1 (N4	3.74
458215	AA028160	Hs. 30925	gb:zn08101.s1 Soares_NFL_T_GBC_S1 Homo s	3.73
425874	AK001061	Hs. 30925	hypothetical protein FLJ10199	3.72
442643	U82756	Hs. 18676	PRP4/STRAW2 splicing factor 2	3.70
447471	AF039843	Hs. 18676	sprouty (Drosophila) homolog 2	3.70
447644	AW861522	Hs. 108646	Homo sapiens cDNA FLJ14534 fs, clone PL	3.67
422616	BE300330	Hs. 116725	serenophosphate synthetase 2	3.64
433160	AW207002	Hs. 134342	TASP for testis-specific adriamycin sens	3.64
418180	BE518087	Hs. 63724	hypothetical protein MGC5456	3.62
425632	A084746	Hs. 119374	RAS p21 protein activator (GTPase activa	3.62
425669	AA359597	Hs. 301701	Homo sapiens cDNA FLJ12073 fs, clone HE	3.62
412156	H29487	Hs. 17110	Homo sapiens mRNA; cDNA DKFZp404C2016 (f	3.61
417426	NM 007291	Hs. 82124	laminin, beta 1	3.61
407168	AA457352	Hs. 82124	gb:aa52111.s1 Stratagene fetal retina S3	3.61
425620	NM 003378	Hs. 171014	VGF nerve growth factor inducible	3.61
440760	AK001145	Hs. 284216	hypothetical protein FLJ10283	3.60
446481	W15284	Hs. 74832	ESTs	3.59
414111	BE047679	Hs. 125982	hypothetical protein FLJ13117	3.59
437862	AW578107	Hs. 5894	Homo sapiens mRNA; cDNA DKFZp666G0224 (f	3.59
409703	NM 006187	Hs. 56009	Z-S-oligoadenylate synthetase 3 (100 k	3.59
406981	S71129	Hs. 56009	acetylcholinesterase (YT blood group)	3.59
431586	AW971100	Hs. 293189	ESTs	3.58
415173	AK501735	Hs. 180059	ESTs	3.57
430512	AF182294	Hs. 241578	U6 snRNA-associated Sm-like protein Lsm8	3.57
446126	AW068909	Hs. 241578	pleckstrin homology domain interacting p	3.57
405305	AA070078	Hs. 3618	gb:zn60005.r1 Stratagene fibroblast (S37	3.57
433867	AK000596	Hs. 3618	hypocretin-like 1	3.56
459721	AZ099000	Hs. 143635	gb:gn1412.x1 NCL_CGAP_Lus5 Homo sapiens	3.56
441412	AJ353657	Hs. 159750	ESTs	3.55
416114	AJ655549	Hs. 183866	glicuronidase, beta	3.55
454670	U8363681	Hs. 10004	gb:PM0.4.T0019-090300-602-e11 L10019 Homo	3.54
443105	XN6753	Hs. 22570	chondroin sulfate proteoglycan 4 (neta	3.53
444680	A1186571	Hs. 22570	ESTs	3.51
413949	AA316077	Hs. 75639	Human T81 gene mRNA, 3' end	3.51
437033	AJ244364	Hs. 5409	RNA polymerase I subunit	3.50
412141	A143838	Hs. 48938	hypothetical protein FLJ21802	3.49
437158	AW050198	Hs. 48938	KIAA1150 protein	3.48
432642	BE297636	Hs. 3069	heat shock 70kD protein 9B (mortalin-2)	3.47
440634	AA821767	Hs. 132447	ESTs	3.47
445652	AL117473	Hs. 13036	DKFZP727A071 protein	3.46
425600	XT8686	Hs. 289114	hexabrachion (hexamer C, cytotactin)	3.43
420460	AA262331	Hs. 48376	Homo sapiens clone HB-2 mRNA sequence	3.43
426141	CO5886	Hs. 279397	ESTs	3.40
424321	WY4048	Hs. 1765	lymphocyte-specific protein tyrosine kin	3.40
445209	BE151830	Hs. 294145	ESTs	3.39
408304	AW810279	Hs. 294145	gb:MR4.ST0125-15129-029-a09 ST0125 Homo	3.37
416561	D87328	Hs. 79375	holocarboxylase synthetase (biotin-lipop	3.35
429247	AA306782	Hs. 122552	G-2 and S-phase expressed 1	3.34
453605	AW055308	Hs. 31803	ESTs, Weakly similar to N-WASP (Hs)sapin	3.34
420430	P21945	Hs. 346738	splicing factor, arginine/serine-rich 5	3.32
417386	AL037228	Hs. 82043	O123 gene product	3.32
400999	AJ951562	Hs. 126370	ESTs, Weakly similar to CNE3_HUMAN COPIN	3.31
407516	X64974	Hs. 126370	gb:H sapiens mRNA: HTPCRMO2 for octacyc	3.31
450065	AL250107	Hs. 24341	transcriptional co-activator with PDZ-li	3.31
416902	AA375634	Hs. 768974	hypothetical protein FLJ12528	3.28
432878	BE386490	Hs. 279663	Pinn	3.28
443296	AF952886	Hs. 313342	ESTs	3.27
429964	AJ918130	Hs. 21374	ESTs	3.25
428044	AA063322	Hs. 301404	RNA binding motif protein 3	3.25
425317	AW205118	Hs. 210546	interleukin 21 receptor	3.25
418064	BE387287	Hs. 83384	S100 calcium-binding protein, beta (neur	3.25
432917	NM 014125	Hs. 241515	PRC00327 protein	3.24
447871	BE297946	Hs. 239532	ESTs	3.24
414829	AA321568	Hs. 77436	pleckstrin	3.24
426996	AW968934	Hs. 173108	Homo sapiens cDNA: FLJ21897 fs, clone H	3.23
416188	BE157260	Hs. 79070	v-myc avian myelocytomatosis viral onco	3.22
428530	AA454191	Hs. 99362	Human DNA sequence from clone RP11-530N1	3.21
445174	AV652850	Hs. 172004	titin	3.19
459277	AW167599	Hs. 172004	ESTs	3.19
439039	AB66707	Hs. 48713	ESTs	3.15
415803	U50079	Hs. 88556	histone deacetylase 1	3.15
420005	AW271106	Hs. 133294	ESTs	3.15
422511	AJ076442	Hs. 117938	collagen, type XVII, alpha 1	3.14
452480	A1903526	Hs. 133131	gb:RC.E0101-090199-963 B01031 Homo sapien	3.14
445701	AF055581	Hs. 133131	lymphocyte adaptor protein	3.14
410878	BE450516	Hs. 293732	hypothetical protein MGC23195	3.13
458664	AJ300427	Hs. 293732	gb:gn1807.x1 NCL_CGAP_Lus5 Homo sapiens	3.13
436315	BE390513	Hs. 279355	hypothetical protein MGC4837	3.13

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	430441	BE390891		dsomoplatin (DPI, DPI)	3.12
	435080	A031760	Ha.155111	hypothetical protein FLJ14428	3.12
	429606	US2112	Ha.158331	reinin-binding protein	3.11
5	432978	AF126743	Ha.279884	DNAJ domain-containing	3.10
	452626	BE426286	Ha.301036	peroxisomal biogenesis factor 6	3.11
	445027	A073016	Ha.15725	hypothetical protein S56048	3.10
	427647	W19744	Ha.180059	Homo sapiens cDNA FLJ20653 fs, clone KA	3.09
	417211	T97617	Ha.269092	ESTs	3.08
10	448740	AF146761	Ha.20450	BCM-like membrane protein precursor	3.08
	448752	AAS3867	Ha.300842	KIAA1508 protein	3.07
	415355	H48875	Ha.268906	ESTs	3.07
	425345	AU077297	Ha.155894	protein tyrosine phosphatase, non-recept	3.07
	410321	Y12860	Ha.62245	solute carrier family 25 (mitochondrial	3.07
	411395	AA836373	Ha.7542	KIAA1802 protein	3.07
15	410951	BE27331	Ha.78596	proliferating cell nuclear antigen	3.06
	432343	NM 002960	Ha.2961	S100 calcium-binding protein A3	3.06
	457991	BE53951	Ha.306996	Homo sapiens, clone IMAGE-3447073, mRNA,	3.05
	433201	AB040896	Ha.21104	KIAA1453 protein	3.03
20	416178	AB050327	Ha.152822	serologically defined breast cancer anti	3.02
	411975	A016058	Ha.144583	ESTs	3.01
	448719	AA033627	Ha.21858	trinucleotide repeat containing 3	3.00
	419870	AW403911	Ha.266175	phosphoprotein associated with GEMs	3.00
	429601	AF237621	Ha.60828	keratin 1 (epidermolytic hyperkeratosis)	2.94
25	415668	AW57084	Ha.306814	hypothetical protein FLJ21685	2.81
	453256	A056587	Ha.32556	KIAA0379 protein	2.81
	436856	AI469355	Ha.127310	ESTs	2.75
	417880	BE215395	Ha.82846	selectin L, lymphocyte adhesion molecule	2.60
	402029	NM 004454	Ha.43637	ets variant gene 5 (ets-related molecule	2.59
	404257	BE387593	Ha.21321	Homo sapiens clone FLB9213 PRQ2474 mRNA,	2.55
30	415314	N88802	Ha.5422	glycoprotein M68	2.51
	434276	AF122659	Ha.93605	luciferase zipper, putative tumor suppress	2.50
	424035	NM 002814	Ha.139226	replication factor C (activator 1) 2 (40)	2.48
	410600	AW575742		ESTs. Moderately similar to S65557 alpha	2.48
35	438180	AJ293742	Ha.199067	v-erb-B2 avian erythroblastic leukemia v	2.43
	444809	BE207568	Ha.208219	oculopontin	2.39
	458337	AL138387	Ha.256126	baculoviral VP repeat-containing 7 (lv	2.37
	410290	AA402307	Ha.322844	hypothetical protein DKF_Zp564A1.76	2.37
	411358	R47479	Ha.94761	KIAA1691 protein	2.36
40	427550	BE242818	Ha.311609	nuclear RNA helicase, DECD variant of DE	2.34
	426312	AF026393	Ha.181874	interferon-induced protein with leucine	2.29
	448659	BE362567	Ha.21406	signal transducer and activator of trans	2.24
	418661	NM 001949	Ha.1189	E2F transcription factor 3	2.23
45	459373	BE408266	Ha.301405	hypothetical protein PP3501	2.21
	417437	US2682	Ha.82132	interferon regulatory factor 4	2.21
	436700	A053690	Ha.301406	hypothetical protein PP3501	2.18
	450690	AA295695	Ha.333418	FXVD domain-containing ion transport reg	2.15
50	432800	BE391046	Ha.278962	AIM-1 protein	2.15
	421773	W69233	Ha.112457	ESTs	2.09
	440415	AA579258	Ha.6083	Homo sapiens cDNA, FLJ21028 fs, clone C	2.03
	433364	A075407	Ha.296083	ESTs. Moderately similar to I54374 gene	2.02
	412609	Z48804	Ha.74124	ocular albinism 1 (Nettleship-Falls)	2.01
55	443950	NM 001425	Ha.9999	epithelial membrane protein 3	2.01
	451537	R56631	Ha.25650	retinol X receptor, gamma	2.00
	427080	A0605287	Ha.301175	ras-related G2 sodium/iron toxin substrate	1.94
	413190	AA151802	Ha.40368	adaptor-related protein complex 1, sigma	1.90
	412626	A079076	Ha.75061	macrophage myristoylated alanine-rich C	1.91
	453779	ND5187	Ha.43388	28kD interferon responsive protein	1.86
	453107	NM 016113	Ha.279746	vavlike receptor-like protein 1	1.86
60	430637	BE160381	Ha.255299	S100 calcium-binding protein A11 (calgiz	1.86
	408561	AJ308037	Ha.84120	hypothetical protein MGCT3016	1.84
	413171	AA318325	Ha.75219	tyrosinase-related protein 1	1.83
	408016			Target E2a	1.82
	446644	NM 003272	Ha.15791	transmembrane 7 superfamily member 1 (wp	1.81
65	431836	AF178532	Ha.271411	beta-site APP-cleaving enzyme 2	1.77
	439496	BE616501	Ha.32243	Homo sapiens, Similar to RIKEN cDNA 1110	1.77
	447604	AW089933	Ha.301342	hypothetical protein MGCA342	1.76
	438865	UA4385	Ha.325495	tissue inhibitor of metalloproteinase 2	1.70
	446072	AF083811	Ha.7345	IMD1 (milklike arrest deficient, yeast, h	1.70
70	416091	AF295370	Ha.283082	defensin, beta 3	1.69
	446291	BE391753	Ha.14623	interferon, gamma-inducible protein 30	1.67
	425532	AL008726	Ha.118126	protective protein for beta-galactosidase	1.67
	418918	Y07871	Ha.69476	C2D antigen (p50), sheep red blood cell	1.67
	412580	AA113262	Ha.17901	Homo sapiens, clone IMAGE-3837015, mRNA,	1.67
75	448258	BE389893	Ha.343214	hypothetical protein FLJ20396	1.66
	414945	BE076358	Ha.77667	lymphocyte antigen 6 complex, locus E	1.66
	425262	DB1719	Ha.155418	CS3553 protein	1.65
	439237	AW408158	Ha.316893	ESTs, Weakly similar to AA7582 B-cell gr	1.64
	427923	AW274357	Ha.301406	hypothetical protein PP3501	1.63
80	424925	AF077069	Ha.153357	procoagulant-fibrin, 2-oxoglutarate 5-ido	1.62
	441539	AW194364	Ha.94814	interleukin-4-induced gene 1 protein (p	1.60
	445682	BE410233	Ha.13501	poecadillo (zebrafish) homolog 1, conlat	1.60
	412939	AW411491	Ha.75069	eukaryotic translation elongation factor	1.58
	417237	H66385	Ha.81737	palmitoyl-protein thioesterase 2	1.56

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412658	BE386745	Hs.74631	basigin (OK blood group)	1.56
447700	BE543146	Hs.281434	Homo sapiens cDNA FLJ14028 fs, clone HE	1.54
459614	BE297412	Hs.25185	hypothetical protein	1.53
459663	H43540	Hs.25292	ribonuclease Hc, large subunit	1.53
423397	NM.001838	Hs.1652	chemokine (C-C motif) receptor 7	1.49
425535	AB079737	Hs.152887	KIAA0468 gene product	1.46
403340	BE174626	Hs.321130	hypothetical protein MG22771	1.46
446755	AW451473	Hs.16134	serine/threonine kinase 10	1.46
454429	BE273437	Hs.301405	hypothetical protein PP3501	1.46
425722	AB590976	Hs.57031	hypothetical protein MGC13047	1.45
414509	AW161211	Hs.76294	CD33 antigen (melanoma 1 antigen)	1.44
422203	X57329	Hs.6557	transporter 1, ATP-binding cassette, sub	1.43
436378	AJ227874	Hs.95244	ESTs	1.42
424218	AF031824	Hs.143212	cystatin F (heukocytein)	1.42
434566	AW256877	Hs.248122	G protein-coupled receptor 24	1.42
439740	AL355512	Hs.6557	hypothetical protein BC1048E5.5	1.42
429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.42
427634	A359745	Hs.18449	hypothetical protein MGC10820	1.40
403409			NM_005299 Homo sapiens antigen p57 (mel)	1.40
434262	AF121858	Hs.12169	sorting nexin 1	1.34
431566	AW604451	Hs.265814	SPRY (Drosophila) homolog 4	1.32
427730	AW250649	Hs.180577	granulin	1.32
411742	AW247593	Hs.71819	eukaryotic translation initiation factor	1.31
450395	BE148545	Hs.161757	ESTs	1.30
413291	NM.025278	Hs.7268	simply-lactonase C (beta-galactosidase	1.26
442609	AL205956	Hs.8518	selenoprotein N	1.24
416929	N20535		melastatin 1	1.21
421975	AW361017	Hs.6459	hypothetical protein FLJ118356	1.21
454478	AW057149		superoxide dismutase 2, mitochondrial	1.20
437723	AB727221	Hs.13256	ESTs	1.18
416350	AF188625	Hs.185907	phospholipase A2, group IID	1.08

TABLE 48B:

Phy: Unique Euc. process identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Phy	CAT	Accession
33640	CAT Number	
40	713_2	BC017171 BC021195 NM_007126 AF100752 AL137377 ZG0768 BM174865 BG754806 AU124376 BG757203 BG764422 BG775028 BG824418 BM045810 AU120387 BG770238 BG566740 BG133231 BF759980 BG359988 BM048875 BE181070 BE313689 BE279144 BG030934 AW245347 AT070171 BF193681 BE355897 AA463876 AJ153792 AA458810 AA948113 AA4930916 AC52963 AA558168 AD240408 AF151843 A1311025 AW768399 AJ355156 AW037384 AW051015 BE465591 AA637648 AB184348 AF721757 AW151143 BE158925 BG110933 BM045810 BE903367 BE732715 BM043200 BE900063 BE900706 BE731097 BE390023 BG7673304 BF996405 BF988300 BM475542 AW246215 BE551897 BE903610 BE561550 BE560537 BE907382 BE732947 BE227204 BG761305 BE626242 BE391848 BE382475 BG020258 AW547991 BA509099 BE39191 BE229420 BE259109 AW245422 AA232847 AB914618 HB0534 BC301004 AL331791 AA35881 BF753112 AL577303 AA373265 BE746965 BF743630 BE797295 AC554913 BM018558 AB65266 AW072450 F20201 AW151405 AW551787 AA773468 BG259594 BE391163 BG021529 AA211288 BG767231 BM465265 BG240524 W52646 AA113434 BE785431 B041681 BG832385 BG323168 BG759470 BF363239 BF981332 BE259418 BE785738 B091658 N72512 W58732 W56860 BG058985 AA205260 H19721 W17051 W77958 BE262610 AA844319 W74143 W72214 N65154 BE723023 BG164095 AA531069 F13645 RA1354 AA022578 BG180977 BE354955 AA812018 AA740241 AC027722 AU150356 AA855395 AW97627 BE220225 AA854092 AW518114 A1243644 AA805453 AA810295 AA525118 A134786 AA31670 AA814436 A1271105 RD7704 AA76506 AA724553 AB15395 A137552 AA491103 AW030168 RD7703 AA89120 AW246235 AW028993 A78992 AU118515 AW071465 AA485611 AW571853 AW151286 BE775356 BE868005 BE007260 BG746251 BE562912 BM454584 AL134894 BF104082 H06991
45		AW062425 AW024111 BM453041 AA750783 BE218582 AJ440046 AW166131 BE515854 AB302996 AA461307 AD950881 AW023059 AA155799 AA115486 AL597396 AW889004 AW571420 AA137082 AA013374 BG619478 BG040189 AL362200 D25517 AU570784 AJ142347 AW269786 A127070C AW1610541 AW793806 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827
50		BC017171 BC021195 NM_007126 AF100752 AL137377 ZG0768 BM174865 BG754806 AU124376 BG757203 BG754422 BG775028 BG824418 BM045810 AU120387 BG770238 BG566740 BG133231 BF759980 BG359988 BM048875 BE181070 BE313689 BE279144 BG030934 AW245347 AT070171 BF193681 BE355897 AA463876 AJ153792 AA458810 AA948113 AA4930916 AC52963 AA558168 AD240408 AF151843 A1311025 AW768399 AJ355156 AW037384 AW051015 BE465591 AA637648 AB184348 AF721757 AW151143 BE158925 BG110933 BM045810 BE903367 BE732715 BM043200 BE900063 BE900706 BE731097 BE390023 BG7673304 BF996405 BF988300 BM475542 AW246215 BE551897 BE903610 BE561550 BE560537 BE907382 BE732947 BE227204 BG761305 BE626242 BE391848 BE382475 BG020258 BA547991 BA509099 BE39191 BE229420 BE259109 AW245422 AA232847 AB914618 HB0534 BC301004 AL331791 AA35881 BF753112 AL577303 AA373265 BE746965 BF743630 BE797295 AC554913 BM018558 AB65266 AW072450 F20201 AW151405 AW551787 AA773468 BG259594 BE391163 BG021529 AA211288 BG767231 BM465265 BG240524 W52646 AA113434 BE785431 B041681 BG832385 BG323168 BG759470 BF363239 BF981332 BE259418 BE785738 B091658 N72512 W58732 W56860 BG058985 AA205260 H19721 W17051 W77958 BE262610 AA844319 W74143 W72214 N65154 BE723023 BG164095 AA531069 F13645 RA1354 AA022578 BG180977 BE354955 AA812018 AA740241 AC027722 AU150356 AA855395 AW97627 BE220225 AA854092 AW518114 A1243644 AA805453 AA810295 AA525118 A134786 AA31670 AA814436 A1271105 RD7704 AA76506 AA724553 AB15395 A137552 AA491103 AW030168 RD7703 AA89120 AW246235 AW028993 A78992 AU118515 AW071465 AA485611 AW571853 AW151286 BE775356 BE868005 BE007260 BG746251 BE562912 BM454584 AL134894 BF104082 H06991
55		AW062425 AW024111 BM453041 AA750783 BE218582 AJ440046 AW166131 BE515854 AB302996 AA461307 AD950881 AW023059 AA155799 AA115486 AL597396 AW889004 AW571420 AA137082 AA013374 BG619478 BG040189 AL362200 D25517 AU570784 AJ142347 AW269786 A127070C AW1610541 AW793806 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827
60		BC017171 BC021195 NM_007126 AF100752 AL137377 ZG0768 BM174865 BG754806 AU124376 BG757203 BG754422 BG775028 BG824418 BM045810 AU120387 BG770238 BG566740 BG133231 BF759980 BG359988 BM048875 BE181070 BE313689 BE279144 BG030934 AW245347 AT070171 BF193681 BE355897 AA463876 AJ153792 AA458810 AA948113 AA4930916 AC52963 AA558168 AD240408 AF151843 A1311025 AW768399 AJ355156 AW037384 AW051015 BE465591 AA637648 AB184348 AF721757 AW151143 BE158925 BG110933 BM045810 BE903367 BE732715 BM043200 BE900063 BE900706 BE731097 BE390023 BG7673304 BF996405 BF988300 BM475542 AW246215 BE551897 BE903610 BE561550 BE560537 BE907382 BE732947 BE227204 BG761305 BE626242 BE391848 BE382475 BG020258 BA547991 BA509099 BE39191 BE229420 BE259109 AW245422 AA232847 AB914618 HB0534 BC301004 AL331791 AA35881 BF753112 AL577303 AA373265 BE746965 BF743630 BE797295 AC554913 BM018558 AB65266 AW072450 F20201 AW151405 AW551787 AA773468 BG259594 BE391163 BG021529 AA211288 BG767231 BM465265 BG240524 W52646 AA113434 BE785431 B041681 BG832385 BG323168 BG759470 BF363239 BF981332 BE259418 BE785738 B091658 N72512 W58732 W56860 BG058985 AA205260 H19721 W17051 W77958 BG262610 AA844319 W74143 W72214 N65154 BE723023 BG164095 AA531069 F13645 RA1354 AA022578 BG180977 BE354955 AA812018 AA740241 AC027722 AU150356 AA855395 AW97627 BE220225 AA854092 AW518114 A1243644 AA805453 AA810295 AA525118 A134786 AA31670 AA814436 A1271105 RD7704 AA76506 AA724553 AB15395 A137552 AA491103 AW030168 RD7703 AA89120 AW246235 AW028993 A789102 AU118515 AW971465 AA485611 AW571853 AW151286 BE775356 BE868005 BE007260 BG746251 BE562912 BM454584 AL134894 BF104082 H06991
65		AW062425 AW024111 BM453041 AA750783 BE218582 AJ440046 AW166131 BE515854 AB302996 AA461307 AD950881 AW023059 AA155799 AA115486 AL597396 AW889004 AW571420 AA137082 AA013374 BG619478 BG040189 AL362200 D25517 AU570784 AJ142347 AW269786 A127070C AW1610541 AW793806 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827
70		BC017171 BC021195 NM_007126 AF100752 AL137377 ZG0768 BM174865 BG754806 AU124376 BG757203 BG754422 BG775028 BG824418 BM045810 AU120387 BG770238 BG566740 BG133231 BF759980 BG359988 BM048875 BE181070 BE313689 BE279144 BG030934 AW245347 AT070171 BF193681 BE355897 AA463876 AJ153792 AA458810 AA948113 AA4930916 AC52963 AA558168 AD240408 AF151843 A1311025 AW768399 AJ355156 AW037384 AW051015 BE465591 AA637648 AB184348 AF721757 AW151143 BE158925 BG110933 BM045810 BE903367 BE732715 BM043200 BE900063 BE900706 BE731097 BE390023 BG7673304 BF996405 BF988300 BM475542 AW246215 BE551897 BE903610 BE561550 BE560537 BE907382 BE732947 BE227204 BG761305 BE626242 BE391848 BE382475 BG020258 BA547991 BA509099 BE39191 BE229420 BE259109 AW245422 AA232847 AB914618 HB0534 BC301004 AL331791 AA35881 BF753112 AL577303 AA373265 BE746965 BF743630 BE797295 AC554913 BM018558 AB65266 AW072450 F20201 AW151405 AW551787 AA773468 BG259594 BE391163 BG021529 AA211288 BG767231 BM465265 BG240524 W52646 AA113434 BE785431 B041681 BG832385 BG323168 BG759470 BF363239 BF981332 BE259418 BE785738 B091658 N72512 W58732 W56860 BG058985 AA205260 H19721 W17051 W77958 BG262610 AA844319 W74143 W72214 N65154 BE723023 BG164095 AA531069 F13645 RA1354 AA022578 BG180977 BE354955 AA812018 AA740241 AC027722 AU150356 AA855395 AW97627 BE220225 AA854092 AW518114 A1243644 AA805453 AA810295 AA525118 A134786 AA31670 AA814436 A1271105 RD7704 AA76506 AA724553 AB15395 A137552 AA491103 AW030168 RD7703 AA89120 AW246235 AW028993 A789102 AU118515 AW971465 AA485611 AW571853 AW151286 BE775356 BE868005 BE007260 BG746251 BE562912 BM454584 AL134894 BF104082 H06991
75		AW062425 AW024111 BM453041 AA750783 BE218582 AJ440046 AW166131 BE515854 AB302996 AA461307 AD950881 AW023059 AA155799 AA115486 AL597396 AW889004 AW571420 AA137082 AA013374 BG619478 BG040189 AL362200 D25517 AU570784 AJ142347 AW269786 A127070C AW1610541 AW793806 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827
80		BC017171 BC021195 NM_007126 AF100752 AL137377 ZG0768 BM174865 BG754806 AU124376 BG757203 BG754422 BG775028 BG824418 BM045810 AU120387 BG770238 BG566740 BG133231 BF759980 BG359988 BM048875 BE181070 BE313689 BE279144 BG030934 AW245347 AT070171 BF193681 BE355897 AA463876 AJ153792 AA458810 AA948113 AA4930916 AC52963 AA558168 AD240408 AF151843 A1311025 AW768399 AJ355156 AW037384 AW051015 BE465591 AA637648 AB184348 AF721757 AW151143 BE158925 BG110933 BM045810 BE903367 BE732715 BM043200 BE900063 BE900706 BE731097 BE390023 BG7673304 BF996405 BF988300 BM475542 AW246215 BE551897 BE903610 BE561550 BE560537 BE907382 BE732947 BE227204 BG761305 BE626242 BE391848 BE382475 BG020258 BA547991 BA509099 BE39191 BE229420 BE259109 AW245422 AA232847 AB914618 HB0534 BC301004 AL331791 AA35881 BF753112 AL577303 AA373265 BE746965 BF743630 BE797295 AC554913 BM018558 AB65266 AW072450 F20201 AW151405 AW551787 AA773468 BG259594 BE391163 BG021529 AA211288 BG767231 BM465265 BG240524 W52646 AA113434 BE785431 B041681 BG832385 BG323168 BG759470 BF363239 BF981332 BE259418 BE785738 B091658 N72512 W58732 W56860 BG058985 AA205260 H19721 W17051 W77958 BG262610 AA844319 W74143 W72214 N65154 BE723023 BG164095 AA531069 F13645 RA1354 AA022578 BG180977 BE354955 AA812018 AA740241 AC027722 AU150356 AA855395 AW97627 BE220225 AA854092 AW518114 A1243644 AA805453 AA810295 AA525118 A134786 AA31670 AA814436 A1271105 RD7704 AA76506 AA724553 AB15395 A137552 AA491103 AW030168 RD7703 AA89120 AW246235 AW028993 A789102 AU118515 AW971465 AA485611 AW571853 AW151286 BE775356 BE868005 BE007260 BG746251 BE562912 BM454584 AL134894 BF104082 H06991

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Table 43A lists about 1127 genes upregulated in primary melanoma and/or melanoma metastases relative to normal body tissues. These genes were selected from 59680 probesets on the Eot/Affymetrix Hu30 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Play Unique Eot probe set identifier number
EaAcch Exemplar Accession number, Genbank accession number
UnigeneID Unigene number
Unigene Title Unigene gene title

R1: 90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of normal tissue AIs
R2: 90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator
R3: 90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of heart, liver, lung, and kidney AIs

Play	EaAcch	UnigeneID	Unigene Title	R1	R2	R3
452838	U55011	Hs.30743	preferentially expressed antigen in melanoma	12.15	13.27	13.15
455555	NM_000372	Hs.2053	tyrosinase (melanocyte-specific tyrosinase)	11.77	14.73	11.77
430377	NM_001922	Hs.301855	dopachrome tautomerase (dopachrome decarboxylase)	10.53	19.55	10.27
420208	BE776055	Hs.55972	shc (mouse homolog) like	9.78	7.09	0.89
431360	NM_000427	Hs.251520	lactacin	9.40	7.20	8.84
421585	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	8.03	10.27	12.84
419628	HA586894	Hs.112408	S100 calcium-binding protein 47 (psoriasin)	7.56	8.92	6.49
435549	BE365801	Hs.21858	desmoglein 1	7.52	5.47	16.47
430686	NM_001942	Hs.2633	tinucleotide repeat containing 3	6.06	4.13	3.31
409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	5.86	8.22	0.77
428270	NL_001394	Hs.2359	dual specificity phosphatase 4	5.84	3.46	5.84
429927	A5321549	Hs.2248	small inducible cytokine subfamily B (C)	5.82	3.94	5.82
414812	X77355	Hs.77367	melanocyte-specific protein	5.81	3.33	6.79
453344	BE349075	Hs.44571	ESTs	5.78	1.07	5.98
425088	A4663372	Hs.169395	hypothetical protein FLJ12015	5.60	3.92	5.60
420275			ENSP00000251056: Plasma membrane calcium	5.12	4.22	5.12
416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte	5.09	3.33	4.14
426052	AF060877	Hs.99236	regulator of G-protein signaling 20	5.06	5.76	5.06
426500	NM_003378	Hs.171014	VGF nerve growth factor inducible	4.77	5.04	9.42
430838	N46564	Hs.165395	hypothetical protein FLJ12015	5.03	3.06	5.03
417542	J04129	Hs.82269	progestagen-associated endometrial protein	4.93	8.13	5.41
425334	AW152225	Hs.165808	ESTs, Weakly similar to 158022 hypophel	4.78	2.93	4.78
408962	BE365436	Hs.44317	SRY (sex determining region Y) box 10	4.75	3.26	4.75
410361	BE391804	Hs.62661	granulin binding protein 1, interferon-gamma	4.70	3.11	4.70
429933	AL134197	Hs.33597	protein kinase C, regulatory subunit	4.68	2.27	4.68
427755	AA116021	Hs.36260	ubiquitin specific protease 18	4.65	3.21	3.31
417166	AA431323	Hs.42146	ESTs	4.55	5.23	4.55
421773	W69233	Hs.112457	ESTs	4.52	11.11	0.96
427211	AF151073	Hs.8646	hypothetical protein	4.37	3.70	4.30
457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	4.37	3.08	6.75
428613	BE220805	Hs.184697	Homo sapiens clone 2285 mRNA sequence	4.32	2.61	4.32
447937	AL109715	Hs.20034	Homo sapiens mRNA full length insert cDNA	4.31	3.13	4.31
451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	4.28	2.89	2.17
433658	U30678	Hs.155110	immunoglobulin kappa constant	4.18	2.68	5.92
420301	AA761526	Hs.22020	paired box gene 5 (B-cell lineage specific	4.15	2.57	4.16
433447	U29195	Hs.5281	neuronal protein 1	4.15	2.26	6.46
445431	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	4.10	4.04	4.64
408380	AF123050	Hs.44532	diacylglycerol	4.02	2.46	5.33
421379	Y15221	Hs.103892	small inducible cytokine subfamily B (C)	4.02	3.48	3.19
421633	AF121860	Hs.106260	sorting nexin 10	4.01	2.61	3.36
454117	BE410100	Hs.40368	adaptor-related protein complex 1, pigma	3.98	3.88	3.98
417355	D13168	Hs.82002	endothelin receptor type B	3.95	2.46	3.66
420667	N37030	Hs.173337	ESTs	3.88	3.87	3.88
412228	AW303785	Hs.73792	complement component (3dE) protein B	3.81	3.04	7.94
427528	AU077143	Hs.179555	manichloromannan maintenance deficient (S	3.79	2.23	3.79
405451			diacylglycerol-like 3	3.78	3.74	4.06
448078	AK001256	Hs.22975	KIAA1575 protein	3.76	2.83	3.76
422759	AW028309	Hs.132706	19A24 protein	3.75	2.36	3.75
456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.73	2.59	6.97
444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibitor	3.72	2.15	3.92
427656	AF191495	Hs.180142	calmodulin-like skin protein (CLSP)	3.69	4.17	1.19
415817	U89657	Hs.70857	protein tyrosine phosphatase, receptor-t	3.64	2.08	3.64
423423	AF283777	Hs.116461	CDV2 antigen	3.64	2.94	3.64
419566	AL137938	Hs.40396	cathepsin B, type 2	3.56	2.22	4.68
420338	AA825955	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	3.55	2.96	4.70
412140	AA219691	Hs.73625	RAB8 interacting, kinesin-like protein	3.54	1.95	3.54
438073	AF196870	Hs.54277	DNA segment on chromosome X (uniquely 992	3.53	2.19	3.27
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothel	3.48	2.83	11.00
447922	BE280074	Hs.23960	cyclin B1	3.48	2.10	4.64
439393	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHA0b	3.47	3.90	4.98
452744	A257652	Hs.246107	Homo sapiens mRNA, cDNA, DRF Zp43ME082 (r	3.45	2.38	3.45
447210	AF103269	Hs.17752	phosphotyrosine-specific phosphatase	3.44	3.83	2.09
428904	AK000713	Hs.193736	hypothetical protein FLJ20705	3.43	2.39	3.43
407846	AA425202	Hs.40403	Cyph300-interacting transactivator, wit	3.41	4.33	5.41
423605	AF047026	Hs.129887	cathepsin B, type 2	3.40	1.97	4.06
421508	NM_004833	Hs.105115	absent in melanoma 2	3.38	2.77	5.46
428001	H97428	Hs.219907	ESTs, Moderately similar to Transforming	3.36	2.11	3.36
430770	AA756694	Hs.123296	ESTs	3.36	2.08	3.83
445784	A253135	Hs.146065	ESTs	3.32	2.02	3.80

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	422173	BE385828	Hs.2506.19	phorbol-like protein M05019 (CEM15)	2.53	1.68	3.16
	418506	AA084248	Hs.85339	G-protein-coupled receptor 39	2.53	2.74	3.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.52	1.62	3.17
	448140	AF167671	Hs.20450	BCAM-like membrane protein precursor	2.51	2.67	1.88
5	442926	AC073662	Hs.332938	hypothetical protein MGC2370	2.51	2.08	4.57
	417427	M02081	Hs.82727	interleukin 15 (lymphocyte chemoattractant)	2.51	1.74	2.68
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.51	1.67	2.24
	432800	BE391046	Hs.278962	AIM-1 protein	2.51	5.55	2.42
10	406896	AY979168	Hs.344296	glycoprotein (transmembrane) nmh	2.50	1.95	2.41
	410326	AC080029	Hs.47650	ESTs	2.50	2.63	2.50
	452833	BE559681	Hs.30736	KIAA0124 protein	2.50	3.14	3.07
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	2.49	3.38	2.91
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.48	1.85	2.70
	416460	AC06315	Hs.85858	CD8 antigen, alpha polypeptide (p32)	2.48	2.33	2.99
15	409142	AL118877	Hs.50758	SMCA (structural maintenance of chromosome	2.48	2.47	1.88
	412970	AB028436	Hs.177534	dual specificity phosphatase 10	2.46	2.00	0.98
	401780			NM_005557: Homo sapiens keratin 16 (foca	2.44	2.30	1.39
	415626	AA180295	Hs.210473	Homo sapiens cDNA FLJ14872, clone PL	2.44	1.57	0.88
20	432904	NM_060204	Hs.3066	granzyme K (serine protease, granzyme 3,	2.42	1.91	2.55
	417880	BE241595	Hs.82848	saractin L (lymphocyte adhesion molecule	2.42	2.31	4.27
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.41	2.73	2.41
	415762	BE314524	Hs.79376	putative transmembrane protein	2.41	2.07	3.41
	402703	NM_006167	Hs.56009	signal recognition particle 720 kD	2.41	2.34	2.26
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.40	1.65	2.40
25	453867	AL080235	Hs.35861	DKFZP586E1621 protein	2.40	2.19	8.13
	411290	AA402307	Hs.322844	hypothetical protein DKFZP56A4178	2.40	2.88	2.46
	403328			Target Exon	2.39	2.00	1.95
	427540	R12014	Hs.20976	ESTs	2.39	1.73	3.24
	448623	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.39	1.96	2.39
30	433648	AF095719	Hs.83764	carboxypeptidase A4	2.38	2.45	2.65
	433501	Z44110	Hs.86149	phosphohistone 3 phosphate-binding prot	2.38	1.85	2.38
	433066	AY926569	Hs.227765	signal recognition particle 720 kD	2.38	2.19	2.38
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2 m	2.37	1.99	6.23
35	450447	AF212223	Hs.25010	hypothetical protein P15 2	2.37	1.72	3.24
	458997	AW937420		ESTs	2.37	1.57	3.27
	451446	AB026286	Hs.171637	hypothetical protein MGC2628	2.35	1.90	2.39
	408838	AB696535	Hs.40369	ESTs	2.35	1.58	3.71
	448276	BE514434	Hs.20830	kinesin-like 2	2.35	2.19	2.35
	424148	BE422274	Hs.1741	integrin, beta 7	2.35	1.89	3.07
40	410700	AA323335	Hs.65941	hypothetical protein FLJ20073	2.35	1.85	2.35
	409105	AW467539	Hs.255977	ESTs	2.35	2.35	2.35
	452882	AW972990	Hs.196270	folate transporter/carrier	2.34	2.12	2.90
	425606	US2112	Hs.158331	renin-binding protein	2.34	2.69	1.69
	433676	BE080715	Hs.161091	ESTs	2.34	3.74	2.34
45	423494	AW054365	Hs.21413	Wiskott-Aldrich syndrome protein interac	2.34	2.08	4.48
	431620	AA126109	Hs.264981	Z-S-aldoladenylate synthetase 2 (65-71	2.33	4.83	2.66
	436614	AW104388	Hs.149091	ESTs	2.33	3.37	2.33
	426289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	2.33	1.67	4.28
	426827	AW067825	Hs.172655	methyltetrahydrofolate dehydrogenase	2.33	1.59	0.40
50	430015	AW768399		ESTs	2.33	1.76	2.33
	421282	AA286914	Hs.40782	ESTs	2.32	1.65	2.49
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	2.32	2.16	1.48
	432540	AB21517	Hs.105898	ESTs	2.32	1.59	2.35
55	419644	BE397287	Hs.83304	S100 calcium-binding protein, beta (neur	2.32	2.42	2.32
	414829	AA321508	Hs.77436	pleckstrin	2.32	1.91	2.32
	425390	AB026634	Hs.156114	protein tyrosine phosphatase, non-recept	2.31	1.63	2.31
	448659	BE383657	Hs.21486	signal transducer and activator of trans	2.31	2.79	2.41
	429819	AL113623	Hs.193811	KIAA0675 gene product	2.30	1.96	2.95
	409512	AW978187	Hs.293591	melanoma differentiation associated prot	2.30	1.85	3.66
60	425231	AA527161		ESTs	2.28	1.96	2.36
	416091	AF255370	Hs.283082	defensin, beta 3	2.28	2.76	2.18
	418478	L03945	Hs.1171	cyclic-dependent kinase inhibitor 2A (me	2.27	2.88	2.46
	427719	AI093122	Hs.134726	ESTs	2.27	1.98	2.29
	431830	Y16645	Hs.217387	small inducible cytokine subfamily A (Cy	2.27	2.16	4.09
65	457465	AW301344	Hs.122908	DNA replication factor	2.26	2.23	2.26
	431639	AK000880	Hs.266175	phosphoprotein associated with GEMs	2.26	2.13	3.16
	424845	BE052285	Hs.29724	Hs.29724	2.26	1.84	2.26
	424867	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.26	3.38	2.56
	439317	AW293413	Hs.132906	19A21 protein	2.26	2.04	2.73
70	449922	Z97630	Hs.226117	H1 histone family, member 0	2.26	1.59	2.38
	441362	BE514410	Hs.23804	RAB26 (R, carboxic) homolog (E coli Ra	2.25	1.86	3.07
	425388	AA332384	Hs.156110	immunoglobulin kappa constant	2.25	1.91	2.25
	417282	AA195203		RAB3C, member RAS oncogene family	2.25	2.20	3.20
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.24	2.69	2.78
75	431782	AW978167	Hs.5884	Homo sapiens mRNA, cDNA DKFZP586C0224 (2.23	2.20	2.51
	408915	AW136771	Hs.244349	epidermal differentiation complex protei	2.23	1.91	2.47
	442503	AF147078	Hs.150853	p53-responsive gene 5	2.23	3.62	0.85
	429747	M81507	Hs.2490	cathepsin 1, apoptosis-related cysteine pr	2.22	1.60	1.69
	424825	AF207009	Hs.153537	procaspase-hydrin, 2-oxopropionyl-5-dio	2.22	5.53	2.46
80	417683	AW958741	Hs.403068	actin-binding protein complex 1, sigma	2.21	1.91	4.32
	422947	AA306782	Hs.122652	G-2 and S-phase expressed 1	2.21	2.05	2.32
	445875	AF070524	Hs.13410	Homo sapiens clone 24453 mRNA sequence	2.20	2.69	2.91
	417366	BE185289	Hs.1076	small proline-rich protein 18 (comelin)	2.20	2.26	3.79

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[illegible]

2.20	1.96	2.44
2.20	3.28	2.59
2.20	1.98	3.40
2.20	1.44	2.31
2.18	2.44	2.70
2.18	1.75	2.70
2.18	1.55	2.44
2.18	1.43	2.37
2.17	3.07	1.76
2.17	1.86	4.15
2.17	2.38	2.91
2.17	2.02	2.22
2.16	1.87	2.49
2.16	1.55	2.26
2.15	1.56	2.84
2.15	1.76	2.97
2.15	1.85	2.74
2.14	1.88	4.85
2.13	2.08	2.13
2.12	1.67	3.41
2.12	1.75	2.27
2.12	2.14	1.48
2.12	2.46	2.67
2.12	2.16	2.82
2.11	2.01	0.68
2.10	2.52	2.10
2.10	1.52	4.01
2.10	1.53	2.10
2.10	1.55	2.41
2.09	2.11	2.86
2.09	2.61	2.09
2.09	1.76	4.10
2.09	3.91	2.38
2.09	1.52	1.28
2.08	1.86	2.08
2.08	2.83	2.08
2.08	1.06	2.23
2.08	1.94	2.60
2.07	1.91	1.52
2.07	3.56	0.97
2.07	1.88	2.68
2.07	1.72	2.22
2.07	2.26	4.22
2.07	1.74	1.90
2.06	2.08	1.43
2.06	2.12	2.06
2.05	1.65	2.91
2.06	1.97	2.42
2.05	2.44	2.05
2.05	2.37	2.05
2.05	1.67	1.82
2.05	1.56	1.99
2.04	1.52	2.07
2.04	2.02	2.11
2.04	4.57	1.84
2.04	1.67	2.05
2.03	1.80	2.21
2.03	1.53	2.31
2.02	1.73	2.02
2.02	1.86	5.47
2.02	1.39	1.67
2.02	1.57	2.02
2.02	2.22	2.15
2.01	2.55	1.75
2.01	2.58	2.39
2.01	1.50	2.01
2.01	1.73	2.09
2.01	2.42	0.78
2.01	1.65	1.72
2.01	1.61	1.03
2.00	2.11	2.33
2.00	1.89	2.24
1.99	1.59	1.50
1.99	2.03	2.29
1.99	1.42	2.17
1.99	1.89	1.99
1.99	2.23	3.44
1.99	2.05	0.32
1.98	2.48	2.79
1.98	1.93	1.96
1.98	2.22	1.91
1.98	1.68	1.96
1.98	1.67	2.18

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	409178	BE183948	Hs.52915	kallikrein 5	1.98	3.76	1.37
	420551	AW504614	Hs.283739	Human sapiens mRNA for FLJ01111 protein.	1.98	1.90	2.63
	414020	NM_002384	Hs.75703	small inducible cytokine A4 (homologous	1.97	1.88	1.23
	443105	X96753	Hs.9004	chondronin sulfate proteoglycan 4 (mela	1.97	1.95	5.55
5	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	1.97	1.77	1.97
	413174	AW572659	Hs.281373	hypothetical protein g434041.3	1.97	1.73	3.88
	420561	AS30037	Hs.84120	hypothetical protein MGC13016	1.97	2.89	2.08
	421866	M24470	Hs.14135	guanosine monophosphate reductase	1.97	1.95	2.65
	405506			Target Exon	1.96	1.72	2.27
10	412490	AW803564	Hs.288850	Human sapiens cDNA: FLJ25250 fs, clone H	1.96	1.74	2.35
	431379	AL139315	Hs.23785	Human sapiens mRNA, cDNA DKFZp447M123 (fr	1.95	2.09	2.77
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.95	1.66	2.58
	453931	AL121278	Hs.25144	ESTs	1.95	2.38	1.95
	424308	AW915531	Hs.154443	mindwzomosome maintenance deficient (S.	1.95	1.63	2.82
15	425947	AW009166	Hs.58376	ESTs	1.94	2.02	1.94
	442084	M42267	Hs.88594	PCNENSH predicted novel secreted protein	1.94	1.49	2.21
	400533			ENSP00000205376-FRED65 protein (Fragmen	1.94	1.69	1.94
	448752	AA593867	Hs.300842	KIAA1608 protein	1.94	1.71	2.40
	408638	BE294925	Hs.46680	CC-12 protein	1.94	1.69	2.25
20	435659	AW602166	Hs.222339	CEP1 protein	1.93	1.62	3.21
	405779			NM_005367:Human sapiens melanoma antigen,	1.93	1.83	1.99
	444670	H58373	Hs.332938	hypothetical protein MGC63170	1.93	1.97	1.93
	448950	AA305900	Hs.5672	hypothetical protein AF40225	1.93	1.56	1.61
	459185	AW961601	Hs.252405	hypothetical protein FLJ12295 similar to	1.93	2.12	2.63
25	409398	AA132672	Hs.7984	pleckstrin homology, Sec7 and collectin	1.92	2.12	2.51
	413916	N49813	Hs.75615	apocipoprotein C-II	1.92	1.98	0.22
	429509	AF002246	Hs.310863	cell adhesion molecule with homology to	1.92	1.65	6.38
	422594			NM_002462:Human sapiens myosin (beta	1.92	2.45	1.89
	427722	A1659076	Hs.97031	hypothetical protein MGC13047	1.92	2.69	2.30
30	421958	AA357185	Hs.109918	ras homolog gene family, member H	1.92	2.10	2.93
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.91	1.57	1.91
	415402	AA116487	Hs.177576	mannosyl (alpha-1,3)-glycoprotein beta-	1.91	1.44	1.68
	432380	AA381256	Hs.237668	interleukin 7 receptor	1.90	1.52	1.14
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	1.90	2.16	1.21
35	427073	AA352702	Hs.37747	Human sapiens, Similar to RIKEN cDNA 2700	1.90	1.84	2.07
	449293	AW274357	Hs.301406	hypothetical protein PP3501	1.90	4.26	1.70
	426470	AA328794	Hs.128644	ESTs	1.90	2.68	2.04
	409527	BE182896	Hs.3686	ESTs	1.90	2.01	1.90
40	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	1.90	2.49	2.52
	428125	AA339071	Hs.18425	leucine aminopeptidase	1.89	1.69	1.49
	427634	AA359745	Hs.182579	hypothetical protein MGC10820	1.89	3.99	1.99
	452874	AK011043	Hs.30525	hypothetical protein FLJ10199	1.89	1.67	1.45
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	1.89	2.55	1.39
	448243	AW369771	Hs.183668	integrin, beta 8	1.89	1.96	1.89
45	416114	A1665549	Hs.183668	glucuronidase, beta	1.89	1.70	1.10
	429335	Z98200	Hs.161374	HSP019 protein	1.88	1.86	2.04
	440672	AF083811	Hs.7345	MAD1 (maltic arrest deficient, yeast, h	1.88	4.16	1.78
	430171	AF086289	Hs.234766	skin-specific protein	1.87	2.70	0.75
	407366	AF028942	Hs.17518	gli Human sapiens cug3 mRNA, partial sequ	1.87	2.25	1.87
50	454284	AB000734	Hs.50640	JAK binding protein	1.87	1.98	1.46
	417370	T28651	Hs.62030	tryptophanyl-tRNA synthetase	1.87	2.73	1.71
	429417	AA158247	Hs.104879	serine (or cysteine) proteinase inhibitor	1.87	1.79	2.72
	401781			Target Exon	1.87	1.88	1.16
	440590	A1663448	Hs.266338	mucic sulfatase	1.86	1.79	1.13
55	428450	NM_014791	Hs.184338	KIAA0175 gene product	1.86	1.72	4.39
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	1.86	1.81	1.86
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	1.86	1.57	1.86
	433001	AF217513	Hs.279505	clone HQ6310 PRD0310p1	1.85	1.71	5.82
60	433107	NM_016113	Hs.279746	vonkillo receptor-like protein 1	1.85	2.75	1.84
	430441	BE398991	Hs.182226	desmoplakin (DPI, DPT)	1.85	1.80	2.79
	417512	TX6534	Hs.82226	glycoprotein (transmembrane) emb	1.85	1.80	1.86
	423673	BE003054	Hs.1695	metin metalloproteinase 12 (macrophage	1.85	1.94	1.85
	431958	X53629	Hs.2077	cathepsin 3, type 1, P-cathepsin (placenta	1.85	1.72	2.82
	414737	A1160386	Hs.125087	ESTs	1.84	1.90	1.94
65	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	1.84	1.57	1.84
	428311	NM_006551	Hs.183671	tryptophan 2,3-dioxygenase	1.84	1.41	0.12
	412141	A1183638	Hs.48938	hypothetical protein FLJ1802	1.84	1.70	3.15
	428515	AF030339	Hs.286229	pnein C1	1.84	1.66	1.94
	427914	AA417350	Hs.20575	ESTs	1.84	2.32	2.17
70	439352	BE514347	Hs.169615	hypothetical protein FLJ20989	1.84	1.55	1.84
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.83	3.20	1.75
	435860	AB51760	Hs.151111	hypothetical protein FLJ11420	1.83	1.62	1.47
	407966	AA295052	Hs.38516	Human sapiens, clone MGC15887, mRNA, com	1.83	1.58	2.11
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntho	1.83	1.73	2.18
75	433029	NM_014322	Hs.279926	opsin 3 (mammalian)	1.83	1.96	1.83
	426158	NM_001892	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.81	1.63	2.46
	423860	AA301657	Hs.41284	ESTs	1.82	2.44	1.82
	411027	AF072059	Hs.67946	leukocyte immunoglobulin-like receptor,	1.82	2.24	2.01
	441859	AW194364	Hs.94814	ESTs, Weakly similar to FIG1 MOUSE FIG-1	1.82	2.72	2.16
80	437435	AA249439	Hs.27227	hypothetical protein DKFZp782H1311	1.82	1.50	1.82
	443327	N30169	Hs.108923	R4B38, member RAS oncogene family	1.82	2.52	1.76
	420674	NM_000055	Hs.1327	butyrylcholinesterase	1.82	1.43	0.68
	439219	N33883	Hs.41322	ESTs	1.82	1.88	2.43

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5	432810	AA863400	ESTs	1.82	1.43	1.82
	447404	NM_007350	He.82101	1.82	1.98	1.82
	447484	AA664839	HS.25266	1.82	1.63	1.82
	436456	AA52677	HS.248122	1.82	2.80	2.18
	418918	XD1871	HS.89476	1.82	2.28	1.80
10	424755	AB033094	HS.152925	1.82	1.85	1.62
	436315	BE390513	HS.27935	1.82	1.74	5.18
	420783	AB59838	HS.59923	1.81	1.87	0.80
	417105	XS0982	HS.81226	1.81	1.98	2.03
	423961	D13666	HS.136346	1.81	1.73	2.45
15	448019	AI362520	histone deacetylase 3	1.81	1.39	2.24
	412580	AA113262	HS.17901	1.81	3.05	1.58
	409415	AA575258	HS.8083	1.80	2.00	1.78
	453684	AK001622	HS.34578	1.80	1.98	1.80
	446921	AB012113	HS.16530	1.80	1.56	1.71
20	453779	N35187	HS.43388	1.80	2.42	2.04
	434706	AB562591	HS.116394	1.80	1.58	1.80
	416065	BE267931	HS.78996	1.80	1.79	2.51
	453331	AC40665	ESTs	1.79	1.43	2.33
	429412	NM_008235	HS.2407	1.79	1.46	4.46
25	428784	Y12851	HS.193470	1.79	2.30	1.79
	453507	AF032217	HS.33085	1.79	1.49	1.51
	452626	BE245286	HS.201636	1.79	1.57	2.00
	439237	AW408158	HS.318893	1.79	2.26	2.22
	406672	M26041	HS.198253	1.79	1.76	1.78
30	413009	BE140782	HS.40556	1.79	1.43	3.32
	452898	NM_001285	HS.301921	1.78	1.66	1.29
	424954	NM_000546	HS.1546	1.78	1.73	2.35
	456378	AJ227874	HS.99244	1.78	1.84	1.78
	421778	AA428000	HS.283072	1.78	1.96	3.67
35	421948	AJ2583	HS.334309	1.78	1.74	3.00
	414915	NM_002482	HS.76391	1.77	2.27	2.02
	437317	AA748613	HS.318777	1.77	1.98	2.32
	427318	AF186081	HS.157583	1.77	1.61	0.92
	418403	D86578	HS.64790	1.76	1.49	2.24
40	421433	AB591182	HS.22380	1.76	1.49	2.52
	450728	AW162523	HS.25363	1.76	1.74	1.76
	428655	H05789	HS.188757	1.76	1.43	1.76
	427536	BE271741	HS.115803	1.76	2.12	1.76
	453364	AB075407	HS.259683	1.76	1.66	1.46
45	401994		Target Exon	1.75	1.44	1.75
	418290	AA278530	HS.83968	1.75	1.69	1.70
	408633	AW983372	HS.46677	1.75	1.46	1.88
	429978	AA249027	HS.333418	1.75	1.60	1.82
	450660	AA256686	HS.168357	1.75	2.13	2.63
50	456667	AW004056	HS.183572	1.74	1.95	1.42
	417866	AW067903	HS.82772	1.74	2.64	2.01
	428746	AW503820	HS.192861	1.74	2.82	2.31
	420642	BE297535	HS.3069	1.74	1.51	1.62
	429505	AW820035	HS.278679	1.73	1.54	3.15
55	417851	AB826502	HS.97269	1.73	1.67	1.05
	453653	AW408337	HS.36672	1.73	2.22	2.28
	430413	AB842182	HS.241392	1.73	2.05	1.47
	415485	AA840023	HS.98907	1.73	1.71	1.73
	447217	BE465754	HS.17778	1.73	1.62	4.70
60	437673	AW665665	HS.153034	1.72	1.55	2.10
	437879	BE362092	HS.5594	1.72	2.50	1.80
	448410	AB001227	HS.21125	1.72	1.48	3.98
	413313	NM_002047	HS.283108	1.72	2.19	1.82
	452203	X57522	HS.9939	1.72	2.68	1.68
65	443950	NM_001425	HS.9939	1.71	2.17	2.24
	402989		ENSP0000034863 Zinc finger protein 131	1.71	1.71	1.71
	450832	AW970602	HS.105421	1.71	1.33	2.38
	453005	AW055308	HS.31803	1.71	1.67	1.95
	439783	AI125760	HS.24835	1.71	2.10	2.20
70	419678	NM_001527	HS.167379	1.71	3.96	1.76
	432259	BE269103	HS.274502	1.71	1.56	1.94
	420340	NM_000724	HS.97087	1.71	2.12	1.98
	428289	M26301	HS.2253	1.71	2.46	0.76
	424006	AF054815	HS.137548	1.70	1.70	2.78
75	440939	Z65188	HS.68174	1.70	2.72	1.60
	406646	M33600	HS.308026	1.70	2.27	1.33
	425367	BE271188	HS.155975	1.70	2.77	2.07
	420286	AF198395	HS.113717	1.70	1.90	3.21
	432355	AW007023	HS.322822	1.69	1.44	1.60
80	445247	AW274290	HS.153997	1.69	2.57	1.69
	436965	Z11894	HS.156110	1.69	1.52	3.13
	410257	BE244044	HS.61459	1.69	1.99	1.97
	424683	NM_002351	HS.151544	1.69	1.76	1.69
	427792	M63526	HS.186841	1.69	2.48	2.48
	458098	BE550224	metallothionein 1E (functional)	1.68	1.83	1.68
	425397	JK0498	HS.156346	1.68	1.57	4.09
	421485	AA243499	HS.104000	1.68	1.64	0.68

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421583	NM_005433	Hs.105906	granulysin	1.68	2.24	1.55
448775	AB025237	Hs.388	nadir (nucleoside diphosphate linked moi	1.68	1.98	2.05
451418	BE387790	Hs.26369	hypothetical protein FLJ20287	1.68	1.35	1.68
440457	BE387593	Hs.21321	Homo sapiens clone FL8711 PRO2474 mRNA,	1.68	1.88	1.63
430866	U4385	Hs.325495	issue inhibitor of metalloproteinase 2	1.67	2.54	1.90
401760			Target Exon	1.67	1.93	1.61
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.67	1.85	4.25
448644	NM_003272	Hs.15791	transmembrane 7 superfamily member 1 (up	1.67	1.54	1.48
415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	1.67	1.55	0.90
450293	N35654	Hs.171118	hypothetical protein FLJ19006	1.67	1.54	1.95
12856	BE386745	Hs.74631	basigin (OK blood group)	1.67	2.71	1.47
439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.66	1.82	1.19
424399	A506587		A505887 JL-8T095-190199-019 8T095 Homo	1.66	1.65	0.44
423255	AA344146	Hs.162185	ESTs, Weakly similar to 542799 gap prec	1.66	1.98	1.45
427239	BE270447		ubiquitin carrier protein	1.66	2.94	1.92
425262	D87119	Hs.155418	GS3655 protein	1.66	2.36	1.66
413869	NM_000878	Hs.75396	interleukin 2 receptor, beta	1.66	1.86	1.90
405688	X03068	Hs.73331	major histocompatibility complex, class	1.65	2.05	1.31
446217	A1651594	Hs.90709	ESTs	1.65	1.50	1.77
400222			NM_020822: Homo sapiens G protein-couple	1.65	1.74	1.81
432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TfT3	1.65	2.50	1.77
417237	H85385	Hs.81737	palmitoyl protein thioesterase 2	1.65	2.89	1.57
423012	NM_020465	Hs.279910	ATX1 (antioxidant protein 1, yeast) homo	1.64	2.76	1.26
446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	1.64	1.96	1.24
433867	AK000596	Hs.3618	hippocampin-like 1	1.64	1.47	1.00
433871	AW138797	Hs.132906	19A24 protein	1.64	2.17	1.96
416371	M13560	Hs.84296	CD74 antigen (exon/variant polypeptide of m	1.64	2.18	1.43
423236	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.64	1.67	1.64
406264	NM_014837	Hs.52463	KIAA0966 protein	1.64	1.46	4.89
431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.64	2.58	1.79
414586	AA306180	Hs.16488	lymphocyte cytosolic protein 1 (L1-plas	1.63	1.72	1.88
418117	AF522013	Hs.83496	leukin for activation of T cells	1.63	1.58	1.99
448304	BE622768	Hs.290356	mesoderm development candidate 1	1.63	1.67	1.86
425535	AB007937	Hs.158287	KIAA0468 gene product	1.63	2.56	1.97
453258	AW293134	Hs.132597	ring finger protein (CH2HC3) type 6	1.63	1.46	2.43
420000	AB030663	Hs.84292	p153-inducible ribonucleotide reductase s	1.63	1.54	1.94
447321	AW271217	Hs.281434	Homo sapiens cDNA FLJ14026 fs, clone HE	1.63	1.96	1.77
422192	AA305159	Hs.113019	fb485	1.62	1.45	1.62
450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	1.62	2.23	1.53
415381	BE023429	Hs.50993	heat shock 70MD protein 4	1.62	1.72	2.38
424779	AL048851	Hs.153053	CD37 antigen	1.62	1.92	2.10
413283	R78669	Hs.23756	hypothetical protein similar to swine ac	1.62	1.41	1.12
414907	X80725	Hs.77597	polo (Drosophila)-like kinase	1.62	2.03	2.13
414159	AW511414	Hs.257352	apoptoprotein L, 6	1.62	1.89	1.32
410055	AF250839	Hs.85241	gene for serine/threonine protein kinase	1.62	1.81	1.27
428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	1.62	1.50	2.13
436251	BE519065	Hs.296555	nucleolar protein (KHEO repeat)	1.61	1.71	2.02
451708	AF306536	Hs.60975	ESTs	1.61	2.31	1.70
418113	A272141	Hs.83484	SRV (sex determining region Y)-box 4	1.61	1.53	2.50
410600	AW575472		ESTs, Moderately similar to S65657 alpha	1.61	1.83	1.69
436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	1.61	1.56	1.61
440201	AL339588	Hs.7041	hypothetical protein DKF2p762B226	1.61	1.58	1.85
414368	W07171	Hs.75939	uridine monophosphate kinase	1.61	1.59	2.75
454429	BE273437	Hs.301406	hypothetical protein IP2801	1.61	2.54	1.52
422257	NM_001716	Hs.113916	Burkitt lymphoma receptor 1, GTP-binding	1.61	2.15	1.54
426437	BE076537	Hs.108995	ubiquitin-conjugating enzyme E2L 6	1.60	2.01	1.38
408626	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.60	2.00	1.60
414761	AU377228	Hs.77726	enhancer of zeste (Drosophila) homolog 2	1.60	1.36	2.23
426612	AF062949	Hs.252587	pituitary tumor-transforming 1	1.60	1.78	2.59
411263	BE297802	Hs.69380	kinasin-like 6 (mitotic centromere-assoc	1.60	1.78	2.07
417324	AW265494		ESTs	1.60	2.48	1.91
430325	AF004602	Hs.293356	synapsin binding protein 1	1.60	1.74	2.53
431797	BE169641	Hs.270134	hypothetical protein FLJ20280	1.60	1.46	2.46
434449	AW553484	Hs.3849	hypothetical protein FLJ22041 similar to	1.60	1.81	3.00
443376	AW392520	Hs.9290	proteasome (prosome, macropain) subunit,	1.59	1.88	1.68
417437	AF526812	Hs.62132	interleukin regulatory factor 4	1.59	1.90	2.26
437949	UT8519	Hs.41654	ESTs, Weakly similar to A46910 X-linked	1.59	2.14	1.59
401797			Target Exon	1.59	1.82	1.78
449720	AA311152	Hs.288708	hypothetical protein FLJ21562	1.59	1.45	4.69
424971	AA479005	Hs.154036	tumor suppressing subtransferrable candi	1.59	1.82	1.68
415474	NM_014252	Hs.78437	-solid cancer family 25 (retinoblastoma)	1.59	1.51	0.30
430017	AA263172	Hs.35	protein tyrosine phosphatase, non-recept	1.58	1.72	2.46
422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.58	1.85	1.94
434694	AA305599	Hs.238205	hypothetical protein PR00013	1.58	1.25	2.09
428844	AW972635	Hs.301994	hypothetical protein FLJ12671	1.58	1.72	1.80
440942	AW246547	Hs.17901	Homo sapiens, clone IMAGE 3937015, mRNA,	1.58	2.68	1.98
419596	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase	1.58	1.84	1.22
401151			Target Exon	1.58	2.43	1.60
441590	A1622207	Hs.190537	ESTs	1.58	1.40	1.58
418877	S83308	Hs.87224	SRV (sex determining region Y)-box 5	1.58	1.98	1.58
416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	1.58	2.28	1.60
418759	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	1.58	2.14	2.10
418216	AA662240	Hs.283099	AF15q14 protein	1.57	1.46	1.57

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	47700	AA022294	Hs.180383	dual specificity phosphatase 6	1.57	1.42	0.88
	438485	X59135	Hs.156110	immunoglobulin kappa constant	1.49	1.57	1.49
	404872			ENSP00000243173?D11109J22.1 (novel home	1.57	1.46	1.36
				hypothetical protein	1.57	1.55	2.73
	448201	AA297567	Hs.43728	synuclein, alpha (non A4 component of am	1.57	1.36	1.57
	414599	A815523	Hs.76830	type I transmembrane protein Fc14	1.57	1.70	1.13
	440406	BC395085	Hs.10086	mannosidase, alpha, class B2, member 1	1.57	1.75	1.57
	432946	U06899	Hs.279854	Human T-cell receptor active alpha-chain	1.57	2.26	2.10
	417929	R27219	Hs.74747	interferon, alpha-inducible protein (do	1.57	2.09	1.57
	431629	AU077025	Hs.265827	NM_022161?Homo sapiens. Iitin inhibitor-	1.56	2.28	1.45
10	402876			hypothetical protein FLJ21841	1.56	2.97	1.56
	414839	XG3692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	1.56	1.75	1.88
	405663	H43540	Hs.25292	ribonuclease H1, large subunit	1.56	2.76	1.67
	425818	AB027225	Hs.155581	matrix metalloproteinase 17 (membrane-	1.56	2.36	1.83
15	422765	AN049701	Hs.1578	baculoviral M1P repeat-containing 5	1.56	1.78	2.06
	422765	AA022764	Hs.123469	ESTs, Weakly similar to AF208855.1 BM-01	1.56	1.32	2.70
	453613	F06838		ESTs	1.56	1.76	1.84
	428379	X06026	Hs.22593	CD3G antigen, gamma polypeptide (TTC3 co	1.56	1.43	1.56
	429500	X78565	Hs.289114	hexanucleotide (tetanase C, cytotactin)	1.56	1.56	1.56
20	444652	BE513613	Hs.11538	actin related protein 23 complex, subun	1.56	2.01	1.56
	420842	A1083668	Hs.50601	hypothetical protein MGC10586	1.55	2.24	1.90
	447513	AA0958776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	1.55	1.24	3.07
	408901	AK001330	Hs.48655	hypothetical protein FLJ10468	1.55	1.79	2.17
	437669	AF381005	Hs.123954	ESTs, Weakly similar to match to ESTs AA	1.55	1.83	1.96
25	439437	A1207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	1.55	1.63	2.20
	418835	AL023594	Hs.88977	hypothetical protein d511E16.2	1.55	1.73	1.50
	485633	AA311426	Hs.21635	tubulin, gamma 1	1.54	2.02	1.67
	447763	BE515911	Hs.112603	hypothetical protein	1.54	2.52	1.52
30	430223	NM_002514	Hs.235935	neuropilin-2, alpha 1 (CD333)	1.54	1.54	3.03
	448258	BC386893	Hs.343214	hypothetical protein FLJ20396	1.54	1.97	1.53
	440165	AF014718	Hs.7753	collagenin	1.54	1.53	2.55
	433376	AI249361	Hs.741122	carcarg-4, apocystin-related cysteine pr	1.54	1.34	1.68
	445982	BE410233	Hs.13501	pescadillo (zebrafish) homolog 1, contai	1.54	2.21	1.54
35	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.54	2.50	1.94
	416526	H03109	Hs.263396	HT018 protein	1.54	1.41	2.01
	431630	NM_002204	Hs.25529	integrin, alpha 3 (antigen CD49c, alpha	1.54	1.89	1.23
	431519	AW153390	Hs.278654	heterochromatin-like protein 1	1.54	1.53	1.79
	420421	AF281133	Hs.343589	exosome component Rps41	1.53	2.47	1.61
40	406973	MA9996	Hs.198253	major histocompatibility complex, class	1.53	1.62	1.19
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.53	1.74	1.37
	423400	BE171364	Hs.128382	Homo sapiens mRNA, cDNA DKFZ01611224 (f	1.53	1.59	1.59
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-i	1.53	2.72	1.54
	429837	NM_003896	Hs.225939	sialyltransferase 9 (CMP-HexA:alphaLactosyl	1.53	1.64	2.40
45	412939	AF0411491	Hs.75069	eukaryotic translation elongation factor	1.52	1.98	0.98
	410678	BE540516	Hs.253732	hypothetical protein MGC3195	1.52	1.39	2.17
	431186	NM_012248	Hs.220697	ras-like protein	1.51	1.91	1.82
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.52	1.57	1.82
	422532	AL008126	Hs.118126	protective protein for beta-galactosidase	1.51	2.08	1.19
	413063	AL035137	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	1.51	1.50	0.67
50	412008	H50720	Hs.81892	HOXA101 (gene product)	1.51	1.42	7.41
	424902	NM_003866	Hs.153687	inositol polyphosphate 4-phosphatase, ty	1.51	2.75	1.51
	405204			NM_002085?Homo sapiens growth factor re	1.51	1.44	1.53
	424481	R19453	Hs.1787	proteolipid protein 1 (Pellicular-Merzbac	1.51	1.92	2.32
55	422516	BE284802	Hs.117650	multicatalytic proteinase similar to S	1.50	1.50	1.47
	418827	BE327311	Hs.47766	HT021	1.50	1.35	3.53
	427550	BE242818	Hs.311609	nuclear RNA helicase, DECD variant of DE	1.50	1.55	2.09
	423992	BE270472	Hs.279900	HSPO15 protein	1.50	1.82	0.82
	442432	BE503589	Hs.38178	hypothetical protein FLJ23468	1.50	1.34	4.87
60	418566	AW504515	Hs.205814	glyoxylate (Drosophila) homolog 4	1.50	3.05	1.51
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	1.50	1.38	0.46
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (spem re	1.50	2.05	1.78
	427861	S78796	Hs.108966	phosphatidylinositol 4-phosphate 5-kinas	1.49	1.52	2.62
	422894	BE561617	Hs.119192	IG2A ligase family, member 2	1.49	2.02	1.49
65	452363	AB627433	Hs.94953	Homo sapiens, Similar to complement comp	1.49	2.02	1.41
	411825	AK000334		hypothetical protein FLJ26327	1.49	2.55	1.38
	409425	U04062	Hs.54462	zinc finger protein, subfamily 1A, 1 (Ik	1.49	1.77	1.49
	431010	AN048164	Hs.249184	transcription factor 15 (TCF1)	1.49	1.79	1.75
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	1.49	1.57	2.14
70	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	1.49	1.42	1.45
	411296	BE207307	Hs.10114	growth suppressor 1	1.49	1.74	1.50
	447894	W02112	Hs.8836	pinin, beta	1.49	2.25	1.51
	416381	AW024907	Hs.68772	ESTs, Weakly similar to CA13_HUMAN COL1A	1.49	2.06	1.89
	424182	AA336229	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.49	1.59	1.65
75	417131	NM_004585	Hs.17466	retinoic acid receptor responder (tozoa	1.49	2.00	1.22
	427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	1.49	2.12	1.41
	422646	BE513934	Hs.1563	neurophilin cytosolic factor 1 (NF2), chr	1.49	1.61	1.67
	417007	AF224741	Hs.80768	chloride channel 7	1.48	1.94	1.88
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	1.48	1.68	1.57
80	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.48	1.43	2.25
	410741	T11895	Hs.324473	mitogen-activated protein kinase 1	1.48	1.31	3.17
	447471	AF025943	Hs.18676	glyoxylate (Drosophila) homolog 2	1.48	1.35	1.48
	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11a (p180),	1.47	1.58	1.48
	442945	A024849	Hs.131853	ESTs, alpha L	1.47	1.73	1.38

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5	447200	BE543146	Hs.281434	Homo sapiens cDNA FLJ14028 fs, clone HE	1.47	1.89	1.53
	424085	NM_002914	Hs.139226	regulation factor C (activator 1) 2 (40)	1.47	2.03	1.47
	422867	L32137	Hs.1594	cartilage oligomeric matrix protein (pse	1.47	1.86	1.93
	416350	AF188625	Hs.189507	phospholipase A2, group IID	1.47	2.92	1.49
	459207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	1.47	1.81	1.73
10	447840	DB0892	Hs.20960	KIAA0229 protein	1.47	1.93	1.74
	446106	AA377165	Hs.44833	ESTs	1.47	1.56	1.53
	425811	AL036104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.47	1.78	1.84
	432615	AA557191	Hs.35028	ESTs, Weakly similar to 154374 gene NF2	1.47	2.04	1.47
	435099	AC004170	Hs.4756	flap structure-specific endonuclease 1	1.46	1.76	1.83
15	402254			Target Exon	1.47	1.27	1.46
	430147	R67074	Hs.234434	hairpinhancer-of-split related with YRP	1.46	2.00	1.59
	414324	Y14768	Hs.890	lymphotxin beta (TNF superfamily, membe	1.46	1.58	2.15
	400270			NM_000025: Homo sapiens adenylylsuccinate	1.46	1.42	2.32
	414806	D14694	Hs.77329	phosphatidylester synthase 1	1.46	2.07	1.40
20	419625	U51616	Hs.182885	nuclear factor of kappa light polypeptide	1.45	1.78	1.53
	430594	AK000790	Hs.245885	hypothetical protein FLJ20783	1.45	1.31	0.90
	419556	U29615	Hs.91763	chitinase 1 (chitinotriase)	1.45	2.13	1.45
	433550	AF171771	Hs.61790	hypothetical protein FLJ23338	1.45	2.00	1.39
	448412	AZ19093	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	1.45	1.37	3.17
25	411619	AI186609	Hs.71040	hypothetical protein FLJ20425	1.45	1.39	3.01
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.45	1.82	1.44
	420395	BE045545	Hs.161757	ESTs	1.45	2.40	1.33
	438555	AZ22089	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	1.45	1.91	1.65
	422497	D29642	Hs.1528	KIAA0053 gene product	1.45	1.94	1.49
30	400991			Target Exon	1.45	2.10	1.42
	431779	AH971178	Hs.268571	apolipoprotein C-I	1.45	1.53	0.42
	424618	L29472	Hs.1802	major histocompatibility complex, class	1.44	1.96	1.44
	423032	AI684746	Hs.119274	RAS p21 protein activator (GTPase activa	1.44	1.34	3.36
	424232	AB015392	Hs.143460	protein kinase C, nu	1.44	1.28	2.94
35	438291	BE514605	Hs.285292	Homo sapiens cDNA, FLJ22380 fs, clone H	1.44	1.63	1.45
	445745	AB007924	Hs.13245	KIAA0455 gene product	1.44	1.44	1.52
	449209	BE16830	Hs.294145	ESTs	1.44	1.35	2.49
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.44	2.10	1.78
	401284			Target Exon	1.44	1.71	1.44
40	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.44	1.68	1.44
	433020	A137576	Hs.279918	hypothetical protein	1.44	1.37	2.02
	400042	AW051540	Hs.161723	ESTs	1.44	2.02	1.29
	453878	AW964440	Hs.19025	DC32	1.44	1.69	1.44
	427268	X78520	Hs.174139	chloride channel 3	1.44	1.45	1.96
45	417386	AL037228	Hs.82043	DT21 gene product	1.43	1.32	2.81
	409197	NS4706	Hs.303025	chromosome 11 open reading frame 24	1.43	1.80	1.17
	411009	W37572	Hs.285964	ESTs	1.43	1.57	1.72
	433160	AW267002	Hs.134342	TASP for testis-specific adriamycin sens	1.43	1.36	1.49
	416084	L16991	Hs.79026	deoxynucleotidyl kinase (thymidylate kn	1.43	2.15	1.57
50	407826	AA128423	Hs.40300	catpain 3, (p64)	1.43	1.61	1.69
	439070	AI733278	Hs.7621	ESTs	1.43	2.10	1.40
	444090	SB9115	Hs.10308	natural killer cell group 7 sequence	1.43	2.09	1.24
	420162	BE378432	Hs.93577	cyclin-dependent kinase 4	1.43	2.13	1.54
	442591	AW292797		hypothetical protein MGC10772	1.43	2.11	1.61
55	451668	Z43948	Hs.328444	cartilage acidic protein 1	1.43	1.49	1.16
	423639	AB037826	Hs.130411	KIAA1405 protein	1.42	2.08	1.51
	424234	BE314534	Hs.168159	apoptosis regulator	1.42	1.57	1.31
	424263	M77642	Hs.1707	L1 cell adhesion molecule (hydrocephalus	1.42	1.88	1.63
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	1.42	1.46	3.18
60	442126	AW150632	Hs.170307	Rat guanine nucleotide exchange factor R	1.42	1.36	1.38
	427471	AF937660	Hs.6298	KIAA1151 protein	1.42	1.58	1.98
	412471	MS3193	Hs.73948	endothelial cell growth factor 1 (platelet	1.42	1.61	1.29
	434262	AF121858	Hs.12169	sorting nexin 8	1.41	3.07	1.41
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKF43K1815 (f	1.41	1.82	1.43
65	402474			NM_004079: Homo sapiens cathepsin S (CTSS	1.41	1.32	1.24
	419897	X90826	Hs.93649	upstream transcription factor 2, c-onc 1	1.41	1.69	1.80
	417621	AW054694	Hs.82316	interleukin-induced, hepatic C-reactivat	1.41	1.22	1.41
	424441	X14850	Hs.147097	H2A histone family, member X	1.41	1.74	2.15
	406663	L24683	Hs.155189	immunoglobulin heavy constant mu	1.41	1.51	2.03
70	409614	BE297412	Hs.152884	hypothetical protein	1.41	1.54	2.20
	423885	HE1806	Hs.152884	ESTs	1.41	1.19	1.41
	412276	BE262621	Hs.73798	neurocytic migration inhibitory factor (1.40	1.88	1.24
	425179	AJ224442	Hs.155020	putative methyltransferase	1.40	1.84	1.47
	418699	BE339630	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.40	1.27	2.79
75	423400	AA508815	Hs.124640	ESTs	1.40	1.83	1.44
	417389	BE206964	Hs.82045	midkine (neurile growth-promoting factor	1.40	1.55	2.51
	422596	AF063611	Hs.118633	2'-5'-diadenylate synthetase-like	1.40	2.57	1.44
	435292	N20514	Hs.172965	ESTs	1.40	1.91	1.43
	419424	BE041820	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.39	1.57	1.37
80	425068	AL048716	Hs.154387	KIAA1053 gene product	1.39	1.27	3.18
	425020	AL110195	Hs.166017	microphthalmia-associated transcription	1.39	2.26	1.40
	427740	BE242604	Hs.180616	CD36 antigen (collagen type I receptor,	1.39	1.76	0.99
	403022			C211007: gp1741207: gpA6: 12.15.1: AF22	1.39	1.74	1.36
	416111	AA032813	Hs.79018	chromatin assembly factor 1, subunit 1 (1.39	1.72	1.39
	410103	AW903666		gpCMA-NN1032: 280300: 122: 802: NN1032: Homo	1.39	1.46	1.34
	439180	AL393742	Hs.190967	v-erb-b2 avian erythroblastic leukemia v	1.39	1.35	1.79
	414057	AB185599	Hs.75730	signal recognition particle receptor (r)	1.39	1.49	1.17

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416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.39	1.52	1.44
423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.39	3.02	1.52
448484	BE513340	Hs.334725	Homo sapiens, Similar to RIKEN cDNA 9430	1.38	1.81	1.39
436855	AI692365	Hs.127310	ESTs, Weakly similar to T14742 hypothel	1.38	1.35	0.99
437179	AA395608	Hs.5912	serologically defined colon cancer antig	1.38	1.26	4.14
437912	BE278594	Hs.5912	F-box only protein 7	1.38	2.03	1.40
448654	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120KD	1.38	1.52	1.38
435981	AD348408	Hs.124675	ESTs, Weakly similar to T14742 hypothel	1.38	1.48	1.38
432812	AB334112	Hs.501562	ESTs	1.38	1.26	1.43
406826	AW515005	Hs.84298	CD74 antigen [invariant polypeptide of m	1.38	1.07	1.28
446962	AI351421	Hs.279709	muscle specific ring finger protein 1	1.38	1.46	2.23
404387	NM_014784	Hs.47822	Rho guanine exchange factor (GEF) 11	1.38	1.98	1.50
428044	AA053322	Hs.331404	RNA binding mol protein 3	1.38	1.29	2.04
412926	AB979075	Hs.75051	microphage myristoylated alanine-rich C	1.38	1.52	2.62
418255	AW135405	Hs.37251	ESTs	1.38	1.44	1.75
419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.37	1.51	1.37
446877	X91809	Hs.22698	regulator of G-protein signalling 19	1.37	1.98	1.45
422909	Z66023	Hs.118721	siladase 1 (lysosomal siladase)	1.37	1.27	1.75
435458	F11872	Hs.4892	Homo sapiens clone Z4841 mRNA sequence	1.37	1.38	2.80
425081	X74794	Hs.154443	minichromosome maintenance deficient (S,	1.37	1.61	1.62
429849	U33053	Hs.2499	protein kinase C-like 1	1.37	1.71	1.45
407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.37	1.52	1.82
425923	BE276018	Hs.288940	five-span transmembrane protein M83	1.37	1.86	1.37
453941	U39817	Hs.36820	Bloom syndrome	1.37	1.59	1.37
449755	AW451473	Hs.16134	serine/threonine kinase 10	1.37	1.82	1.48
439755	AW748402	Hs.77873	BT homolog 3	1.36	2.10	1.35
447930	AA065149	Hs.486595	lymphoid enhancer-binding factor 1	1.36	1.79	1.67
413821	AA644126	Hs.55964	ESTs, Weakly similar to C4H1/complement	1.36	1.91	1.39
448823	AA78563	Hs.145519	FKBP37 protein	1.35	1.29	0.33
451570	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	1.36	1.33	2.01
402542			Target E3on	1.36	1.56	1.36
451050	AW937420		ESTs	1.36	2.00	1.36
444501	AW247624	Hs.11342	ninjabin 1	1.36	1.59	1.14
413291	NM_006278	Hs.75258	sialyltransferase 4C (beta-galactosidase	1.36	2.55	1.42
438129	AA735647	Hs.177873	glucosylated/ST1 Soares_testis_NHT Homo sap	1.36	1.46	1.32
428388	AD243568	Hs.95558	ESTs	1.36	1.26	4.86
439704	AW020018	Hs.293257	ESTs	1.36	1.84	1.48
432942	X12630	Hs.193400	interleukin 6 receptor	1.36	1.27	0.58
437316	AB634584	Hs.46901	CD74 antigen (invariant polypeptide of m	1.35	2.10	1.29
403409			membrane-associated tyrosine- and leucine	1.35	1.81	1.53
446342	BE298666	Hs.14546	NM_005929:Homo sapiens antigen p87 (meta	1.35	1.64	1.35
437740	AA610265	Hs.122915	Homo sapiens mRNA: cDNA DKFpZ64D015 (r	1.35	1.37	2.33
428073	AF938451	Hs.136574	ESTs	1.35	1.91	1.35
421506	BE302796	Hs.105697	arachidonate 12-lipoxygenase, 12R type	1.35	1.53	1.10
457780	AA568123	Hs.134170	thymidine kinase 1, soluble	1.35	1.89	1.57
439769	AA448828	Hs.30596	ESTs	1.35	2.03	1.43
408824	AW515961	Hs.84298	Homo sapiens mRNA full length insert cDN	1.35	2.06	1.41
429852	AD010445	Hs.225848	CD74 antigen (invariant polypeptide of m	1.35	1.77	1.27
421777	BE562088	Hs.108195	small inducible cytokine subfamily C, 3	1.35	1.52	0.51
400328	X97344		HSPCD37 protein	1.34	1.65	1.61
421445	AA910559	Hs.104433	transporter 2, ATP-binding cassette, sub	1.34	1.77	1.02
428077	AK001404	Hs.194980	Homo sapiens, clone IMAGE-405498b, mRNA	1.34	1.77	1.15
418283	S79895	Hs.83942	cyclic B2	1.34	1.53	1.62
425848	BE242709	Hs.159637	cathepsin K (glycosaminoglycosidosis)	1.34	1.33	3.45
431211	MB8849	Hs.323733	valyl-tRNA synthetase 2	1.34	2.11	1.32
422758	AF152329	Hs.284180	gap junction protein, beta 2, 26KD (conn	1.34	1.27	1.97
421579	NM_002975	Hs.105927	proteolipidic gamma subfamily C, 3	1.34	1.61	1.75
416374	NM_001154	Hs.300711	stem cell growth factor, lymphocyte secr	1.34	1.76	1.81
451092	AI207259	Hs.13766	amnesin AS	1.34	1.68	1.55
424778	AF351048	Hs.153842	Homo sapiens mRNA for FLJ00074 protein,	1.34	1.87	0.81
421703	AB365313	Hs.1416	lymphocyte antigen 9	1.34	1.94	1.42
416700	AW498958	Hs.343475	Fc fragment of IgG, low affinity II rec	1.33	2.19	1.48
425923	NM_005026	Hs.167808	cathepsin D (lysosomal aspartyl protease	1.33	1.96	1.18
418803	U50679	Hs.88556	phosphomethyl-3-kinase, catalytic, de	1.33	1.70	1.80
427730	AW255549	Hs.105577	histone deacetylase 1	1.33	1.28	2.65
441174	BE312775	Hs.294005	granulin	1.33	2.73	1.35
412738	N34731	Hs.74562	Homo sapiens, clone IMAGE-305047, mRNA	1.33	2.05	1.33
424528	AW039737	Hs.238954	siab binding protein 1, FBP interacting	1.33	1.85	1.35
422598	BE387202	Hs.118638	ESTs, Weakly similar to KIAA1204 protein	1.33	1.31	2.06
422997	BE182121	Hs.122908	Homo sapiens, clone 1, protein (NM23A)	1.33	1.77	1.43
415323	BE293352	Hs.949	DNA replication factor	1.33	1.91	1.39
409119	AA531138	Hs.4253	neutrophil cytosolic factor 2 (65KD, chr	1.33	1.16	0.60
419952	AL151485	Hs.97873	hypothetical protein MGC2574	1.33	1.52	1.34
415697	AD365803	Hs.188271	hypothetical protein	1.32	2.07	1.29
434359	AF129536	Hs.284226	DNFZP5694024 protein	1.32	2.00	1.33
442932	AA457211	Hs.8858	F-box only protein 6	1.32	2.07	1.29
444029	AW165993	Hs.326292	bromodomain adjacent to zinc finger doma	1.32	1.25	1.91
425974	MT2529	Hs.169401	hypothetical gene DKFpZ64A11114	1.32	1.63	1.44
447733	AF157482	Hs.19400	acetylphosphatase E	1.32	1.47	1.32
448610	NM_006157	Hs.21602	MAD2 (mitotic arrest deficient, yeast, h	1.32	2.51	1.23
426490	NM_001621	Hs.170087	nel (chicken)-like 1	1.31	3.12	1.31
427584	BE410293	Hs.179718	aryl hydrocarbon receptor	1.31	1.21	1.65
			v-myb avian myeloblastosis viral oncogen	1.31	1.68	1.47

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	417059	AL033762	Hs.B1071	intracellular matrix protein 1	1.31	1.30	2.14
	407777	AA161071	Hs.71465	squalene epoxidase	1.31	1.45	1.43
	408536	AW381532	Hs.135188	ESTs	1.31	1.38	0.90
5	410243	AW402432	Hs.6349	protein tyrosine phosphatase, non-recept	1.31	1.81	1.49
	422468	BES14492	Hs.117487	gene near HD on gp15.3 with homology to	1.31	1.63	1.31
	420754	U72382	Hs.30042	interferon-induced protein 35	1.31	1.69	1.29
	428003	AF119046	Hs.154149	apurinic/apyrimidinic endonuclease/APEX	1.31	1.74	1.39
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	1.31	1.43	0.94
	421375	AW961017	Hs.6459	hypothetical protein FLJ11856	1.30	2.53	1.34
10	417361	AA020275	Hs.20677	hypothetical protein FLJ11856	1.30	1.38	1.38
	420676	AA410656	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.30	2.11	1.36
	427289	AJ097346		phosphoserine aminotransferase	1.30	2.27	1.48
	427747	AAW11425	Hs.180655	serine/threonine kinase 12	1.30	1.68	1.79
	422298	AA360231	Hs.114416	Homo sapiens, similar to transducin (bet	1.30	1.50	1.30
15	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.30	1.42	2.13
	423062	NM_003655	Hs.5637	ESTs	1.30	1.58	1.30
	439740	AL365512	Hs.6657	hypothetical protein BK1048E35	1.30	1.77	1.35
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	1.30	1.57	1.51
	416920	AA176455	Hs.30475	protein kinase (RNA) II (DNA directed) poly	1.30	1.67	1.44
20	430451	AA836472	Hs.297939	cathepsin B	1.30	1.49	1.16
	457400	AF032906	Hs.252549	cathepsin Z	1.30	1.40	1.21
	430506			C200H12.2:gp67764.7:trfNP_033602.1:zn	1.29	1.68	1.26
	424687	AJ024660	Hs.153591	Nucleo (D, nucleoprotein)-like protein	1.29	2.64	1.31
	408815	AW957574	Hs.25485	hypothetical protein FLJ22341	1.29	1.79	1.36
25	416322	BE019494	Hs.79217	pyrimidine 5-carboxylate reductase 1	1.29	1.59	1.80
	440795	AA026213	Hs.59741	ESTs, Weakly similar to PHIL1_HUMAN PEANU	1.29	2.01	1.43
	421646	AA017077	Hs.1432	protein kinase C substrate 50K-H	1.29	1.70	1.34
	425966	NM_001761	Hs.1573	cyclin F	1.29	1.63	1.50
	446766	AF063208	Hs.16178	apoptosis antagonizing transcription fac	1.29	1.71	1.40
30	406827	AA571409		glap0202a.1: NC_CGAP_Lu6 Homo sapiens	1.29	2.04	1.35
	419813	AA144529	Hs.86575	mitogen-activated protein kinase kinase	1.29	1.41	1.29
	433936	AW577125		size specific homodimer (Disophila) homole	1.29	1.24	1.29
	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.29	1.99	1.36
35	434388	AA121098	Hs.3638	serum-inducible kinase (SINK)	1.29	1.19	1.32
	418322	AA284166	Hs.84113	cyclic-dependent kinase inhibitor 3 (CDK	1.29	1.31	1.29
	402681			Est Control	1.29	1.59	1.36
	413781	J05272	Hs.850	UMP (inosine monophosphate) dehydrogenas	1.29	1.67	1.53
	421315	AW936678		gb:PM2-DT023-080300-004-004 DT0023 Homo	1.28	1.26	1.07
40	420372	AW960049	Hs.293660	Homo sapiens, clone IMAGE3636475, mRNA,	1.28	1.85	1.40
	425549	AW577125	Hs.157441	apical focus forming virus (SFFV) provir	1.28	1.45	1.38
	456478	AW805740		superoxide dismutase 2, mitochondrial	1.28	2.29	1.07
	410275	U85659	Hs.61796	transcription factor AP-2 gamma (activat	1.28	1.20	0.93
	406016			Target Exon	1.28	1.47	1.31
45	449609	BE246434	Hs.289206	guanine nucleotide binding protein (G pr	1.28	1.26	3.02
	425559	BE282642	Hs.186120	interferon regulatory factor 7	1.28	1.76	1.23
	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.28	1.60	1.30
	452700	AJ850390	Hs.288940	five-span transmembrane protein M53	1.28	1.51	1.22
	403543	N73093	Hs.44289	ESTs	1.28	2.02	1.08
50	408822	AA5300715	Hs.57079	Homo sapiens cDNA FLJ13267 kl, clone OV	1.27	1.28	3.51
	420580	AA807465	Hs.208184	potassium voltage-gated channel, shaker-	1.27	1.66	1.39
	444681	AJ243937	Hs.288316	chromosome 5 open reading frame 9	1.27	1.47	1.55
	430794	NM_0010166	Hs.333303	gap junction protein, beta 2, 28kd (conn	1.27	1.81	0.89
	430637	BE180081	Hs.256290	S100 calcium-binding protein A11 (calgi	1.25	1.35	1.69
55	440502	AJ341113	Hs.78281	regulator of G-protein signalling 12	1.27	1.67	1.31
	441598	AJ733219	Hs.53262	ESTs	1.27	1.30	1.30
	431921	NA6466	Hs.58870	ESTs	1.27	2.00	1.16
	459345	AW953672		gb:U46-BM045-b-11-AJ01.1 NH_MGC_50	1.26	1.44	1.33
	42426	BE077546	Hs.31447	ESTs, Moderately similar to A49010X-In	1.26	1.20	1.45
60	426334	BE305081	Hs.189358	hypothetical protein	1.26	1.22	1.89
	414044	BE514194	Hs.75721	protein 1	1.26	1.48	1.51
	405268			ENSF00000223174:XA04783 PROTEIN.	1.26	1.19	2.25
	416882	NM_006190	Hs.79389	Protein kinase C-binding protein NELL2	1.26	1.69	1.49
	439529	BE293492	Hs.293884	hypothetical protein MGC13102	1.26	1.83	1.19
	421254	AK001724	Hs.102590	coat protein gamma cop	1.26	1.61	1.23
65	417785	X59812	Hs.82568	cytochrome P450, subfamily XXIVA (stero	1.26	1.84	0.68
	419395	BE363326	Hs.92080	5-aminimidazole-4-carboxamide ribonucle	1.26	1.66	1.26
	418988	NM_000078	Hs.856338	cholesterol ester transfer protein, plas	1.26	1.42	1.19
	441553	AA281219	Hs.121296	ESTs	1.26	1.29	1.28
	446819	AJ076643	Hs.31313	resected phosphoprotein 1 (pseoponin,	1.25	1.22	0.65
70	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for sec	1.25	1.17	2.85
	430067	BE293180	Hs.240373	MuH2 protein	1.25	1.78	1.26
	429604	AK001851	Hs.210778	hypothetical protein FLJ10989	1.25	1.18	1.25
	429380	AF023268	Hs.200600	secretory carrier membrane protein 3	1.25	2.22	1.25
	440251	AW796016	Hs.332012	Homo sapiens, clone IMAGE3687782, mRNA,	1.25	1.90	1.39
75	416059	AA060978	Hs.76141	hypothetical protein FLJ10116	1.24	1.32	1.53
	435466	BES19165	Hs.32003	G-protein beta subunit-like	1.24	1.96	1.32
	450521	AW297288	Hs.55918	hypothetical protein FLJ11354	1.24	1.61	1.27
	400214	H91923	Hs.119024	NM_007002:Homo sapiens cell membrane gly	1.24	1.88	1.32
80	435013	BES14535	Hs.147333	NM_020142:Homo sapiens NADPH-dependent	1.24	1.76	1.25
	406851	AA609784	Hs.77171	mitochondrion maintenance deficient (S	1.24	1.82	1.42
	448498	AA148276		motor histocompatibility complex, class	1.24	1.68	1.19
	440007	Y25999	Hs.77118	ESTs	1.24	1.73	1.29
				hypothetical protein FLJ22678	1.24	1.70	1.38

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41365	MS477	Hs.289082	GMD ganglioside activator protein	1.24	1.61	1.16
426502	Y0759	Hs.170157	myosin VA (heavy polypeptide 12, myosin)	1.24	2.65	1.24
452056	AW555065	Hs.101150	Homo sapiens, clone IMAGE:4064156, mRNA,	1.24	1.49	1.50
427390	AA432163	Hs.288231	Homo sapiens cDNA: FLJ23111 fls, clone L1	1.24	1.17	2.10
429954	AS01130	Hs.21374	ESTs	1.23	1.19	4.17
421178	BE257994	Hs.102419	zinc finger protein	1.23	1.62	1.28
42609	AL020996	Hs.8518	selenoprotein N	1.23	2.30	1.24
416188	BE157260	Hs.793070	v-myc avian myeloblastomatosis viral oncog	1.23	1.18	0.90
410127	AA354313	Hs.58685	CD5 antigen (p56-62)	1.23	1.68	1.23
452244	N3330	Hs.176674	ESTs	1.23	1.53	1.23
406718	AA505525	Hs.169476	glyceraldehyde 3-phosphate dehydrogenase	1.23	1.56	1.29
436939	AB453680	Hs.5345	arginyl aminopeptidase (aminopeptidase B	1.23	1.68	1.23
414457	AW514320	Hs.76159	ATPase, H transporting, lysosomal (vacuo	1.23	1.58	1.20
416029	N29355	Hs.84	metastasin	1.23	1.92	1.20
401106			Target Exon	1.23	1.82	1.29
408981	MS00797	Hs.49427	Gem-interacting protein	1.23	1.40	1.59
413317	US3225	Hs.75283	sorting nexin 1	1.23	1.43	1.44
422461	AL050163	Hs.117339	DNA-activation protein 10	1.23	1.71	1.24
425455	AL137522	Hs.157777	casein kinase 1, gamma 1	1.23	1.95	1.26
451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.23	2.07	1.27
414399	L47345	Hs.155202	transcription elongation factor B (SII)	1.22	1.87	1.19
422034	AC209486	Hs.333069	EB2 repressor factor	1.22	1.55	1.21
434224	AA380731	Hs.84	interleukin 2 receptor, gamma (severe co	1.55	1.22	1.51
429574	BE264321	Hs.208912	hypothetical protein MGC861	1.22	1.49	1.46
411742	AW247593	Hs.71819	eukaryotic translation initiation factor	1.22	1.64	1.40
449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.22	1.63	1.30
418004	U27519	Hs.87339	adenylate dehydrogenase 3 family, member	1.24	1.22	0.71
451481	AA300228	Hs.259666	hypothetical protein DKFZ344N1923	1.22	2.20	1.26
422739	H20106	Hs.119391	adaptor-related protein complex 2, sigma	1.21	1.55	1.21
424326	NM_014479	Hs.142526	ADAM-like disintegrin protease, deysin	1.21	1.11	3.29
404186			HLA-DPB2-like Homo sapiens leukoprotein-like	1.21	1.59	1.21
441604	AB089933	Hs.301342	hypothetical protein MGC4342	1.21	1.26	2.00
427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	1.21	1.14	1.26
414509	AW161311	Hs.76294	CD63 antigen (melanoma 1 antigen)	1.21	1.39	1.25
428468	AA171386	Hs.164482	DNF ZP565D0624 protein	1.21	1.86	1.22
419700	AF084636	Hs.92367	galactosylase 1	1.21	1.53	0.74
430948	AA347578	Hs.124016	hypothetical protein MGC2605	1.21	1.48	1.21
448143	AF039704	Hs.20478	ceroid-lipofuscinosis, neuronal 2, late	1.20	1.75	1.23
448469	BE613280	Hs.77550	hypothetical protein MGC1780	1.20	1.54	1.29
442173	WT501	Hs.8127	KIAA0144 gene product	1.20	1.54	1.31
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	1.20	1.18	1.11
448230	BE395949	Hs.94814	hypothetical protein MGC2865	1.20	1.83	1.19
403817			NM_015271: Homo sapiens tripartite motif-	1.20	1.22	1.61
411578	AF071114	Hs.71465	squaleone epoxidase	1.20	1.15	2.01
452423	AA691724	Hs.180535	hypothetical protein MGC10996	1.20	1.29	1.20
424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.20	2.34	1.20
447223	AA246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.20	1.93	1.20
427585	BE329035	Hs.118400	arginet (Drosophila)-like (sea urchin fas	1.20	1.32	1.52
446199	NM_013379	Hs.14089	dipeptidyl peptidase 7	1.19	1.64	1.22
434563	AW085994	Hs.9469	pleckstrin homology domain-containing, f	1.19	1.53	1.45
421541	NM_003942	Hs.105584	ribosomal protein S6 kinase, 90kD, polyp	1.19	1.75	1.27
450706	AW167578	Hs.14691	ESTs, Moderately similar to CB0022 hypox	1.19	1.71	1.22
433381	NM_006411	Hs.240534	1-acylglycerol-3-phosphate O-acyltransfer	1.19	1.66	1.21
426339	AL389951	Hs.271623	nucleoprotein SMD	1.19	1.17	1.55
421612	AF161254	Hs.106196	BD6 antigen	1.19	1.73	1.30
410182	NM_001983	Hs.59544	excision repair cross-complementing rode	1.19	1.75	1.18
434171	BE247688	Hs.347349	KIAA0945 protein	1.18	1.73	1.09
424837	BE276113	Hs.333034	N-acetyltransferase, homolog of S. cerevis	1.18	1.22	1.22
428293	BE250944	Hs.181556	solute carrier family 1 (neutral amino a	1.18	1.45	1.30
453764	AW972580	Hs.172753	ESTs	1.18	1.71	1.35
439012	BE383814	Hs.6455	PuvB (E. coli homolog)-like 2	1.18	1.60	1.23
422286	MS4673	Hs.1469	hist. shock transcription factor 1	1.18	1.68	1.28
439683	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.18	1.89	1.18
430513	AJ012008	Hs.241586	G6C protein	1.18	2.07	0.81
427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	1.18	1.13	3.25
441646	H05734	Hs.30559	ESTs	1.18	1.56	1.23
418219	AA731836	Hs.137319	ESTs	1.18	1.77	1.23
406422			Target Exon	1.18	1.43	1.31
414823	AA156531	Hs.103902	ESTs, Weakly similar to A44851 keratin,	1.18	1.66	1.23
425720	AA362394	Hs.293984	hypothetical protein MGC131902	1.18	1.36	1.15
419250	AW770185	Hs.1067	U5 snRNP-specific protein, 116 kD	1.17	1.74	1.21
454390	AB020713	Hs.56966	KIAA0905 protein	1.17	1.33	1.35
428471	XS7348	Hs.184510	stratelin	1.17	1.19	1.24
430200	BE561333	Hs.234986	germin	1.17	1.13	1.96
412665	U26419	Hs.75933	procollagen-prolyse, 2-oxoglutarate 5-ido	1.17	1.17	1.22
430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	1.17	1.69	1.32
430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein Lsm5	1.17	1.12	2.44
417080	BE392846	Hs.1063	small nuclear ribonucleoprotein polypept	1.17	1.93	1.18
423102	AW067812	Hs.303825	chromosome 11 open reading frame 24	1.17	1.89	1.17
408393	AW015318	Hs.231165	ESTs	1.16	1.10	1.91
424292	AA308432		gh-EST43554 Fetal brain I Homo sapiens c	1.16	1.61	1.21
446759	RS1463	Hs.16165	expressed in activated TAAK lymphocytes	1.16	1.45	1.23
427324	AA159587	Hs.285932	hypothetical protein FLJ23322	1.16	1.50	1.23

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446055	AIB15981	Hs.12909	macropin 1	1.16	1.49	1.10
414432	BE378174	Hs.26506	Homo sapiens clone CDA6P0005 mRNA sequen	1.16	1.67	1.20
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevisiae)	1.16	1.66	1.32
411305	BE241596	Hs.69547	myelin basic protein	1.16	1.15	4.29
438930	AW893633	Hs.343281	hypothetical protein AL110115	1.16	1.37	1.34
407239	AA495550	Hs.678465	leukocyte immunoglobulin-like receptor,	1.15	1.82	1.17
427458	BE208364	Hs.29283	ESTs, Weakly similar to UKHU proteoglyca	1.15	1.46	1.32
402160			Target Exon	1.14	1.23	1.12
415881	N35205	Hs.141368	ESTs	1.14	2.42	1.14
420223	N27807	Hs.25450	abscisic acid protein L4	1.12	1.23	1.14
450778	U81375	Hs.139322	solute carrier family 29 (nucleoside tra	1.14	1.38	1.27
429538	BE162592	Hs.139322	small proline-rich protein 2A	1.14	1.16	3.52
428342	AI739166	Hs.120487	Homo sapiens cDNA FLJ13458 fs, clone PL	1.13	1.13	1.13
435996	AA725678	Hs.9275	ESTs	1.13	1.22	1.13
448950	AF288980	Hs.5790	CG1-152 protein	1.12	1.52	1.19
437696	Z63844	Hs.154151	hypothetical protein dJ37E16.5	1.12	1.31	1.08
425009	X58288	Hs.73165	protein tyrosine phosphatase, receptor t	1.12	1.08	1.20
412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.12	2.93	1.12
427951	W77162	Hs.289502	antigen identified by monoclonal antibod	1.12	1.11	3.43
408116	AA251393	Hs.24756	Homo sapiens, Similar to RIKEN cDNA 5430	1.12	1.50	1.12
450296	AL041949	Hs.26605	hepatocyte growth factor-regulated tyros	1.11	1.48	1.12
420597	AA827705	Hs.255661	ESTs	1.11	2.19	1.11
435915	AA260174	Hs.84753	Williams-Beuren syndrome chromosome reg	1.10	2.73	1.11
418399	AF131781	Hs.24907	hypothetical protein FLJ12442	1.10	1.43	1.14
450358	AB010698	Hs.62180	coronin, actin-binding protein, 2B	1.10	1.35	1.19
444783	AK001468	Hs.63405	arilin (Drosophila) Scrapie homolog, act	1.10	1.43	1.10
420301	AI969590	Hs.134729	Homo sapiens, clone IMAGE360533, mRNA,	1.10	1.53	1.14
426222			C10033957.gli12314272[emb]CAC05951.1) (A	1.10	1.59	1.06
418961	NM_001949	Hs.1189	E2F transcription factor 3	1.09	1.62	1.09
442680	BE270707	Hs.6563	similar to APOBEC1	1.09	1.49	1.24
4330702	AW085525	Hs.65964	ESTs	1.09	1.68	1.09
423856	AL137326	Hs.134729	Homo sapiens mRNA; cDNA DKFZp434B0050 (f	1.09	1.10	1.73
443759	BE390632	Hs.76057	FX1Y domain-containing ion transport reg	1.09	1.23	1.25
414396	BE546266	Hs.10336	galactose-4-epimerase, UOP-	1.09	1.07	1.23
401558			ENSP00000220470[5]-SECRETOGRANIN III.	1.08	1.54	1.08
428411	AW3291464	Hs.11024	ESTs	1.08	1.07	6.19
420521	AW327546	Hs.76907	solute carrier family 25 (mitochondrial	1.08	1.25	0.93
414594	NM_015362	Hs.347524	HSPC002 protein	1.08	1.18	1.12
453883	A163816	Hs.205738	cofactor required for Sp1 transcriptions	1.07	1.15	1.31
420356	BE513294	Hs.66154	HLA class II region expressed gene NE2	1.06	1.47	1.08
412265	AA101325	Hs.292911	hypothetical protein FLJ12457	1.06	1.12	0.73
429269	AA420450	Hs.62042	Plastophen	1.06	1.06	1.23
417381	AF164142	Hs.76877	solute carrier family 23 (nucleoside tra	1.05	1.04	0.84
415825	Y19024	Hs.322469	involial 1,4,5-trisphosphate 3-kinase B	1.05	1.09	1.37
444436	N27875	Hs.10336	ESTs	1.04	1.13	1.05
407394	AF005061	Hs.49378	gb: Homo sapiens skin-specific protein (x	1.04	1.22	0.79
404960			eyes absent (Drosophila) homolog 3	1.04	1.06	1.04
408972	AL030100	Hs.63563	DKFZP566D0919 protein	1.04	1.09	1.13
414477	UA1635	Hs.5422	amplified in osteosarcoma	1.03	1.11	1.03
403327	LA1162	Hs.5422	collagen, type IX, alpha 3	1.03	1.02	2.33
435056	AW023337	Hs.5422	glycoprotein M6B	1.03	1.02	3.56
415314	N68602	Hs.46452	glycoprotein M6B	1.02	1.02	4.02
426891	AF015224	Hs.113261	memaglobin 1	1.00	1.41	0.05
401203			Target Exon	1.00	1.02	0.98
400304	AF005082	Hs.69752	Homo sapiens skin-specific protein (gp33	1.00	1.49	0.56
407395	AF005082	Hs.69752	gb: Homo sapiens skin-specific protein (x	1.00	1.69	0.91
411388	X72525	Hs.1530	desmocollin 1	1.00	3.12	1.00
428616	AA885390	Hs.5509	Target CAT	1.00	1.77	1.00
402660			ENSP00000239210.DJ50O24.4 (novel protein	1.00	1.53	1.00
437211	AA382207	Hs.22752	ecotopic viral integration site 2B	1.00	1.39	1.00
402929	AA576653	Hs.50964	stenoal 5 alpha-reductase 2-like; HSAR g	1.00	1.46	1.00
409190	AL076516	Hs.194093	sarcoma amplified sequence	1.00	0.80	1.00
416143	A1955650	Hs.176376	glutaminyl-peptidyl cyclotransferase (glu	1.00	1.96	1.00
401588			C150001807.gli544344ip3qC6659FORA, MOUS	1.00	2.04	1.00
419519	A1198719	Hs.22151	ESTs	1.00	1.91	1.00
448816	AB033052	Hs.7120	KIAA1226 protein	1.00	1.82	1.00
440270	NM_015966	Hs.86724	cytokine receptor like molecule 9	1.00	1.15	1.00
418618	U66097	Hs.108105	GTP cyclohydrolase 1 (dopa-responsive dy	1.00	1.56	0.74
422836	AL037365	Hs.108105	AKAP-binding sperm protein noppin	1.00	2.21	1.00
452461	N16223	Hs.334562	transcription factor	1.00	1.61	1.00
426479	Y00272	Hs.1524	cell division cycle 2, C1 to S and G2 to	1.00	1.42	1.00
422420	U03398	Hs.6656	tumor necrosis factor (ligand) superfam	1.00	1.81	1.00
429477	AI725514	Hs.21065	ESTs	1.00	1.67	1.00
454027	R40192	Hs.130313	Human DNA sequence from clone GS1-115M3	1.00	1.05	1.00
416209	AA236776	Hs.184341	MA2D (mucic acid deficient, yeast, h	1.00	1.79	1.00
451993	AA765776	Hs.184341	ESTs	1.00	2.15	1.00
416947	N23282	Hs.21065	ESTs, Weakly similar to B34087 hypotheti	1.00	1.67	1.00
441606	R37263	Hs.21065	ESTs, Moderately similar to PC4259 fimb	1.00	1.87	1.00
442590	AI060886	Hs.184376	ESTs	1.00	2.59	1.00
404631			C1002837.gli7499200[pi]qT26903 hypotheti	1.00	1.44	1.00
428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	1.00	1.47	1.00
419717	U07970	Hs.52458	G-protein-coupled receptor 19	1.00	1.76	1.00
408611	NM_004367	Hs.46468	chemokine (C-C motif) receptor 6	1.00	1.64	1.00

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421666	AL032520	Hs.1408	endostatin 3	1.00	0.63	1.00
446155	A053695	Hs.159422	Homo sapiens cDNA FLJ13397 fs, clone Y7	1.00	1.60	1.00
423859	NM_001427	Hs.134586	engrailed homolog 2	1.00	2.91	1.00
423130	AW697586	Hs.21213	ESTs	1.00	1.85	1.00
435843	NM021423	Hs.112819	ESTs	1.00	2.08	1.00
435874	AW384438	Hs.135265	Homo sapiens clone FLDB836 PRG2277 mRNA, carbonic anhydrase XIV	1.00	1.00	1.00
430205	AB025904	Hs.235168	G antigen 7B	1.00	1.41	1.00
427335	AA484542	Hs.251677	ESTs	1.00	1.15	1.00
439591	AF27067	Hs.124536	ESTs	1.00	1.80	1.00
428048	AF271191	Hs.44714	ESTs	1.00	2.15	1.00
446259	AA425204	Hs.334721	hypothetical protein FLJ13391	1.00	2.35	1.00
447164	AF026941	Hs.17518	vapc, similar to inflammatory respon	1.00	1.53	1.00
447289	AF024017	Hs.36578	melanoma antigen, family A, 3	1.00	1.73	1.00
408751	NM_003686	Hs.47524	exonuclease 1	1.00	1.55	1.00
453745	AA552685	Hs.63908	hypothetical protein MGC14726	1.00	1.73	1.00
436609	AK022514	Hs.131380	ESTs	1.00	1.96	1.00
413308	NA0321	Hs.17518	gh-y80g07.r1 Scores melanocyte 2048 Hs	1.00	2.26	1.00
421650	AA781795	Hs.122587	ESTs	1.00	1.74	1.00
435570	AW615338	Hs.304451	ESTs	1.00	2.16	1.00
446152	AJ292036	Hs.36708	ESTs	1.00	1.66	1.00
449579	AW027260	Hs.134014	ESTs, Weakly similar to T46425 hypot	1.00	2.04	1.00
418673	NM_005582	Hs.87205	lymphocyte antigen 54 (mouse) homolog	1.00	1.75	1.00
415504	AA158525	Hs.240459	ESTs, Weakly similar to GSP1_HUMAN INTER	1.00	1.85	1.00
425274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily	1.00	1.92	1.00
452922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	1.00	1.72	1.00
417791	AW966339	Hs.44259	ESTs	1.00	1.52	1.00
424595	NM_002467	Hs.153734	NIMA (never-in-mitosis gene a)-related k	1.00	2.02	1.00
416445	AL043004	Hs.75337	KIAA0135 protein	1.00	1.28	1.00
408376	AJ224520	Hs.40830	ESTs	1.00	1.92	1.00
406564	M21305	Hs.46320	FGFES predicted novel secreted protein	1.00	0.46	1.00
408522	AB511214	Hs.74621	Small proline-rich protein SPRK (human,	1.00	1.00	1.00
412828	AL133286	Hs.114062	protein protein (p27-30) (Crest)-like jakob	0.98	0.98	3.24
422270	AF114454	Hs.114062	protein tyrosine phosphatase-like (prol	0.95	0.95	3.08
446488	AB037782	Hs.15119	KIAA1361 protein	0.94	0.96	1.61
433435	BE345277	Hs.349659	Ts transition elongation factor, mitoch	0.94	0.94	0.76
425402	AF208234	Hs.658	cystatin B (protein B)	0.93	0.91	1.55
423542	AF205704	Hs.159407	glycylid transfer protein	0.92	0.93	2.09
414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	0.91	0.91	4.08
425211	AF052653	Hs.198249	gap junction protein, beta 5 (connexin 3	0.90	0.81	0.73
417632	R20555	Hs.5422	glycoprotein 1460	0.92	0.92	3.89
449692	U51641	Hs.171921	alpha2,8-sialyltransferase	0.89	0.79	0.84
426716	NM_006379	Hs.72291	sema domain, immunoglobulin domain (lg),	0.89	0.92	3.70
445033	AV522402	Hs.72291	cyclic-dependent kinase inhibitor 2B (p1	0.88	0.90	2.02
405349	BE346947	Hs.44276	homeo box C10	0.88	0.87	0.73
425345	R11141	Hs.193636	hypothetical protein	0.85	0.84	0.63
451621	AB75148	Hs.26770	fatty acid binding protein 7, brain	0.84	0.85	1.32
417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	0.84	0.88	3.37
405885	Hs.80905	Hs.80905	Tat1 Exon	0.81	0.71	1.00
407788	B514082	Hs.38591	S100 calcium-binding protein A2	0.78	0.78	0.90
417515	L51203	Hs.82233	ataxia telangiectasia group D-associated	0.77	0.73	0.71
421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fs, clone C	0.75	0.78	4.69
440274	R24595	Hs.7122	scrapie responsive protein 1	0.74	0.78	5.42
425071	NM_013589	Hs.154424	oxidase, iodothyronine, type II	0.70	0.75	4.29
412719	AW018610	Hs.816	ESTs	0.70	0.77	3.59
432467	T03667	Hs.239368	Human DNA sequence from clone RP1-304B-1	0.69	0.73	3.59
437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.65	0.64	1.11
425247	AW207659	Hs.8530	Homo sapiens cDNA FLJ13329 fs, clone OV	0.61	0.61	3.28
448133	AA723157	Hs.73769	folate receptor 1 (folur)	0.61	0.22	0.49
439559	AW570780	Hs.55483	Homo sapiens cDNA FLJ14471 fs, clone MA	0.49	0.39	0.67
415092	J05581	Hs.89603	mucin 1, transmembrane	0.41	0.11	0.34
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	0.23	0.30	0.35

TABLE 496

Play:	Unique Ex probe identifier number
CAT number	Gene cluster number
Accession:	Genbank accession numbers

Play	CAT Number	Accession
430540	713_2	
70		BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AJ124376 BG757203 BG754000 BG775026 BG824418 BM045810 AJ120387 BG770238 BC066140 BC031323 BI799860 BG365968 BM046875 BE681070 BE133768 BE739144 BM30834 AW245847 AJ707171 BF190461 BE766872 AF443075 A375277 AA046810 AG461515 AA450516 AA58583 AB01189 A020409 A151943 A131025 AW68539 A365196 AW337584 AW026150 BA766591 BE674596 AB18438 AA772197 A051927 AW151143 BI198025 BG19003 BM045874 BE003357 BE723215 BM043200 BE500023 BE500706 BE731097 BE300022 BC075384 BF996405 BF980930 AW426215 AW426215 BE150187 BE030610 BE561530 BE560542 BE503782 BE732947 B1227004 BG761305 BE782642 BE181048 BE87475 BE000258 BE547951 B1459095 BE31351 BE259420 BE736105 AW245422 AHC2847 AB194161 H05254 BE301004 AL331791 AHC5851 BE730112 AL577033 AA73395 AA73395 BE749685 BF743530 BE75296 A352453 BM116598 AB63260 AW02450 F20021 AW151405 AW151752 GA773468 BG25694 BE391163 BG521529 AA121728 BG767231 BM467953 BG340524 W52648 AA113434 BE785431 B1041981 BG832385 BG253168 BG759470 BF303299 BF981332 BE225941 BE785738 B1091658 N75212 W68732 W58590 BG958389 A1265206 H19721 W17051 W77958 BE262010 AB84319 W7143 W72714 K85194 BE734033 BG184049 AAS31085 F13845 R41384 AW025756 BE18097 BE348545 AB12016 AA740241 AB1212 AAT7222 A1152356 AAB8395 AAY97167 BE228225 AA584052 A151818 A24344 AA89453 AA461029 AB25716 AL47866 AA431670 AA81436 A251190 R07704 AA76506 AA724553 AB153395 A5137550 AA451103 AW08188 R07703 AA89129 AA746235 AW029893 AA789102 A187551 AW71465 AA429681 AW971853 AB612096 BE077936 B1608095 BE02780 BG746251 BE362912 BM454584 AL134894 BF140482 HB0591 AW570501 A0613395 AA500435 AA500282 N91138
75		
80		

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Play	Ref	Strand	NT position
4024025	18117407	Plus	121501-122033, 122804-122921, 124019-124116
405451	7422717	Minus	145930-146217
405451	7593692	Plus	165856-168816, 191119-191244, 119609-11978
405451	7593692	Plus	11968-11952
405451	1054740	Plus	18677-118801, 191091-119296, 121682-12182
401780	729190	Minus	21837-28617, 26204-29045, 29135-29296, 2941
405326	6469396	Minus	120426-120578
405447	7593692	Plus	12547-125501, 124914-125050
405332	10675842	Plus	193481-194253
405500	6190607	Plus	198991-199168, 199358-199548
405556	14549691	Plus	80401-80401, 805933-81125
405533	7280331	Plus	27172-27225
405579	7280331	Plus	32042-33866
405594	2956641	Plus	47448-49595
401781	7269190	Plus	83215-83435, 83531-83663, 847-847, 83001-8423
401781	7269190	Plus	43243-431421, 431421-431433, 44607-4453, 4519
403669	8959895	Plus	3127-3137, 24405-3506
401780	9955999	Plus	30138-83250, 85320-86540, 94719-95267
401780	9730720	Plus	6973-7113
401151	9417614	Plus	30469-31228
404872	7280331	Minus	18540-18718
402876	9654663	Plus	16740-16727, 7495-7584
405204	7200116	Plus	156750-126754
402294	7280331	Plus	2975-3009
400991	8096825	Plus	1195917-159320
401284	9008119	Minus	10103-101421
402404	7471775	Plus	5326-5328, 5575-55920, 5730-5730, 5757
402404	7471775	Plus	31233-31233
402542	9601558	Plus	67076-67594
403409	9438936	Plus	6860-7054, 12573-12717
403306	7598683	Plus	105000-105060
406016	7872661	Plus	4134-4141, 4040
402588	4156811	Plus	24404-24251
401106	8486931	Plus	12264-12283
404186	4418393	Plus	829-1110
403817	7862095	Plus	110207-11052
406422	9256141	Plus	15303-153311
402160	8515611	Plus	166063-165354
402622	9256141	Plus	12891-12009
401584	7892878	Plus	11919-11940
404960	7408010	Plus	14686-14673, 14717-147943
402603	9743387	Plus	172951-17306, 173880-173928
402860	908237	Minus	7425-76560
401588	72306	Plus	4200-46681
404831	0524702	Plus	18633-17020, 20007-20121, 61665-21799, 21333
405885	7677703	Minus	4254-42998

Playr:	Unique Esr probset identifier number
ExAccon:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	70th percentile of primary melanoma and melanoma metastatic AIs divided by the maximum AI of benign nev.
R2:	70th percentile of primary melanoma and melanoma metastatic AIs divided by the maximum AI of benign nev, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator.

Play	EaCon	UnigeneID	Unigene Title	R1	R2
422424	A1186431	Hs.29536	prostate differentiation factor	13.73	16.82
446619	Hs.313		secreted phosphoprotein 1 (osteopontin)	11.67	11.81
407846	A442602	Hs.40403	Casp10-interacting transducer, wif	9.35	7.89
407846	SBC37335	Hs.263713	protein kinase SIK3	7.50	7.90
417880	B2741566	Hs.82848	sialin L lymphocyte adhesion molecule	8.21	6.09
424321	W70448	Hs.1785	lymphocyte-specific protein tyrosine kinase	7.13	6.10
447210	A503569	Hs.17752	phosphatidylinositol-specific phospholipase C	6.79	6.26
417650	AW569741	Hs.40386	adren- related protein complex 1, sigma	6.55	6.36
429819	Z87655	Hs.2881	hemopoietic precursor C, cytochrome monokine induced by gamma interferon	6.43	7.51
416812	X72755	Hs.73787	ESTs, weakly similar to ALU7_HUMAN ALU element (C-X-C motif), receptor	6.31	4.28
451736	AA060356	Hs.23889	ESTs, weakly similar to ALU7_HUMAN ALU element (C-X-C motif), receptor	6.20	4.32
418291	A174204	Hs.89414	chemokine (C-X-C motif), receptor 4	6.03	4.35
410370	AA53409	Hs.153687	KIM-1-like gene product	6.02	4.30
417338	H40720	Hs.21486	signal transducer and activator of tau	5.99	7.51
448569	SBC26257	Hs.21486	ESTs	5.95	4.79
439310	A098120	Hs.102793	ESTs	5.95	4.79
425238	US0011	Hs.30743	preferentially expressed antigen in melanoma protein tyrosine phosphatase, receptor 1	5.95	5.55
422700	Y00652	Hs.170121	protein tyrosine phosphatase, receptor 1	5.76	4.80
424237	NM_004613		jaagsen-vanegas and LG notropod protein	5.79	2.19

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409274	NI0_00390	HS.52544	SKAP65 homologue
447739	NI0_00774	HS.8519	cytosolic acyl coenzyme A thioester hydrolase
447711	AF1501073	HS.8645	hydrolytic protein
425118	AD016611	HS.154672	myofibrillar beta-hydroxylate dehydrogenase
425120	BE53557	HS.154672	myofibrillar beta-hydroxylate dehydrogenase
428125	AA93301	HS.182579	enzyme anionopoligase
446921	AD012113	HS.16530	small inducible cytokine subfamily A (Cp)
431183	NI0_00685	HS.250096	CDX1, Lys-Arg-Glu-Lys endoprotease; iqt
420510	WD0510	HS.250096	CDX1, Lys-Arg-Glu-Lys endoprotease; iqt
426600	NI0_003378	HS.171014	UGV nerve growth factor receptor
415444	BE427495	HS.174852	sulfate carrier family 20 (phosphate tran-
436701	NI0_959033	HS.277447	sfers, Moderately similar to 178895, same
436702	NI0_959033	HS.277447	major histocompatibility complex, class
410950	AA5953801	HS.307328	II, beta chain, beta 2 (anion carrier, beta
429950	AA279530	HS.33668	CG-100 protein
404645	AD198004		Target Epon
415701	NI0_00378	HS.73619	Target Epon
425397	J04087	HS.156346	Target Epon
408958	J09688	HS.43346	Target Epon
455495	AD017716	HS.30927	Target Epon
427650	AF765930	HS.54477	Target Epon
440245	AK001193	HS.1100	Target Epon
412228	AA502765	HS.73792	Target Epon
411834	BE127008	HS.52869	Target Epon
425596	AF505996	HS.75812	Target Epon
424507	BE373796	HS.23558	Target Epon
425268	NI0_003512	HS.78777	Target Epon
413111	NI7543	HS.233699	Target Epon
414041	AA455131	HS.49407	Target Epon
425706	AA046678	HS.122559	Target Epon
450293	NI0574	HS.171118	Target Epon
406336	AA951400	HS.158110	Target Epon
413574	AC9374	HS.43387	Target Epon
431129	AF131751	HS.263671	Target Epon
418506	AA084248	HS.85339	Target Epon
411060	NI0_006074	HS.131861	Target Epon
411700	AD11119	HS.131861	Target Epon
437763	AA469369	HS.5281	Target Epon
440199	BE114999	HS.7503	Target Epon
417274	NI02306	HS.81848	Target Epon
410285	NI3187	HS.80985	Target Epon
410321	BE34477	HS.84987	Target Epon
430154	AA583059	HS.234726	Target Epon
428450	NI0_017491	HS.184339	Target Epon
425297	AA236251	HS.135383	Target Epon
425298	AA598334	HS.135383	Target Epon
405956	NI0_014018	HS.55097	Target Epon
424432	BE039389	HS.20178	Target Epon
404471	XS5956		Target Epon
425571	NI0_002260	HS.10082	Target Epon
425922	BE565343	HS.28988	Target Epon
450091	AA504814	HS.287379	Target Epon
449722	BE280074	HS.23960	Target Epon
449723	AF123650	HS.44532	Target Epon
427127	AA050222	HS.12255	Target Epon
417933	X02308	HS.82962	Target Epon
432828	AB042326	HS.287402	Target Epon
450308	AF123650	HS.24706	Target Epon
410266	AA080829	HS.1902	Target Epon
404951	NI0_077762	HS.79015	Target Epon
427337	ZAC222	HS.176663	Target Epon
408895	AA36166	HS.45500	Target Epon
427421	AF17421	HS.201639	Target Epon
422946	BE513934	HS.1583	Target Epon
415786	T89844	HS.78712	Target Epon
444207	AB581004	HS.101005	Target Epon
424131	AC261133	HS.82712	Target Epon
438718	AD104058	HS.80654	Target Epon
437802	AF15995	HS.122910	Target Epon
446359	AF142419	HS.154803	Target Epon
446361	AA302169	HS.154803	Target Epon
450921	AA392121	HS.171403	Target Epon
414359	ME2194	HS.75299	Target Epon
450071	AD018283	HS.74359	Target Epon
452882	AF079590	HS.196270	Target Epon
414522	AF575584	HS.76325	Target Epon
450506	AA116621	HS.38760	Target Epon
404756	NI0_10712	HS.301005	Target Epon
447157	AA02482	HS.125917	Target Epon
413215	AA955112	HS.75597	Target Epon
450000	NI0_00378	HS.73619	Target Epon

5.65	4.63
5.58	3.41
5.45	5.79
5.42	5.56
5.36	4.31
5.33	48.3
5.33	5.13
5.30	6.27
5.16	5.31
5.12	13.12
5.03	4.93
5.03	3.42
4.99	3.36
4.98	5.30
4.98	48.5
4.95	4.46
4.87	4.49
4.82	3.80
4.81	5.26
4.78	2.34
4.78	5.18
4.77	4.14
4.74	1.55
4.73	4.25
4.67	4.69
4.62	3.02
4.61	5.45
4.60	2.88
4.60	4.34
4.60	3.24
4.59	3.58
4.57	3.82
4.57	9.27
4.56	3.60
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4.47	3.72
4.47	3.96
4.45	2.40
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4.42	3.91
4.41	3.80
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4.36	4.65
4.36	3.44
4.36	3.21
4.35	3.10
4.34	5.61
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4.32	2.90
4.31	5.79
4.30	3.62
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4.28	5.06
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4.24	3.15
4.23	3.65
4.22	4.21
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4.20	4.26
4.19	2.65
4.18	4.18
4.16	4.28
4.16	4.89
4.16	3.39
4.14	3.82
4.14	3.02
4.12	4.18
4.12	3.87
4.11	3.80
4.11	4.25
4.10	2.91
4.10	4.25
4.09	3.99
4.09	4.60
4.08	3.64
4.07	2.43
4.07	6.55
4.06	4.18

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6.43
2.45
3.22

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5	421508	NM_004933	Ha.105115	abraxin in melanoma 2	4.05	4.39
	408688	A054522	Ha.152925	KIAA1028 protein	4.05	3.32
	439453	BE264974	Ha.6566	thyroid hormone receptor interactor 13	4.04	3.53
	445701	AF055581	Ha.13131	thymocyte adaptor protein	4.02	4.20
	451131	A026798	Ha.768012	fatty-acid-Coenzyme A ligase, long-chain	4.01	3.96
10	445291	BE.15993	Ha.23440	KIAA1105 protein	4.01	2.34
	443071	AL080021	Ha.5986	complement component 1, q subcomponent,	4.00	6.97
	417615	BE548541	Ha.82214	hypocauline phosphoribosyltransferase-1	3.99	4.27
	408246	N55669	Ha.333923	mitochondrial ribosomal protein L13	3.98	3.06
	408819	AW164839	Ha.45320	double ring-finger protein, Dofin	3.98	3.76
15	424058	AL121516	Ha.138617	thyroid hormone receptor interactor 12	3.97	2.38
	418942	A1566004	Ha.141269	Homo sapiens cDNA: FLJ21550 fs, clone C	3.97	3.40
	424756	AW504657	Ha.152531	lamin B receptor	3.93	2.67
	427155	AA357185	Ha.103918	rac homolog gene family, member H	3.89	2.39
	446952	AL031591	Ha.7370	phosphotyrosyl transfer protein, b	3.88	3.73
20	433001	AF217513	Ha.279905	clone HQ0310 PROX10p1	3.88	4.24
	418255	AW135405	Ha.37251	ESTs	3.87	2.53
	444371	BE540274	Ha.239	forkhead box M1	3.86	4.29
	420515	AW084226	Ha.15370	bifunctional hydrolase-like (serine hydrolase	3.85	3.73
	416114	A085549	Ha.183668	glucuronidase, beta	3.85	3.74
25	440596	H13032	Ha.103378	hypothetical protein MGC11034	3.84	1.90
	417020	T78413		heterogeneous nuclear ribonucleoprotein	3.82	2.04
	448503	BE243146	Ha.21332	ETE (POZ) domain containing 1	3.81	3.07
	446506	A012318	Ha.15159	chondrin-like factor; alternatively spliced	3.81	3.69
	417059	AL036762	Ha.81071	extracellular matrix protein 1	3.80	6.01
30	410668	BE379794	Ha.159651	hypothetical protein	3.80	5.22
	420107	AL042980	Ha.7886	peptide (Drosophila) homolog 1	3.79	3.53
	446071	N51527	Ha.13650	hypothetical protein DNF2-006F2423	3.79	2.74
	419731	S47242	Ha.92909	SON DNA binding protein	3.77	1.85
	443370	A1928116	Ha.9691	Homo sapiens cDNA: FLJ23249 fs, clone C	3.77	4.98
35	409837	R70292	Ha.156110	immunoglobulin kappa constant	3.77	7.42
	436481	AA379597	Ha.5159	HSP150 protein similar to ubiquitin-con	3.76	3.55
	419381	AB023420	Ha.90093	heat shock 70kD protein 4	3.76	1.81
	423679	AF229181	Ha.136644	CS box-containing WD protein	3.76	3.97
	402474			NM_004075 Homo sapiens cathepsin S (CTSS	3.76	4.01
40	412628	AL133396	Ha.74521	p10n protein (p27-30) (Cere2-like-Jakob	3.75	3.77
	454060	A1199711	Ha.576	fosfotransferase, alpha-L-1, tissue	3.74	6.15
	409085	N25929	Ha.342849	ADP-ribosylation factor-like 5	3.74	2.92
	426096	D87436	Ha.166318	lipin 2	3.72	2.98
	417105	X50982	Ha.81226	CD6 antigen	3.72	2.78
45	415322	AA204166	Ha.84113	cyclic-dependent kinase inhibitor 3 (CDK	3.72	2.72
	447735	AA75258	Ha.6127	Homo sapiens cDNA: FLJ23020 fs, clone L	3.70	4.09
	409264	NM_014937	Ha.52463	KIAA0956 protein	3.69	4.75
	429170	NM_001394	Ha.2369	dual specificity phosphatase 4	3.69	2.94
	423398	A124308	Ha.98258	ESTs	3.68	3.82
50	423494	AW094365	Ha.25143	Wiskott-Aldrich syndrome protein interac	3.67	3.52
	413236	BE243445	Ha.75248	topoisomerase (DNA) II (beta) (180kD)	3.67	2.79
	423712	W48802	Ha.81988	disabled (Drosophila) homolog 2 (mlnogen	3.66	3.42
	409703	NM_005187	Ha.56009	Z-5-oligodeoxylate synthetase 3 (100 k	3.66	6.44
	447225	R63676	Ha.17820	Rho-associated, coiled-coil containing p	3.65	2.93
55	414829	AA321558	Ha.77436	pleckstrin	3.65	2.30
	400219			Eos Control	3.64	2.76
	427239	AW503395	Ha.6541	ATPase, Ca transporting, ubiquitous	3.63	2.73
	422445	BE2114	Ha.1526	ATPase, Ca transporting, cardiac muscle	3.62	3.60
	445971	AA807345	Ha.288581	Homo sapiens cDNA: FLJ14296 fs, clone PL	3.62	3.62
60	424460	BE257979	Ha.296014	polymerase (RNA) II (DNA directed) poly	3.62	3.06
	427659	AK000436	Ha.179791	hypothetical protein FLJ20429	3.62	2.31
	420750			Target Eosin	3.61	2.74
	424541	AW092551	Ha.180559	ESTs, Weakly similar to A56194 thrombox	3.61	2.26
	427051	BE178110	Ha.173374	Homo sapiens cDNA: FLJ10500 fs, clone NT	3.60	4.20
65	433867	AK000596	Ha.3518	Hypocaulin-like 1	3.59	4.19
	427586	AL137438	Ha.110454	SEC15 (S. cerevisiae) like 1	3.59	1.58
	414841	H15601	Ha.77490	glutathione S-transferase theta 1	3.58	3.98
	429693	BE254962	Ha.211612	SEC24 (S. cerevisiae) related gene fami	3.57	3.00
	425204	NM_002436	Ha.1861	membrane protein, palmitoylated 1 (SGK)	3.56	3.09
70	441689	R76195	Ha.29692	Homo sapiens cDNA: FLJ11436 fs, clone HE	3.56	3.26
	420433	BE567620	Ha.99210	ESTs	3.55	3.36
	406636	L12054		glt: Homo sapiens cDNA: WRN.12VL) and h	3.55	1.83
	446341	AL040763	Ha.310735	ESTs, Moderately similar to ALLU7_HUMAN A	3.54	3.52
	423485	N80866	Ha.278770	CDWS2 antigen (CAMPATH-1 antigen)	3.54	4.66
75	422785	AW097071	Ha.1576	bicucullarin UAP repeat-containing 5 (ur	3.54	3.25
	413630	AA738437	Ha.25265	Homo sapiens cDNA: FLJ1286 fs, clone C	3.54	1.87
	432841	M53425	Ha.62	protein tyrosine phosphatase, non-recept	3.53	3.96
	425177	AF127577	Ha.155017	nuclear receptor interacting protein 1	3.53	3.40
	426643	AA857131	Ha.171595	HN 1A1 specific factor 1	3.51	2.21
80	420137	AA358478	Ha.93537	CBX3 (chromatin, delta polycomb) (TbT3 co	3.51	2.21
	429248	U96759	Ha.198307	von Hippel-Lindau binding protein 1	3.51	2.85
	452852	AK001972	Ha.30822	hypothetical protein FLJ11110	3.51	2.71
	451791	T73407	Ha.27023	vesicle transport-related protein	3.49	2.91
	418310	AA841100	Ha.68693	ESTs	3.49	1.45
85	406858	AA505445	Ha.300697	immunoglobulin heavy constant gamma 3 IG	3.48	6.81
	400200			NM_002788 Homo sapiens profilome (pro	3.48	2.51
	438746	A085815	Ha.184727	Human melanoma-associated antigen p97 (m	3.47	6.94

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5	441646	AB023169	Hs.7935	KIAA0952 protein	3.47	3.38
	427968	A1857607	Hs.181301	cathepsin S	3.45	2.71
	440201	AL359588	Hs.7041	hypothetical protein DKF-Zp762626	3.45	3.45
	434608	AA054543	Hs.17909	hypothetical protein FLJ22595	3.44	3.68
	427572	A1809057	Hs.153051	immunoglobulin heavy constant mu	3.44	6.70
10	413385	MG4455	Hs.640	indoleamine-pyruvate 2,3 dioxygenase	3.44	2.72
	435550	A1224456	Hs.324507	H.sapiens polyA site DNA	3.43	2.76
	435857	AL080235	Hs.35961	DKF-ZP5661621 protein	3.43	3.64
	423032	AA195037	Hs.163341	HTFAP protein	3.43	2.25
	418440	MG3315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	3.43	2.76
15	435915	AA588721	Hs.286218	ribosomal protein L44	3.41	3.06
	447485	BE092785	Hs.29724	hypothetical protein FLJ13167	3.41	4.23
	433506	NM_002104	Hs.3056	granzyme K (serine proteinase, granzyme 3;	3.40	3.83
	417410	AF536020	Hs.82110	PCF and SPST-1, interacting protein	3.40	2.12
	436810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) ho	3.40	4.70
20	422545	X02761	Hs.287820	fibrinectin 1	3.39	7.58
	408142	AL136877	Hs.50758	SMCA3 (structural maintenance of chromoso	3.36	4.12
	434826	AF155651	Hs.22285	pyruvate dehydrogenase phosphatase	3.34	5.05
	440410	AK000227	Hs.21176	hypothetical protein FLJ20220	3.33	4.31
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.33	4.60
25	432642	BE267635	Hs.3069	heat shock 70kD protein 98 (mortalin-2)	3.32	4.49
	425234	AW157235	Hs.165909	ESTs, Weakly similar to 180222 hypoxanth	3.24	4.22
	443923	AA345519	Hs.3641	complement component 1, q subcomponent,	3.23	12.31
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23	5.07
	443958	BE241980	Hs.10029	cathepsin C	3.16	4.97
30	412577	Z22968	Hs.74076	CD163 antigen	3.14	4.75
	441050	NM_004766	Hs.75724	cutaneous protein complex, subunit beta 2	3.13	4.00
	421633	AF121860	Hs.106260	sorting nexin 10	3.12	4.45
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibitor	3.11	4.00
	428767	AA446205	Hs.193700	Homo sapiens mRNA, cDNA, DKF Zp5890324 (f	3.10	4.03
35	430314	AA365601	Hs.238138	yea-B cell colony-enhancing factor	3.06	4.49
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.04	4.98
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	3.03	4.49
	452139	AA059569	Hs.16331	Homo sapiens cDNA, FLJ121482 ts, clone C	3.01	4.75
	430237	AW408158	Hs.318653	ESTs, Weakly similar to AA17582 B-cell g	2.95	5.65
40	422684	BE361617	Hs.119192	H2A histone family, member 2	2.94	4.64
	406782	AA303373		gb-w2011.1.s1 Soares ovary tumor NHOT H	2.93	10.28
	438549	BE868801	Hs.21858	trinucleotide repeat containing 3	2.91	5.40
	450455	AL117424	Hs.25035	chloride intracellular channel 4	2.90	4.86
	427528	AJ077143	Hs.175665	minicolumnous maintenance deficient (S,	2.89	4.04
45	422530	AW572300	Hs.118110	bone marrow stromal cell antigen 2	2.87	9.61
	423605	AF047826	Hs.129887	cadherin 19, type 2	2.83	4.86
	410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	2.82	5.02
	419556	AL137538	Hs.400596	cathepsin 15, type 2	2.80	4.30
	416511	NM_006762	Hs.79356	Lysosomal-associated membrane protein	2.79	5.80
50	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	2.78	4.21
	448517	AA082750	Hs.42194	hypothetical protein FLJ22649 similar to	2.78	4.23
	416784	AA334592	Hs.79914	lumican	2.78	4.40
	427792	MG3978	Hs.180841	tumor necrosis factor receptor superfam	2.77	4.23
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (calcikins	2.77	4.17
55	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.76	4.43
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	2.75	4.20
	437179	AA393528		serologically defined colon cancer antig	2.74	4.07
	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	2.72	4.63
	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-4	2.71	4.53
60	405902	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.68	4.15
	426124	AJ265396	Hs.250697	phosphatidylinositol glycan, class F	2.67	4.00
	422672	X12704	Hs.119129	collagen, type IV, alpha 1	2.67	4.72
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.65	7.77
	409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ22224 ts, clone C	2.65	4.47
65	410341	AW599885	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.64	5.61
	433027	AF191018	Hs.250697	putative nucleotide binding protein, est	2.63	4.34
	424687	JO5070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.62	4.95
	409430	R21945	Hs.346735	splicing factor, arginine/serine-rich 5	2.60	6.00
	424779	AL046651	Hs.153053	CD33 antigen	2.60	4.27
70	423854	BE6186	Hs.153472	Homo sapiens cDNA: FLJ22224 ts, clone H	2.60	4.64
	427550	BE242818	Hs.311609	nuclear RNA helicase, DEAD domain of DE	2.57	4.27
	426143	BE379836		proteasome (prosome, macropain) subunit,	2.56	4.20
	421563	NM_004433	Hs.105806	granzysin	2.54	4.13
	425553	AA237621	Hs.1908	prolactinogen 1, secretory granule	2.54	5.55
75	428166	AS029884	Hs.182783	poly phosphoprotein 2	2.54	5.78
	429600	AA333375	Hs.223014	antemycin inhibitor	2.50	5.15
	407241	M34516	Hs.107526	gb1 human omega tight chain protein 14.1	2.50	4.98
	421739	AB004580	Hs.740405	UDP-Gal-4-epiGalNAc 6-epi-4- galactosyl	2.45	5.58
	412819	T75825	Hs.24143	FGFR3 binding protein precursor	2.45	7.20
80	412025	A1827451	Hs.24143	Wiskott-Aldrich syndrome protein interact	2.44	4.11
	435523	T82849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.44	4.67
	445350	AF052112	Hs.17540	hypothetical protein FLJ23015 ts, clone L	2.44	5.44
	440296	AL137257	Hs.234538	Homo sapiens cDNA: FLJ23015 ts, clone L	2.41	4.31
	440065	W03476	Hs.266331	hypothetical protein MG45495	2.41	4.25
	400223			Eco Control	2.39	5.68
	423658	AF231981	Hs.250175	homolog of yeast long chain polyunsatur	2.39	6.62
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (fo	2.38	7.22

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414622	A1752666	Hs.76669	nicotinamide N-methyltransferase	2.38	5.21
415149	X12451	Hs.78056	cathespin L	2.37	7.71
435099	AC004770	Hs.4796	flap structure-specific endonuclease 1	2.37	5.68
427407	BE268549	Hs.177765	ADP-ribosyltransferase (NAD ⁺ poly (ADP-ribose) polymerase 2	2.31	4.83
425432	AF010161	Hs.169851	paraoxonase 2	2.29	4.53
430555	A015486	Hs.243901	Homo sapiens cDNA FLJ20738 fs, clone HE	2.27	5.03
413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	2.25	4.41
412517	AK001364	Hs.808	heterogeneous nuclear ribonucleoprotein	2.21	4.31
447547	NM_007229	Hs.18842	protein kinase C and cation kinase subet	2.19	4.62
416232	AW502676	Hs.76090	exorpin 1 (CTAM1, yeast, homolog)	2.18	4.84
420842	A108368	Hs.50601	hypothetical protein MGC10586	2.14	4.22
411388	R47479	Hs.94761	KIAA1691 protein	2.13	4.65
428227	A4321649	Hs.2248	small inducible cytokine subfamily B (cy	2.13	4.03
426587	M01176	Hs.75239	matric metalloproteinase 11 (stromelyn	2.11	1.16
417331	AW411297	Hs.81972	SHC (Src homology 2 domain-containing) I	2.11	4.25
450344	AW994032	Hs.8768	hypothetical protein FLJ10849	2.11	4.09
429542	X68264	Hs.211579	melanoma cell adhesion molecule (MCAM) (2.11	5.42
416446	L13210	Hs.75239	lectin, galactoside-binding, soluble, 3	2.10	6.42
418613	AA744529	Hs.86575	mitogen-activated protein kinase kinase	2.10	4.00
453532	T10445		ESTs	2.09	4.48
409220	BE243323	Hs.51233	tumor necrosis factor receptor superfamily	2.09	4.98
414045	NM_002951	Hs.75722	atrophin II	2.07	4.59
422451	AA310763	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	2.07	4.09
414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.06	5.06
452363	A158743	Hs.94553	Homo sapiens, Similar to complement com	2.04	4.17
438033	AA351815	Hs.50740	Homo sapiens cDNA FLJ22722 fs, clone H	2.03	3.36
413313	NM_002047	Hs.263108	glycyl-tRNA synthetase	2.02	4.79
412994	D32757	Hs.75113	general transcription factor IIA	2.00	4.67
424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.98	4.79
421897	AW583693	Hs.100253	N-terminal acetyltransferase complex and	1.98	4.17
442159	AW163390	Hs.278554	histone chromatin-like protein 1	1.95	2.53
429451	BE408861	Hs.202833	heme oxygenase (decycling) 1	1.95	4.63
416957	BE16731	Hs.80645	interferon regulatory factor 1	1.95	4.31
402023			Eos Control	1.94	5.03
437317	AA748613	Hs.311977	ESTs, Highly similar to SWI5NF related,	1.94	4.03
414845	BE076398	Hs.77667	lymphocyte antigen 5 complex, locus E	1.92	4.63
416224	NM_002902	Hs.79068	reticulocalbin 2, EF-hand calcium bindin	1.92	4.12
445411	AL137255	Hs.12646	hypothetical protein FLJ2693	1.91	4.23
413845	NM_000591	Hs.75627	CD14 antigen	1.90	5.00
413317	US0205	Hs.75023	sorting nexin 1	1.90	4.20
448719	AA033677	Hs.21858	trunculeotide repeat containing 3	1.89	4.26
430838	N46664	Hs.169395	hypothetical protein FLJ12015	1.88	4.15
427239	BE270447		ubiquitin carrier protein	1.87	5.72
450440	AB204334	Hs.29001	tyrosine 3-monoxygenase/tyrosinophan 5-mo	1.87	5.81
433671	AW138797	Hs.132906	18A24 protein	1.85	4.27
413190	AA151602	Hs.40368	adaptor-related protein complex 1, sigma	1.85	5.19
414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	1.85	4.31
430840	AW503115	Hs.227623	p45 protein	1.83	5.57
417929	U72219	Hs.74547	Human T-cell receptor active alpha-chain	1.82	4.29
414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.81	4.39
414416	AW403985	Hs.76084	hypothetical protein MGC27221	1.80	4.20
426977	AK001404	Hs.194698	cyclic B2	1.79	4.17
418707	U97562	Hs.67497	bicyclopilin, subfamily 3, member A2	1.78	4.30
425367	BE771188	Hs.155975	protein tyrosine phosphatase, receptor I	1.78	5.44
425811	AL039104	Hs.159657	karyopherin alpha 2 (RAG cohort 1, impor	1.77	5.11
422009	AF472845	Hs.110713	DER oncogene (DNA binding)	1.77	4.37
424909	ST8187	Hs.153372	cell division cycle 25B	1.74	5.00
461514	U72882	Hs.50842	interferon-induced protein 35	1.74	4.66
413892	AA878921	Hs.79607	myristoylated alanine-rich protein kinas	1.73	4.37
444954	AW247076	Hs.12163	eukaryotic translation initiation factor	1.71	5.02
424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrophobates	1.70	4.68
424825	AF707069	Hs.153357	procollagen-hyaline, 2-oxoglutarate 5-dio	1.69	7.70
427376	BE515037	Hs.177556	melanoma antigen, family D, 1	1.67	5.59
413322	AA380158	Hs.75290	ADP-ribosylation factor 4	1.67	4.39
442414	BE408738	Hs.8297	nucleotidase 5 precursor	1.65	4.03
410129	BE244074	Hs.58631	regulator of Fas-induced apoptosis	1.64	2.64
422976	AJ076657	Hs.1600	chaperonin containing TCP1, subunit 5 (e	1.64	4.91
443051	AA330660	Hs.71331	hypothetical protein MGC5350	1.64	4.08
452472	AW557300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	1.63	4.41
446163	BE245342	Hs.30679	scs1 homolog	1.62	4.70
431142	AA482686	Hs.258641	Insomycin A	1.62	1.52
407752	AA573581	Hs.13328	ESTs	1.62	4.19
416322	BE019494	Hs.73217	pyrimidine 5-carboxylate reductase 1	1.61	4.51
414572	AJ077174	Hs.288181	cathespin H	1.60	5.25
415017	PR4434	Hs.77805	ATPase H transporting, lysosomal (vacuo	1.56	6.60
452056	AW555065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNM,	1.58	5.46
413976	BE265452	Hs.75655	procollagen-proline, 2-oxoglutarate 4-di	1.58	4.06
414420	AA043424	Hs.76095	immediate early response 3	1.58	4.00
419638	NA5504	Hs.91749	prolin 2	1.57	5.57
427624	BE166678	Hs.76152	KDEL (Lys-Asp-Glu-Lys) endoplasmic retic	1.57	4.44
415819	AJ077330		transcription elongation factor A (SII),	1.55	4.89
439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.55	6.66
425243	N89487	Hs.155291	KIAA0065 gene product	1.54	4.38

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424799	BE550223	Hs.153179	fatty acid binding protein 5 (peroxisome-uncoupling protein 2 [mitochondrial, pro	1.53	4.22
416971	R34857	Hs.80658	interferon regulatory factor 7	1.53	7.41
426059	BE292842	Hs.166120	Tax1 (human T-cell leukemia virus type I	1.51	4.12
418879	AW162087	Hs.24737	Rac homolog enriched in brain 2	1.50	4.02
432969	BE264029	Hs.51993	proscapsin (variant Gaucher disease and	1.50	4.18
415561	AF057307	Hs.78375	protein disulfide isomerase-related prot	1.48	4.9
428098	AL077258	Hs.182429	transmembrane 9 superfamily member 2	1.49	5.74
452264	AL077013	Hs.28757	natural killer cell transcript 4	1.47	4.95
415198	AW003480	Hs.943	phosphatase, glycoprotein, brain	1.45	4.51
411794	AL111577	Hs.75558	nucleolar protein family A, member 3 (p/	1.45	4.15
433271	BE521697	Hs.14317	adenylate cyclase-associated protein	1.42	4.67
421416	BE302950	Hs.104125	ribosomal protein S26	1.41	5.19
415089	N25117	Hs.299465	hypothetical protein FLJ11855	1.41	4.44
421975	AW961017	Hs.5459	NM_002767 Homo sapiens, proteasome (pro	1.41	4.44
400202			interferon-stimulated protein, 15 kDa	1.41	4.57
413278	BE563085	Hs.833	atanyl-RNA synthetase	1.40	4.25
412968	AW005058	Hs.75102	insulin-like growth factor binding prote	1.39	4.11
440704	M69241	Hs.162	coronin, actin-binding protein, 1C	1.39	4.51
447099	AB030556	Hs.17377	transcription elongation factor (B) (SII)	1.38	4.90
428511	AW109912	Hs.184693	CD151 antigen	1.37	4.44
413825	BE299181	Hs.75564	adenosine deaminase, RNA-specific	1.36	4.29
441737	X79449	Hs.7957	hypothetical protein FLJ22676	1.36	4.10
440087	W28969	Hs.77119	sprouty (Drosophila) homolog 4	1.35	4.50
413566	AW504451	Hs.285814	low density lipoprotein-related protein-	1.35	5.14
413019	BE281604	Hs.75140	HSPC035 protein	1.35	4.14
433026	AW160616	Hs.279292	interferon gamma receptor 2 (interferon	1.34	4.24
427380	NM_055334	Hs.177589	complement component 2	1.33	4.23
428289	M63091	Hs.2253	vitamin A responsive; cytoskeleton relat	1.32	4.61
419715	AF070523	Hs.92384	calretinin	1.31	4.76
422299	AW905214	Hs.153550	guanine nucleotide binding protein (C pr	1.30	5.30
442942	AJ251760	Hs.273385	Homo sapiens clone FLB215 PRK2474 mRNA,	1.29	4.90
449463	AA326392	Hs.21321	EST	1.29	4.56
407143	C14076	Hs.332329	glyoxalase I	1.26	5.56
413125	BE244589	Hs.75207	chaperonin containing TCP1, subunit 2 (b	1.26	4.98
430503	BE244589	Hs.8456	collagen, type IV, alpha 2	1.25	4.5
413929	BE251659	Hs.75147	calcium-regulated heat-stable protein (2	1.24	4.56
419563	AA394208	Hs.92198	S100 calcium-binding protein A9 (calgran	1.21	8.96
422166	W72424	Hs.112405	solute carrier family 16 (monocarboxate	1.21	4.02
416536	N32536	Hs.42645	folate-binding protein	1.16	4.29
425335	BE394327	Hs.286367	S100 calcium-binding protein A13	1.17	4.32
446211	AB021993	Hs.14331	KUAA078 protein	1.13	4.17
428642	NM_014899	Hs.10432	adaptor-related protein complex 1, sigma	1.00	4.00
454117	BE410100	Hs.40358	protein kinase, cAMP-dependent, regulato	1.09	4.40
428216	M18468	Hs.183037	gap junction protein, beta 2, 250D (conn	1.00	4.7
432121	M6849	Hs.322933	protease inhibitor 3, skin-derived (SKAL	0.98	4.40
422158	L10343	Hs.112341	Small proline-rich protein SPRK (human,	0.90	4.78
408522	A541214	Hs.46320			

Table 50B

Play:	Unique Ecol protease identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

55	Play	CAT Number	Accession
412918	2764_3		BE794583 AL151009 AV755430 AV756363 AV711927 BE152343A A521453 AA846815 AW024829 AW949702 BG218526 AE426658 AA456211 A452815 AA945555 AA723580 AA512925 BG105326 BG332618 AW513994 AW602165 AJ373448 AA907951 AW135104 BG186652 W69209 BG219754 BE774875 BG190378 AA483598 BE696966 BE696967 BE056602 AW304207 BE393581 AW795659 BG210552 AW795544 BE393368 AW102686 BE655977 BG182971 H70742 D58090 BG403551 H61248 AV750112 AW372079 CG5492 D56287 D57835 AA350395 BF070019 BG215802 BG195459 AW68947 BG495535 BG333177 B087967 BE541579 BF130753 Z69892 AA210833 BM353155 AJ473754 AJ147901 AB031059 AA843296 AA418925 AA478522 AA020067 A363004 AAT411828 AW330173 BE218552 A532604 EF433224 AA394157 BF780471 BE467036 AA379724 AW209940 A222671 A3477424 AW207111 A228652 AA336810 A457582 AA1915396 AA390825 CT5102 N30295 H50440 AW19304 AB043599 A338362 AJ123606 AA64851B A5156758 BE653321 A228652 AA486101 A5580792 AA758196 AA214630 AJ373791 AJ1594733 EF433447 A250291 BF437165 AA757592 BF086994 AW655502 AW952466 BF445858 A535327 BF333845 AW145064 AJ01629 N50021
60	436701	28142_1	BC016556 BC016365 NM_016040 AF151858 BS61037 AF1966873 AF1966749 BE219482 BE01850 AW770511 AA469095 AA70133 BM150181 BM153977 BE24135 A532345 AJ129838 BM47484 AJ252112 BE246667 AA251084 AW536359 BM13986 BM151481 BF445862 AJ597435 BF000262 AA24386 AB098100 AW076274 A685793 AL080384 BG33686 BE02940 BG179242 BM69554 A226289 AA255771 AW664511 AA451523 H00335 BF370359 AW954201 BM145846 BG111760 AF150065 BG65579A A564086 BG494071 BM059066 A575331 BE302224 AJ476456 AE62980 BM144561 AJ184022 A343932 AJ135856 AW029464 A1708651 AA824243 BM145917 AA652210 AA825708 AJ335858 AJ27304 A6652171 A48974 A497616 AJ344537 A490593 A873901 AW05895 AA68358 AA765611 AJ150322 A662816 BE1149674 A368062 AA019347 A8977692 A8311100 A688495 BE231185 AJ271219 A681078 AJ112676 A702407 BG217152 BE066462 A33302 BE574255 A49521 B048744 AF300223 BF138690 AW966873 A363405 BF115146 AF4910851 A4013059 N28878 AA287813 BE348728 BG361646 AL159953 AL159952 BF381073 AW505055 AA094735 H03613 A2487114 H27168 RS4718 BF72697 AV693603 BG685883 BG619956 BF541504 BF216789 AA3119751 BM452652 BF335838 AA280397 BF771509 BF571997 AA490239 AW388161 BE42126 BF166309 BF1903 A955387 BF42040 F09178 AA772421 AA450218 M78543 A244114 AA013686 A202971 BE1785477 AF150810 AF593131 A338271 N11926 H74297 A265604 AA45055 A281647 BF37670 T52670 BE322893 BG271680 AA025143 H27167 AW00226 BC849487 BF65889
65	432469	5664_1	BE379786 AW152543 AB034550 A564343 A092711 A140525 A512516 A562074 A554589 A161209 A29C242 A339745 A374611 A347368 A585296 A140529 A368124 A493912 AA60235 AA493889 A8057160 AW02266 A905727 A1144126 A080051 AA96329 AA805057 N53469 AA436737 H81163 N70626 A424267 A4983537 BF003004 A4626688 A4235971 A607152 A006366 A005356 AA458946 AW134479 AA150433 A373222 AW571777 A359198 A458373 BE516384 BE73829 A47083 A00344 T55584 BE1658 A098074 A0501565 AA382765 AA370208 A24539 A371515 BE24680 A548596 AAW49675 A1911008 BF223749 N07052 N22626 A191012 A0007601 A119106 BF215651 BF315148 BQ042356 A147466 BE858217 BF793358 AW756758 BG483603 A003724 BF593395 BG45345 A7142294 T59549 A8811773 BF4849575

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A1246746 A1531453 A1189679 A5594592 A0396309 AAB62764 A6644332 AA012423 AA061502 AA069405 AA068949 BF941650
AA0597886 BF941649 A017854 A027442 AA705602 AW020757 B0491734 A0871753 A0653873 B052334 AA398723 A208083 A0119671 AW009199
AA496011 A0114401 A035840 BF741690 BF741680 BA11900 AV724108 AW955578 B0598790 T29312 B0954488 B33175 B183261 BF74200
BE091493 H02122 B0614879 AW933709 A216562 H44107 AA393030 BE173154 B0285854 BF751883 AA483008 BF741676 B64496 B0183198
BF7057 AW062534 BF039420 AW182614 BF431707 N3055 AA629072 B0254498 A0431616 B0390567
BE373890 BF741695 AA156207 AS753157 AW874610 AA916387 N75963 B0833306 AW044671 B013008 NM_002795 D26598 B0118716 B018910891
BF972660 BF119842 B094093 AL538757 BE271653 B0565308 BE309573 D0109626 BE784430 DE89525 B1833873 B0110809 BE621321 B0584956
BE904726 B0871370 A0708990 BF971483 BE298241 B1197007 BE272092 B0120374 AW963505 BE405072 AV744947 B09430401 AW327463
B0472870 BE350897 N03533 AA316042 M02043 AA404246 AW626294 AA379896 AW001110 AW400597 AA379791 B0841889 B011564 AA368459
AA379395 AA320559 B0942616 D31230 AA330404 AA380371 AA371337 AA973257 AA494244 W02225 BF745937 A0383690 B0202590

TABLE 50C:

Play: Unique number corresponding to an Eos probe
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham, et al. (1999) Nature 402:489-495.
Stand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Play	Ref	Strand	NL_position
404854	7143420	Plus	14260-14537
405506	6466489	Plus	8014-80401,80593-81125
402474	7547175	Minus	53526-53628,55735-55920,57530-57757
400750	B119067	Plus	198991-199108,199316-199540

TABLE 51A: ABOUT 453 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO NORMAL SKIN

Table 51A lists about 453 genes upregulated in primary melanomas, relative to normal skin. Genes were selected from 59560 probesets on the Eos/Altmeterix Hs03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI). A normalized value reflecting the relative level of mRNA expression. Play: Unique Eos probe set identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of primary melanoma AIs divided by 90th percentile of normal skin AIs
R2: 90th percentile of primary melanoma AIs divided by 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Play	ExAccn	UnigeneID	Unigene Title	R1	R2
452838	U65011	Hs.30743	preferentially expressed antigen in melan	14.06	15.56
430377	NM_001922	Hs.301865	dopachrome tautomerase (tyrosinase)	13.54	11.62
426555	NM_000372	Hs.2053	tyrosinase (tyrosinase-related protein 1)	13.50	9.98
438549	BE386801	Hs.21688	trinucleotide repeat containing 3	12.78	13.80
422424	A1196431	Hs.296638	prostate differentiation factor	11.88	15.56
426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	10.14	22.46
430822	AJ005371	Hs.148017	glyceroldehyde-3-phosphate dehydrogenase	9.33	7.25
427211	AW972565	Hs.32269	ESTs, Weakly similar to SS1707 reocidist	8.86	9.62
438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	7.87	9.58
417355	D13168	Hs.82002	endothelin receptor type B	7.66	4.63
447210	AF356289	Hs.17752	phosphatidylserine-specific phospholipase	7.39	9.04
413554	AA319146	Hs.75428	secretogranin II (chromogranin C)	6.54	7.32
415752	BE314524	Hs.78776	putative transmembrane protein	6.46	4.65
421508	NM_004833	Hs.105115	absent in melanoma 2	6.44	7.00
449644	AW960707	Hs.148324	ESTs	6.43	5.92
426312	AF029939	Hs.181674	interferon-induced protein with tetra	6.27	6.47
448821	AB012113	Hs.16530	small inducible cytokine subfamily A (C)	6.17	3.70
429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	6.09	3.92
414812	X72755	Hs.77367	monokine induced by gamma interferon	6.04	7.73
452973	H88409	Hs.40527	ESTs	6.04	5.89
420075			ENSP00000251057: Plasma membrane calcium	5.96	5.90
436856	A469355	Hs.127310	ESTs	5.72	5.29
425088	AA663372	Hs.169395	hypothetical protein FLJ12015	5.68	5.88
439310	AF086120	Hs.102793	ESTs	5.62	6.30
429170	NM_001194	Hs.2259	dual specificity phosphatase 4	5.62	3.30
413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	5.50	4.28
409512	AW979187	B235991	melanoma differentiation associated prot	5.36	4.14
430540	AW245422	Hs.27935	Homo sapiens cDNA: FLJ2105 fs, clone H	5.36	4.64
436315	BE380513	Hs.332038	hypothetical protein MGC8370	5.35	4.31
442426	A1373662	Hs.332038	hypothetical protein MGC8370	5.28	4.03
435056	AW023337	Hs.5422	glycoprotein M6B	5.23	3.25
432828	AA042326	Hs.287402	chondroitin 4-sulfotransferase	5.20	5.52
430294	AJ538226	Hs.32976	guanine nucleotide binding protein 4	5.14	4.82
431639	AA000680	Hs.266175	phosphoprotein associated with GEMs	5.09	4.35
430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.06	3.68
414004	AA737033	Hs.7155	ESTs, Moderately similar to 21153574 TYK	5.04	4.23
407366	AF026942	Hs.17518	gb.Homo sapiens cigs3 mRNA, partial sequ	4.94	6.29
422192	AA305159	Hs.113018	64455	4.88	5.62
420208	BE780555	Hs.95972	silver (mouse homolog) like	4.84	6.00
446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.77	4.33
440065	W03476	Hs.266331	hypothetical protein MGC4595	4.74	9.85
421574	AJ000152	Hs.105924	defensin, beta 2	4.74	5.75
440274	R24395	Hs.7122	serpin responsive protein 1	4.72	2.79
417166	AA431323	Hs.42146	ESTs	4.68	4.28
415314	N88802	Hs.5422	glycoprotein M6B	4.65	3.73
443983	H04482	Hs.163724	ESTs	4.64	3.06

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432642	BE297635	Hs.3069	heat shock 70kD protein 90 (mortalin-2)	4.62	2.87
437179	AA393508		serologically defined colon cancer antigen	4.62	5.08
417933	QX2308	Hs.82962	thymidylate synthetase	4.58	3.02
431820	AA128109	Hs.264381	Z'-5'-oligoadenylate synthetase 2 (69-71)	4.50	4.37
431529	AL077025	Hs.265427	interferon, alpha-inducible protein (ds)	4.46	16.82
477937	AL105716	Hs.20034	homo sapiens mRNA full length insert cDN	4.44	5.95
409264	NM_014937	Hs.52463	KIAA0956 protein	4.42	2.94
434203	BE262677	Hs.293558	hypothetical protein PR01855	4.42	3.54
422309	U79745	Hs.114924	soluble carrier family 16 (monocarboxylic	4.38	3.30
447222	BE280074	Hs.233601	cyclin B1	4.32	4.07
446619	AL076643	Hs.313	secreted phosphoprotein 1 (ectoposin,	4.30	3.82
450065	AL050107	Hs.24341	transcriptional co-activator with PDZ-ti	4.28	4.36
424247	X14008	Hs.234734	lysosome (renal amyloidosis)	4.27	3.05
413915	N09613	Hs.75615	cytochrome C- β	4.25	4.68
420267	N37030	Hs.173337	ESTs	4.24	4.24
442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	4.21	3.00
433576	BE060715	Hs.161091	ESTs	4.20	6.31
412652	AB017777		ESTs	4.20	2.73
438209	AL120659	Hs.6111	aryl hydrocarbon receptor nuclear transf	4.20	5.18
441553	AA281219	Hs.121295	ESTs	4.14	4.94
407856	AA045281	Hs.266175	phosphoprotein associated with GEMs	4.14	3.14
438926	AW014875	Hs.137007	ESTs	4.12	4.76
429903	AL134197	Hs.53597	cyclin-dependent kinase 5, regulatory su	4.12	4.85
409860			Target Exon	4.10	5.20
409415	AA579258	Hs.6083	Homo sapiens cDNA: FLJ21028 ts, clone C	4.08	6.02
415636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	4.08	2.42
428265	BE243286	Hs.301638	serotransferrin biogenesis factor 5	4.06	2.95
407748	AL079409	Hs.38176	KIAA0605 protein; SCN Circadian Oscillat	4.06	2.28
417632	R20855	Hs.5422	glycoprotein M68	4.01	2.98
418064	BE387287	Hs.83384	S100 calcium-binding protein, beta (neur	4.00	4.82
446111	AA053498	Hs.20210	interferon-induced protein 47	4.02	4.00
429674	NM_000055	Hs.1327	butyrylcholinesterase	4.00	2.90
451668	Z43948	Hs.326444	cartilage acidic protein 1	3.99	5.17
430015	AW768399		ESTs	3.96	3.89
407756	NM_115021	Hs.38260	reticulon specific protease 18	3.94	2.91
430223	NM_002514	Hs.236935	neuroblastoma overexpressed gene	3.93	3.89
433364	AI075407	Hs.296083	ESTs, Moderately similar to IS4374 gene	3.93	4.70
448719	AA033627	Hs.21958	thymidine repeat containing 3	3.92	7.78
419381	AA024240	Hs.90093	heat shock 70kD protein 4	3.87	3.34
420609			KIAA1275 protein	3.87	3.69
409083	BE383668	Hs.42494	hypothetical protein FLJ10618	3.86	4.04
409703	NM_006187	Hs.58009	Z'-5'-dipolyadenylate synthetase 3 (100 k	3.85	3.64
420218	AW959037		ribosomal protein L4	3.84	3.20
434826	AF155661	Hs.72265	pyruvate dehydrogenase phosphatase	3.84	5.19
410600	AW575742		ESTs, Moderately similar to S65657/alpha	3.82	5.74
442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE-447	3.82	2.96
428513	BE220806	Hs.184697	Homo sapiens clone Z3785 mRNA sequence	3.82	4.03
417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	3.80	3.56
420094	AF685890	Hs.61428	Homo sapiens mesenchymal stem cell prote	3.79	3.23
443105	X36753	Hs.9004	chondroitin sulfate proteoglycan 4 (meta	3.77	3.66
423605	AF047826	Hs.129887	cadherin 19, type 2	3.72	2.28
407846	AA426202	Hs.40403	Copp300-Interacting transactivator, wit	3.72	5.34
442578	AA020163	Hs.83395	hypothetical protein FLJ10781	3.71	3.42
448956	AW372914	Hs.86149	phosphoinositid 3-phosphate-binding prot	3.68	3.31
428227	AA321649	Hs.2248	small inducible cytokine subfamily 1 (Cy	3.68	4.24
400750			Target Exon	3.68	2.74
447217	BE465754	Hs.17778	Neurexin 2	3.66	3.60
456373	BE408296	Hs.301406	hypothetical protein PP2501	3.66	3.48
419628	H67546	Hs.49768	ESTs	3.62	4.13
406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	3.61	4.40
421868	N24470	Hs.1435	guanosine monophosphate reductase	3.59	3.53
421709	AA162304	Hs.107056	CE2-6 protein	3.57	2.93
438501	Z44110	Hs.86149	phosphoinositid 3-phosphate-binding prot	3.56	3.54
409662	BE386436	Hs.44317	SRY (sex determining region Y)-box 10	3.55	2.70
425139	AW530488	Hs.25338	protease, serine, 23	3.50	2.90
428411	AW291464	Hs.103338	ESTs	3.50	2.48
452744	AB257652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (r	3.48	4.61
411305	BE241596	Hs.69547	myelin basic protein	3.48	3.37
447343	AA256641	Hs.236994	ESTs, Highly similar to 502392 alpha-2-m	3.47	2.68
429954	AF918130	Hs.21374	ESTs	3.47	2.63
417821	AA164694	Hs.862316	interferon-induced, hepatitis C-associated	3.46	2.34
435296	AF193766	Hs.13872	cytokine-like protein C17	3.46	2.47
450534	AF570189	Hs.25132	KIAA074 gene product	3.42	3.65
421100	AW351839	Hs.124680	Homo sapiens cDNA: FLJ21763 ts, clone C	3.41	2.63
418506	AA084248	Hs.85339	G protein-coupled receptor 39	3.40	3.42
442711	AF151073	Hs.8645	hypothetical protein	3.39	2.95
453344	BE345075	Hs.44571	ESTs	3.38	2.38
436700	AB93690	Hs.301406	hypothetical protein PP3501	3.36	4.60
418007	M13526	Hs.33189	matrix metalloproteinase 1 (interstitial	3.36	2.61
433867	AQ000056	Hs.3618	hippocampin-like 1	3.36	4.26
408393	AW015318	Hs.23165	ESTs	3.36	2.10
447484	AA446439	Hs.292566	hypothetical protein FLJ14697	3.36	2.49
412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeldt-Jakob	3.35	2.27

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5	426158	NM_001982	Hs.199067	v-erb-b2avian erythroblastic leukemia v	3.35	2.58
	440325	NM_003812	Hs.7154	a disintegrin and metalloproteinase doma	3.34	2.55
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	3.34	5.96
	439963	AW247529	Hs.6733	platelet-activating factor acetylhydrola	3.34	2.73
	406653	U24683	Hs.6733	immunoglobulin heavy constant mu	3.31	5.21
10	427540	R12014	Hs.20576	ESTs	3.30	3.40
	412141	A1183838	Hs.48938	hypothetical protein FLJ21802	3.29	2.80
	400282			NM_005313 Homo sapiens glucose regulated	3.29	3.46
	419870	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.28	5.20
	416539	Y07909	Hs.79368	apical membrane protein 1	3.28	2.79
15	431518	AA743462	Hs.165337	ESTs	3.27	2.51
	402994			NM_024653 Homo sapiens myosin (beta	3.26	6.38
	419566	AL137939	Hs.40296	cadherin 19, type 2	3.26	3.48
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.26	3.71
	444331	BE540274	Hs.239	forkhead box M1	3.25	3.72
20	432874	W54322	Hs.279651	melanoma inhibitory activity	3.25	5.33
	411782	AA195203		RAB35, member RAS oncogene family	3.24	3.20
	438669	AW602166	Hs.222399	GCEP1 protein	3.24	2.32
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.24	6.20
	403817			NM_015271 Homo sapiens tripartite motif	3.23	3.70
25	407567	AJ528445	Hs.92254	synaptotagmin-like 2	3.22	2.49
	426334	BE30581	Hs.168358	hypothetical protein	3.21	2.46
	453837	AL138387	Hs.256126	baculoviral NP repeat-containing 7 (liv	3.19	5.50
	427283	AL119796	Hs.174165	ectonucleotide pyrophosphatase/phosphodi	3.18	2.04
	437379	AL339575	Hs.23765	Homo sapiens mRNA, cDNA DNFX547M123 (fr	3.18	3.73
30	424090	X98699	Hs.135262	XAP, associated factor-1	3.18	4.44
	410491	AA485131	Hs.54051	Homo sapiens clone 25218 mRNA sequence	3.18	3.25
	409418	AW963897	Hs.44743	KIAA1435 protein	3.16	2.21
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.16	4.04
	402829			C100250.0 g167542547.e1p (NC_034610.1) hea	3.15	4.57
35	437862	AW978107	Hs.5884	Homo sapiens mRNA, cDNA DNFX2586C2224 (f	3.15	3.07
	425935	Z98200	Hs.163724	HSPC019 protein	3.14	3.08
	417124	BE122762	Hs.25338	ESTs	3.14	2.73
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.11	2.16
	412490	AW603564	Hs.288550	Homo sapiens cDNA FLJ22528 fs, clone H	3.10	2.43
40	442271	AF000652	Hs.8190	synectin binding protein (p180)	3.10	2.83
	415917	U89867	Hs.78867	protein tyrosine phosphatase, receptor-1	3.10	1.78
	429083	Y09397	Hs.227817	BCL2-related protein A1	3.10	3.17
	437873	AW665665	Hs.154334	ESTs	3.10	3.32
	407813	AL132247	Hs.401109	KIAA4827 protein	3.10	3.90
45	457456	AB007924	Hs.13245	KIAA0455 gene product	3.10	3.35
	451537	R56631	Hs.26550	retinoid X receptor, gamma	3.09	4.45
	406654	BE011882	Hs.46721	UCP1 protein	3.08	3.65
	444484	AK021726	Hs.11260	hypothetical protein FLJ11264	3.08	2.12
	446019	A1362520		lysine deacetylase 3	3.08	2.26
50	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppresso	3.08	5.29
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE-3507281, mRNA,	3.05	3.36
	403532			NM_024638 Homo sapiens hypothetical prot	3.05	3.37
	433160	AW207002	Hs.143442	TASP for telomeric-specific adenylylation	3.04	3.17
	446341	AL040763	Hs.310735	ESTs, Moderately similar to ALU7_HUMAN A	3.03	2.98
55	426501	AW043782	Hs.238616	ESTs	3.03	2.01
	450325	AB935862	Hs.91973	ESTs	3.02	2.19
	418941	AA452970	Hs.239527	EB1B-58Da associated protein 5	3.02	3.29
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.02	2.54
	442064	A422867	Hs.88594	ESTs	3.00	1.96
60	405451			dihydropyrimidinase-like 3	3.00	2.98
	414915	NM_024662	Hs.76391	myosin (beta) resistance 1, homo	2.99	6.41
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.98	3.25
	452958	AA883929	Hs.40527	ESTs	2.98	4.14
	427647	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fs, clone KA	2.96	3.30
65	403190	AL075536	Hs.50884	sarcoma amplified sequence	2.96	2.96
	428819	AL135623	Hs.193914	KIAA825 gene product	2.96	4.16
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.96	2.41
	414219	W20010	Hs.75823	ALL1 fused gene from chromosome 1q	2.95	2.79
	411358	R47479	Hs.94761	KIAA1691 protein	2.95	4.70
70	423467	T03667	Hs.235386	Human DNA sequence from clone RP1-304B14	2.95	2.94
	400222			NM_020828 Homo sapiens G protein-couple	2.94	2.69
	405785			NM_025184 Homo sapiens hypothetical pro	2.94	2.55
	405960	AA307840		gh-EST10534 Adipose tissue, while 1 Homo	2.94	2.97
	418113	A272141	Hs.83484	SRY (sex determining region) Y-box 4	2.93	2.53
75	409038	T57490	Hs.55002	small inducible cytokine subfamily A (Cy	2.93	2.43
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	2.92	3.20
	459710	AU01596	Hs.127592	ESTs	2.91	4.45
	411395	AA889673	Hs.7542	KIAA1802 protein	2.90	2.72
	427528	AU077143	Hs.179565	retinoid homeobox maintenance deficient (S	2.90	2.90
80	406964	M21305	Hs.339315	FGFR3S predicted novel secreted protein	2.90	2.03
	428634	AW899713	Hs.339315	ESTs	2.89	3.55
	431390	AA151802	Hs.40368	adaptor-related protein complex 1, sigma	2.89	3.87
	438619	AB032713		TUJ2B1-TY protein	2.88	2.88
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	2.87	2.00
	428782	X12830	Hs.193400	interleukin 6 receptor	2.85	2.51
	454027	R40192	Hs.21527	Human DNA sequence from clone GS1-115M3	2.85	3.07
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	2.85	5.58

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414737	A1160386	Hs.125087	ESTs	2.84	2.79
412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines	2.84	3.80
447735	AA775268	Hs.61727	Homo sapiens cDNA: FLJ23020 fls, clone L	2.83	2.11
416091	AF953570	Hs.263082	defensin, beta 3	2.83	3.32
442445	AA082855	Hs.209561	KIAA1715 protein	2.81	2.17
408208	BE018177		ESTs	2.81	2.43
430066	A092959	Hs.237825	signal recognition particle 72kD	2.80	2.25
424755	AB033094	Hs.152625	KIAA1268 protein	2.80	2.74
422616	BE300330	Hs.118745	selenophosphate synthetase 2	2.79	2.01
405506			Target Exon	2.78	2.85
411619	AM18609	Hs.71040	hypothetical protein FLJ20425	2.78	3.10
400236			Eos Control	2.78	2.21
452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.78	3.15
444588	AB037182	Hs.15119	KIAA1361 protein	2.78	2.80
439778	AL109129	Hs.95364	putative transmembrane protein	2.78	3.78
420005	AW271106	Hs.133294	ESTs	2.78	2.86
428542	NM_014859	Hs.10432	KIAA0878 protein	2.77	3.07
453773	N35187	Hs.43388	28kD interferon-gamma responsive protein	2.76	4.96
425269	AW133342	Hs.155530	interferon, gamma inducible protein 16	2.76	1.83
437723	A672731	Hs.13256	ESTs	2.76	4.23
416730	T99937		gbcy720d4.1 Scores fetal liver spleen	2.76	2.98
426153	AF057169	Hs.162771	vitelliform macular dystrophy (Best disc	2.76	3.71
444670	H58372	Hs.332528	hypothetical protein MGC2570	2.76	3.97
421351	AJ076567	Hs.103755	receptor-interacting serine-threonine ki	2.74	3.50
406673	M34996	Hs.198253	major histocompatibility complex, class	2.74	3.24
427288	X78520	Hs.174139	chloride channel 3	2.74	2.82
425403	AJ303408	Hs.326159	leucine rich repeat (in FLJ) interaction	2.74	1.55
409417	AA156247	Hs.104879	serine (or cysteine) proteinase inhibito	2.74	2.99
419705	AW368634	Hs.154331	ESTs	2.74	2.28
440457	BC387553	Hs.21321	Homo sapiens clone FLJ85213 PR02474 mRNA,	2.72	3.80
413599	AJ006239	Hs.75438	cytosolic dihydropyrimidine reductase	2.72	2.43
447164	AF028941	Hs.17518	vimentin, similar to inflammatory respon	2.72	4.77
430594	AK000790	Hs.246885	hypothetical protein FLJ20783	2.72	3.67
413278	BC563085	Hs.833	interferon-stimulated protein, 15 kDa	2.71	12.06
424572	M19650	Hs.179500	2',3'-cyclic nucleotide 3' phosphodiester	2.70	2.40
429142	AL138877	Hs.50758	SMC4 (structural maintenance of chromoso	2.70	3.81
425996	W67330		hypothetical protein AL110115	2.69	3.85
430441	BC386091		desmoplakin (DPI, DPK)	2.68	2.55
442355	AA485539	Hs.8262	lysosomal associated membrane protein 2	2.68	1.67
421382	AK000550	Hs.103853	hypothetical protein FLJ22043	2.68	2.94
437158	AW050198		KIAA1150 protein	2.68	1.89
411215	AW536678		gbc.M2-DT0023-080300-004-g04 DT0023 Homo	2.68	2.80
432878	BC364490	Hs.279663	Pitin	2.68	2.58
408822	AW500715	Hs.57079	Homo sapiens cDNA: FLJ13267 fls, clone OV	2.68	2.74
428759	AJ590401	Hs.21213	ESTs	2.68	2.35
405486			Target Exon	2.67	2.70
410326	AJ368909	Hs.47650	ESTs	2.67	3.33
434040	AW446113	Hs.288809	hypothetical protein FLJ22059	2.66	2.54
437396	BE140396	Hs.21521	hypothetical protein DKFZp7620076	2.66	1.91
412719	AW016610	Hs.816	ESTs	2.66	4.21
451708	AO305336	Hs.60975	ESTs	2.66	5.69
418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p55), Iy	2.66	2.31
425017	AL119305	Hs.26409	ESTs	2.66	2.73
400205			NM_005336.Homo sapiens high density lipo	2.66	2.29
444809	BE207568	Hs.208219	oculoparin	2.64	2.86
436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.64	3.33
406382			C160012757.gli12698037.tssB0821837; H (2.64	2.64
432241	AJ937060	Hs.6298	KIAA1151 protein	2.63	2.16
417308	H60720	Hs.81892	KIAA0101 gene product	2.63	2.10
429294	AA059571	Hs.198793	Homo sapiens cDNA: FLJ22463 fls, clone H	2.62	2.43
453935	A633770	Hs.42572	ESTs	2.62	1.99
401464			NM_0142287.Homo sapiens renal tumor anti	2.62	2.62
436456	AW262677	Hs.248122	G protein-coupled receptor 24	2.62	5.94
418478	U38945	Hs.1174	cyclin dependent kinase inhibitor 2A (me	2.61	3.02
453266	AE565587	Hs.32556	KIAA0379 protein	2.60	2.68
451622	AW139587	Hs.30579	Homo sapiens cDNA: FLJ23070 fls, clone L	2.61	2.51
424005	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.60	2.56
409354	N68188	Hs.159472	Homo sapiens cDNA: FLJ22224 fls, clone H	2.59	3.00
425392	N39725	Hs.15220	zinc finger protein 106	2.58	3.52
427286	AW732802		epidermal growth factor receptor pathway	2.58	1.86
418166	AW54416	Hs.21132	Calc-42 receptor protein 3	2.58	2.15
413794	AF234532	Hs.61638	myosin X	2.58	2.54
445707	AJ248720	Hs.114390	ESTs	2.58	1.95
416940	BE267478	Hs.79404	neuron-specific protein	2.57	2.46
427987	NM_016156	Hs.181326	KIAA1073 protein	2.56	2.46
439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.56	2.22
455339	BE145814		gbc.MF0-HIT0208-101299-202-g04 HIT0208 Homo	2.55	2.34
447737	AK000563	Hs.19404	DKFZP564L0862 protein	2.55	2.31
423799	AW026300	Hs.132906	19A-24 protein	2.54	2.11
442762	AF035119	Hs.8700	deleted in liver cancer 1	2.54	2.47
432886	BE159028	Hs.279704	chromatin accessibility complex 1	2.54	2.99
440576	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	2.54	2.96
424481	R19453	Hs.1787	proteolipid protein 1 (Pellicanus-Merzbac	2.53	6.98

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	422340	AWQ96219	Hs.115325	RAB7, member RAS oncogene family-like 1	2.53	3.05
	428844	AW5972635	Hs.301904	hypothetical protein FLJ12671	2.53	3.13
	458997	AW597420		ESTs	2.53	1.63
5	414801	AF090900	Hs.91353	Homo sapiens cDNA: FLJ21887 flc, clone H	2.52	2.30
	414807	AJ736616	Hs.77348	hydroxyproline-L-glutamate dehydrogenase 15 (N	2.52	1.80
	422234	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor 1	2.52	3.02
	423882	NM_013257	Hs.279656	serum/glucocorticoid-inducible kinase-l	2.52	3.05
	407260	L09095		gb:Homo sapiens mRNA fragment.	2.50	5.00
	431185	NM_012249	Hs.250697	ras-like protein	2.49	6.16
10	411542	J04121	Hs.82269	progestin-associated endometrial prote	2.49	4.71
	419556	U29615	Hs.91093	olivine-1 (chionotidase)	2.48	5.77
	408209	NM_004454	Hs.43897	ets variant gene 5 (ets-related molecule	2.48	3.77
	405885			Target Exon	2.46	3.11
	406837	R70292	Hs.156110	immunoglobulin kappa constant	2.44	3.10
15	412650	Z48804	Hs.74124	ocular albinism 1 (Netteschep-Falls)	2.44	4.90
	421633	AF121860	Hs.106260	sorting nexin 10	2.44	4.31
	419929	AA724373	Hs.49344	hypothetical protein FLJ11006	2.42	3.19
	413171	AA318325	Hs.75219	tyrosinase-related protein 1	2.37	3.57
	406621	XST809	Hs.8997	immunoglobulin lambda locus	2.36	5.87
20	414142	AW368397	Hs.334485	hemiconin (litxin II)	2.36	3.04
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	2.36	3.66
	414283	AW960011	Hs.154993	ESTs	2.34	4.95
	453931	AL121278	Hs.251444	ESTs	2.34	4.18
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	2.32	3.45
25	435292	N20514	Hs.172955	ESTs	2.32	4.94
	412926	AI970676	Hs.75061	macrophage myristoylated alanine-rich C	2.31	3.78
	440197	AW540708	Hs.317714	palmit (mouse) homolog, palatin	2.30	3.95
	425262	DB7119	Hs.155418	CS3555 protein	2.29	5.08
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.28	4.05
30	403969			ENSPO0000034963:Zinc finger protein 131	2.28	3.64
	403969	AB011158	Hs.106794	KOA0554 protein	2.26	3.31
	421686	BE391046	Hs.278962	AIM-1 protein	2.24	4.08
	426800			gb:zw20111.1 Scores ovary tumor NHT01 H	2.24	3.47
	406782	AA430373		BMP-R18	2.22	3.66
35	415539	AI733881	Hs.72472	hypothetical protein FLJ12492	2.20	3.43
	447523	Y18328	Hs.21938	PCSK5 cell-derived leucine-zipper-like pr	2.20	3.52
	433180	AB030851	Hs.31854	incisal1 1,4,5-triphosphate 3-kinase B	2.19	3.76
	415825	Y18024	Hs.78817	gb:human omega light chain protein 14.1	2.18	3.17
	407241	M34516		hypothetical protein MGC1250	2.18	3.26
40	422243	AW803733	Hs.23505	FKS05 binding protein precursor	2.16	3.85
	411324	AW265494	Hs.24048	plasminogen activator, tissue	2.14	3.49
	412819	T52625	Hs.274404	interferon regulatory factor 4	2.13	4.39
	427923	AW274357	Hs.301405	interferon regulatory factor 4	2.13	5.49
	417437	US2682	Hs.82132	interferon regulatory factor 4	2.13	3.08
45	425535	AB007937	Hs.158287	KIA0450 gene product	2.13	8.66
	429638	AI916962	Hs.211577	kinecin 1 (kinesin receptor)	2.12	3.01
	409154	U78882	Hs.50842	interferon-induced protein 35	2.12	4.66
	429951	AL040521	Hs.15220	zinc finger protein 106	2.12	3.71
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.11	4.27
50	419200	AW964045		EST	2.11	3.58
	416448	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.10	5.34
	425069	AA687465	Hs.298184	potassium voltage-gated channel, shaker-	2.07	7.86
	445133	AW157646	Hs.198689	ESTs	2.06	3.68
55	411492	T48946	Hs.70332	immunoglobulin superfamily, member 4	2.04	3.36
	408015	AW136771	Hs.244349	epidermal differentiation complex protein	2.03	3.41
	424412	AI55122	Hs.10043	hypothetical protein FLJ13074	2.03	3.62
	431657	AI45227	Hs.105448	ESTs, Weakly similar to B34087 hypothet	2.02	3.03
	427536	BE277141	Hs.115803	gb:01178656F1 NH_MJC_20 Homo sapiens c	2.02	3.03
	400533			ENSPO00000295374-PRC065 protein (Fragment	2.00	3.29
60	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	1.99	3.07
	410129	BE244074	Hs.58831	regulator of Fas-induced apoptosis	1.97	4.52
	417312	AW856411	Hs.258811	leukemia-associated phosphoprotein p18 (1.95	3.25
	423952	AW877787	Hs.136102	KJAA0853 protein	1.94	3.79
65	455705	AW161061		ESTs, Weakly similar to zinc finger pro	1.93	3.16
	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae)	1.93	3.11
	438866	UA4345	Hs.325495	tissue inhibitor of metalloproteinase 2	1.92	3.00
	448410	AK002227	Hs.21126	hypothetical protein FLJ20220	1.92	3.07
	400292	AA250737	Hs.72472	BMP-R18	1.92	4.00
70	436797	AA731491	Hs.334477	hypothetical protein MGC14879	1.90	3.04
	406851	AA659794		major histocompatibility complex, class	1.90	6.53
	428437	AV165017	Hs.184325	CS3-76 protein	1.89	3.39
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.89	4.04
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.87	3.64
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	1.85	4.21
75	425271	AV165984	Hs.156108	TATA box binding protein (TBP)-associa	1.85	3.13
	420162	BE376432	Hs.96517	cyclic-dependent kinase 4	1.85	3.04
	443530	BE563088	Hs.9552	bindin of Arf Two	1.85	3.20
	433671	AW138797	Hs.132906	19A24 protein	1.84	3.39
	424415	NM_001975	Hs.146580	endocase 2, (gamma, neuronal)	1.82	3.22
80	400991			Target Exon	1.82	4.11
	418677	SE8308	Hs.87224	SRV (sex determining region Y)-box 5	1.82	3.43
	424441	X14850	Hs.147097	H2A histone family, member X	1.81	3.12
	424825	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	1.79	5.31

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425818	AB021225	Hs.155681	matrix metalloproteinase 17 (membrane-in	1.79	3.40
416426	AA180256	Hs.210473	Homo sapiens cDNA FL14872 fs, clone PL	1.78	3.38
414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.77	3.69
440542	AY246547	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	1.77	3.12
401591			Target Exon	1.76	4.30
425923	NV_005026	Hs.162808	phosphoglucoisomerase-3-kinase, catalytic, de	1.75	3.68
412844	AI828045	Hs.18016	Homo sapiens mRNA, cDNA DKFZp588H0324 (f	1.74	3.53
417237	H85385	Hs.81737	palmitoyl-protein thioesterase 2	1.73	3.06
419849	BC214326	Hs.53379	anti-apoptotic transition inhibitor factor	1.72	4.38
544529	BE273437	Hs.301406	hypothetical protein PP3501	1.72	4.38
440572	AF038311	Hs.7345	MAD1 (mitotic arrest deficient, yeast, h	1.72	3.61
402804	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m	1.72	3.06
430146	BC337620	Hs.234489	lysate dehydrogenase B	1.71	4.38
426502	Y07755	Hs.170157	myosin VIA (heavy polypeptide 12, myosin)	1.70	4.13
413317	U53225	Hs.75283	sorting nexin 1	1.70	3.08
417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	1.68	3.15
407223	H96850	Hs.26515	ghywl03b12s1 Soars melanocyte 2N6HM Ho	1.68	4.19
413566	AW604451	Hs.285814	apodys (Drosophila) homolog 4	1.67	5.74
404067			Target Exon	1.67	4.73
447630	A660149	Hs.44665	lymphoid enhancer binding factor 1	1.66	3.22
443337	Y07604	Hs.9235	non-metastatic cells 4, protein expressed	1.65	3.17
427747	AN111425	Hs.180655	protein tyrosine kinase 12	1.64	3.35
437912	BE278594	Hs.5912	F-box only protein 7	1.64	3.24
404140			NM_006510 Homo sapiens ret finger protei	1.64	3.10
412124	D49958	Hs.75819	glycoprotein M5A	1.64	3.45
427239	BE273447		ubiquitin carrier protein	1.62	3.58
427289	AB073346		phosphoserine aminotransferase	1.62	5.89
452923	BE276018	Hs.288490	live-span transmembrane protein M83	1.62	3.23
426020	AL110195	Hs.165017	microphallium-associated transcription	1.62	4.00
439627	BE267102	Hs.29076	hypothetical protein FLJ121841	1.61	5.00
451489	NM_005503	Hs.26468	synuclein, beta (A4 precursor protein-bio	1.60	3.60
414659	AB15523	Hs.76530	synuclein, alpha (non A4 component of am	1.58	3.34
411825	AK000334		hypothetical protein FLJ20327	1.56	3.18
438552	AJ245820	Hs.6314	type I transmembrane receptor (leukine-r	1.56	3.23
420801	AA421048	Hs.95011	synuclein, beta 1 (dystrophin-associat	1.55	3.10
401914			Target Exon	1.54	3.33
424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ly	1.54	3.15
416448	H05734	Hs.30559	ESTs	1.52	3.36
437679	AA448829	Hs.30596	Homo sapiens mRNA full length insert cDN	1.52	3.17
427696	Z53844	Hs.5790	hypothetical protein d3DTE.16.5	1.52	4.93
413019	BE281604	Hs.75140	low density lipoprotein-related protein-	1.52	3.01
419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.52	3.83
422596	AF063611	Hs.118633	Z-5-oligoadenylate synthetase-like	1.50	3.04
421851	R19886	Hs.108096	amido-crystallin	1.50	3.10
448499	BE513280	Hs.77550	hypothetical protein MGIC1780	1.44	3.07
427378	BE515037	Hs.177556	melanoma antigen, family D, 1	1.44	3.00
412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	1.42	3.66
448143	AF035704	Hs.20478	cerebellar lipofuscinosis, neuronal 2, like	1.42	4.16
413291	NM_006278	Hs.75268	calcyltransferase 4C (beta-galactosidase	1.41	3.30
435968	AW161481	Hs.111577	integral membrane protein 3	1.41	3.30
424486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	1.40	3.01
443759	BE393832	Hs.134729	FXRD domain-containing ion transport reg	1.39	3.82
444441	AW513841	Hs.301394	hypothetical protein MGIC3101	1.43	3.36
430205	AB025904	Hs.231568	carbonic anhydrase XIV	1.36	3.32
406827	AA971400		glt0p92d04s11 NCJ_CGAP_L55 Homo sapiens	1.35	3.03
406906	Z25424		glt0p92d04s11 NCJ_CGAP_L55 Homo sapiens	1.34	3.25
426880	AA395167	Hs.41294	ESTs	1.34	3.68
433320	D06047	Hs.250879	ESTs, Highly similar to CTXN RAT CORTXN	1.34	6.18
450358	AB010098	Hs.24907	coronin, actin-binding protein, 28	1.33	3.19
421612	AF161254	Hs.106196	80kD antigen	1.33	3.03
438915	AA260174	Hs.285681	Williams-Beuren syndrome chromosome reg	1.32	3.68
428342	AF739168		Homo sapiens cDNA FL131458 fs, clone PL	1.32	3.10
449444	AW181846		solute carrier family 16 (monocarboxylic	1.30	3.30
404700			Target Exon	1.30	3.14
403043			Target Exon	1.30	4.22
420858	NM_005846	Hs.56828	histone H2B repeat containing 5	1.09	1.29
424679	AL117477	Hs.115960	DKFZP772G051 protein	1.27	3.13
406908	Z25437		glt0p92d04s11 NCJ_CGAP_L55 Homo sapiens	1.27	3.66
422665	AW603880		ATPase, H transporting, lysosomal (vacuo	1.26	3.09
423130	AW697588	Hs.21213	ESTs	1.25	3.09
453220	AB033089	Hs.32452	Homo sapiens mRNA for KIAA1263 protein,	1.24	3.15
442680	BE270707	Hs.8563	similar to APOBEC1	1.22	3.94
422319	AA400342	Hs.115232	splicing factor 3a, subunit 2, 66kD	1.21	3.36
420408			NM_030920 Homo sapiens hypothetical pro	1.04	3.37
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.00	3.02

TABLE 51B:

Key: Unique Exon probe identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Key CAT Number Accession

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5	400660	9757499	Minus	151830-152104,152649-152744
	402609	9926446	Minus	113464-113633,114264-114654
	400750	8119067	Plus	198991-199168,199316-199548
10	402594	2598643	Minus	4727-4989
	403817	8962065	Plus	110297-110352
	402829	8918414	Plus	101532-101852,102006-102263
15	403532	8076842	Minus	81750-81901
	405451	7622517	Minus	145949-146227
	405785	5581533	Minus	98702-98925
20	405598	6465489	Plus	80014-80401,80503-81125
	405486	6651379	Plus	179441-179598
	406382	9256148	Plus	122336-122851
25	401454	9186923	Minus	114659-114832
	405885	7677703	Minus	42574-42598
	403969	8569909	Plus	31237-31375,32405-32506
30	400533	6981826	Minus	277132-277595
	400991	8096825	Plus	159187-159320
	401591	9969377	Minus	55419-55835
35	404067	3282162	Plus	1415-2071
	404140	9843520	Plus	37761-38147
	401914	9369520	Plus	62537-62945,63155-63308
40	404700	9800123	Minus	159521-160203
	403043	7788753	Minus	314423-316252
	402408	9796239	Minus	110326-110491

TABLE 52A: ABOUT 204 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO MELANOMA METASTASES

Table 52A lists about 204 genes upregulated in primary melanomas relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Altmetrix Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Play: Unique Eos probe set identifier number
 Ex/Con: Exemplar Accession number, Genbank accession number
 UnigenID: Unigen number
 UnigenID: Title: Unigen gene title
 R1: 90th percentile of primary melanoma AIs divided by the 90th percentile of melanoma metastasis AIs
 R2: 90th percentile of primary melanoma AIs divided by the 90th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Play	Ex/Con	UnigenID	Unigen Title	R1	R2
40	421548	LC583	keratin 6A	21.90	16.66
	422168	AA568894	S100 calcium-binding protein A7 (psoriasin)	21.35	43.65
	401781		Target Exon	18.70	18.58
	401780		NM_005557*Homo sapiens keratin 16 (kera)	15.34	16.00
45	431360	NM_000427	keratin 16	12.34	9.96
	409632	W74001	serine (or cysteine) proteinase inhibitor	11.24	8.73
	412636	NM_004415	desmoplakin (DPL, DP1)	11.20	6.62
	417366	BE185289	small proline-rich protein 18 (comelin)	10.46	12.75
	409601	AF237621	keratin 1 (epidermolytic hyperkeratosis)	10.41	25.49
50	420555	AW485297	S100 calcium-binding protein A8 (calgranulin A)	8.53	8.53
	420783	A1659838	lectin, galactoside-binding, soluble, 7	8.11	11.14
	422511	AU076442	collagen, type XVII, alpha 1	7.90	8.92
	422158	L10343	protease inhibitor 3, skin-derived (SKAL)	7.14	22.14
	427666	AF791495	calmodulin-like skin protein (CLSP)	7.03	8.90
55	430686	NM_001942	desmoglein 1	6.88	5.39
	431369	BE184456	secretory leukocyte protease inhibitor (SLPI)	6.60	12.79
	458525	AW486387	S100 calcium-binding protein A9 (calgranulin B)	6.44	6.19
	437191	NM_006846	serine protease inhibitor, Kazal type, 5	6.34	7.77
	427146	W7424	S100 calcium-binding protein A9 (calgranulin B)	6.15	8.91
60	418067	A1127958	cystatin E/M	6.08	9.24
	408536	AW381532	ESTs	6.04	17.40
	402075		ENSP000000251056*Pleura membrane calcium	5.96	8.41
	413554	AA319146	secretoglycin II (chromogranin C)	5.46	3.32
	410001	AB041036	kallikrein 11	5.38	5.36
	421100	AW351839	Homo sapiens cDNA: FLJ21763 fa, clone C	5.32	3.84
65	407788	BE154982	S100 calcium-binding protein A2	5.19	5.30
	419329	AW007220	S100-type calcium binding protein A14	4.94	5.03
	429504	X99133	lipocalin 2 (oncoferrin 24p3) (INGAL)	4.86	5.22
	421773	W69233	ESTs	4.82	12.41
	442577	AA252998	ESTs	4.82	4.40
70	401760		Target Exon	4.60	11.03
	408522	AI541214	Small proline-rich protein SPRK1 (human)	4.50	11.35
	417515	L24203	ataxia-telangiectasia group D-associated	4.47	12.43
	431211	M86849	gap junction protein, beta 2, 26MD (connexin 43)	4.45	2.99
	446989	AK001958	hypothetical protein FLJ11036	4.39	4.23
75	423017	AW1178161	serine (or cysteine) proteinase inhibitor	4.38	4.58
	418663	AK001100	desmocollin 3	4.36	5.16
	424620	AA101043	kallikrein 7 (chymotrypsin, stratum com)	4.29	5.19
	401747		Homo sapiens keratin 17 (KRT17)	4.28	5.41
	414807	AJ238616	hydroxyprostaglandin dehydrogenase 15- (N)	4.20	4.24
80	411274	NM_000776	kallikrein 10	4.22	4.82
	439496	BE165051	Homo sapiens, similar to RIKEN cDNA 11110	4.21	8.26
	420039	NM_004605	sulfotransferase family, cytosolic, 2B,	4.18	4.73
	429538	BE182592	small proline-rich protein 2A	4.16	7.30

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5	431842	NM_005764	Hs.271473	epithelial protein up-regulated in cancer	2.36	2.23
	453931	AL121278	Hs.25144	ESTs	2.34	1.69
	452308	AI167560	Hs.61297	ESTs	2.31	3.82
	431048	RS0253	Hs.249129	cell death-inducing DFFA-like effector a	2.31	2.18
	403752			NM_002753? Homo sapiens mitogen-activate	2.30	2.38
10	425225			NM_002699? Homo sapiens POU domain, class	2.30	2.36
	420223	N27807		ribosomal protein L4	2.30	1.73
	452023	AB032999	Hs.27566	KIAA1173 protein	2.29	4.54
	443172	AW62984	Hs.199061	p300/CBP-associated factor	2.28	2.02
	439793	AW60291	Hs.6823	hypothetical protein FLJ19430	2.28	1.71
15	414004	AAV37033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	2.27	1.81
	429554	NM_012275	Hs.207224	interleukin 1, delta	2.26	2.17
	436995	AF037335	Hs.5338	carbonic anhydrase XII	2.26	2.51
	404029			NM_018939? Homo sapiens prolactinadherin be	2.26	2.19
	424049	AB014524	Hs.138380	KIAA624 protein	2.26	2.99
20	442423	BE326264	Hs.246842	ESTs	2.26	1.75
	408452	AA054683	Hs.192455	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.26	2.29
	4410471	X57346	Hs.104510	striflin	2.25	2.40
	410541	AA085003	Hs.54179	synectin-2 protein	2.24	2.46
	415639	AF13681	Hs.72472	BMP-R1b	2.22	1.64
25	425701	AA361850	Hs.240443	Human clone 137308 mRNA, partial cds	2.22	3.04
	423973	AF034861	Hs.136574	arachidonate 12-lipoxygenase, 12R type	2.22	3.24
	402178	BE393949	Hs.50915	kallistatin 5	2.19	4.74
	433091	Y12542	Hs.3185	lymphocyte antigen 6 complex, locus D	2.19	7.96
	430171	AF066299	Hs.234766	skin-specific protein	2.17	3.56
30	401994			Target Exon	2.14	3.34
	448228	AAJ03107	Hs.148590	protein related with psoriasis	2.11	5.52
	444292	AF081497	Hs.279682	Rb type C glycoprotein	2.11	5.78
	426150	NM_003698	Hs.167218	Barf1-like homeobox 2	2.05	2.96
	452554	AAW452434	Hs.58006	ESTs, Weakly similar to ALUS_HUMAN ALU S	2.04	4.17
35	443162	T45995	Hs.9029	DKFZP434G032 protein	1.98	3.20
	402004	AF005082		Homo sapiens skin-specific protein (p33	1.94	3.20
	407395	AF005082		glt; Homo sapiens skin-specific protein (x	1.92	3.24
	412507	L35645	Hs.73964	EphA4	1.92	3.08
	410310	J02931	Hs.62152	coagulation factor III (thromboplastin,	1.90	3.18
40	425415	NI3923	Hs.157091	interleukin	1.89	5.26
	417324	AW269494		ESTs	1.88	3.82
	412446	AF168015		ESTs	1.88	3.36
	451092	AI207258	Hs.13765	Homo sapiens mRNA for FLJ000074 protein,	1.87	3.75
	444726	NM_006147		interferon regulatory factor 5	1.86	4.11
45	424399	AA05687		AS256971L, BT005-150109-019 BT005 Homo	1.85	4.20
	434346	AA630445		ESTs	1.84	3.08
	446051	BE048031	Hs.37054	ephrin-A3	1.83	3.44
	423725	AAJ03108	Hs.132127	hypothetical protein LOC57822	1.78	3.45
	413819	AW199235	Hs.8364	Homo sapiens pyruvate dehydrogenase kinase	1.76	2.99
50	411908	L27943	Hs.72924	cytidine deaminase	1.74	3.60
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGI-8	1.71	3.56
	413966	AA133935	Hs.173704	ESTs, Moderately similar to AS3593 throm	1.71	3.38
	424046	AF027895	Hs.138202	serine (or cysteine) protease inhibitor	1.70	3.92
	425600	NM_001564	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	1.68	3.25
55	429299	AW620463	Hs.347408	hypothetical protein MG13102	1.67	2.92
	429002	AW248439	Hs.2340	junction plakoglobin	1.66	3.35
	421335	X39977	Hs.103505	ARS component B	1.65	4.31
	433662	W07162	Hs.159826	PRAS2, PRAS2, member RAS oncogene family	1.65	3.65
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.64	4.04
60	414214	DH9958	Hs.75819	glycoprotein M6A	1.64	3.59
	437897	AF075661	Hs.146170	hypothetical protein FLJ22969	1.62	3.13
	423390	NM_003248		transglutaminase 3 (E, polypeptide, prote	1.62	2.92
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor I	1.57	3.09
	422106	DB4239	Hs.111732	Fc fragment of IgG binding protein	1.53	3.39
65	427751	AF000152		conserved gene amplified in osteosarcoma	1.52	3.53
	416881	N32520	Hs.141358	ESTs	1.52	3.08
	435013	H91523	Hs.110024	NM_020142 Homo sapiens NADH:ubiquinone o	1.49	2.91
	434574	AA424459	Hs.33470	ESTs	1.48	3.05
	454478	AW805749		superoxide dismutase 2, mitochondrial	1.48	3.54
70	444730	BE279949	Hs.18141	iodinin 1	1.46	4.48
	414583	AA362907	Hs.75944	proline arginine-rich and leucine-rich r	1.41	2.99
	433640	AW350125	Hs.240443	Homo sapiens cDNA: FLJ23538 fs, clone L	1.40	3.71
	427461	AA531527	Hs.332040	hypothetical protein MG13010	1.36	2.98
	430205	AG025904	Hs.235168	carbonic anhydrase XIV	1.36	3.14
75	450796	NM_001988	Hs.25482	emovotin	1.34	3.94
	407394	AF066081		glt; Homo sapiens skin-specific protein (x	1.30	3.26
	430513	AJ012008	Hs.241586	G6C protein	1.28	3.26
	411388	X72925	Hs.695752	desmocollin 1	1.22	3.94
	431089	BE041395		ESTs, Weakly similar to unknown protein	1.21	3.71
80	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	1.00	3.20
	443672	AA323362	Hs.9667	lutylubostaine (gamma)-, 2-oxoglutarate d	1.00	3.26

TABLE S2B:

Phy:

CAT number:

Accession:

Unique Ecol probe identifier number

Gene cluster number

Genbank accession numbers

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	418970	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (lvs	3.74	3.91
	450293	N36754	Hs.171118	hypothetical protein FLJ00006	3.74	2.89
	430606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3,	3.72	2.65
	408548	AA055449	Hs.83187	ESTs, Weakly similar to ALUC_HUMAN Hs.	3.72	2.43
5	429490	AI011311	Hs.250619	ESTs, Weakly similar to ALU1_HUMAN AU.S	3.71	2.23
	414821	M63835	Hs.77424	FC fragment of IgG, high affinity Ia, re	3.70	2.36
	419749	X73608	Hs.93029	sparc1/stonectin, ovary and kazal-like d	3.67	3.30
	410016	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	3.67	6.72
	433858	U03678	Hs.156110	immunoglobulin kappa constant	3.66	2.49
10	424153	AA451737	Hs.141436	MAGE-like 2	3.64	2.65
	421666	AL035290	Hs.1408	endothelin 3	3.64	5.92
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activat	3.61	2.69
	429732	U020158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.60	1.95
	422173	BE358828	Hs.250619	ESTs, Weakly similar to ALU1_HUMAN AU.S	3.59	3.08
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	3.57	11.26
	442079	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	3.56	4.91
	439869	AY292872	Hs.124554	ESTs	3.53	4.15
	453064	R01534	Hs.89463	potassium large conductance calcium-acti	3.51	2.88
20	411292	AB018549	Hs.69328	MD-2 protein	3.46	1.82
	414324	Y14768	Hs.890	lymphotxin beta (TNF superfamily, membe	3.45	4.65
	420286	AI796395	Hs.111377	ESTs	3.42	2.47
	413385	M04455	Hs.840	indoleamine pyrolyse 2,3 dioxygenase	3.42	3.09
	442104	L29971	Hs.188	phosphodiesterase 4B, cAMP-specific (du	3.41	2.22
	405545			Target Exon	3.40	2.46
25	416373	AA195845		ESTs, Weakly similar to S12558 cysteine-	3.40	5.64
	417410	AF053620	Hs.82110	PC4 and SFRS1 interacting protein 1	3.37	4.27
	418122	AA055038	Hs.7149	Homo sapiens cDNA: FLJ21556 fl, clone H	3.32	2.37
	433470	AW960564		transmembrane 4 superfamily member 1	3.33	3.13
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lym	3.32	2.51
30	442149	AB014550	Hs.8118	KIAA0650 protein	3.30	2.29
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypophel	3.29	3.85
	447023	AA356754	Hs.17109	integral membrane protein 2A	3.24	2.79
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.23	1.78
	414176	BE140638	Hs.75794	EDG-2 (endothelial differentiation, lys	3.22	2.90
35	447513	AW655776	Hs.31350	ESTs, Moderately similar to ALU1_HUMAN A	3.18	4.16
	421983	NM_001078	Hs.109225	vascular cell adhesion molecule 1	3.17	3.59
	424148	BE242274	Hs.17441	integrin, beta 7	3.14	2.29
	408648	AA563730	Hs.277477	major histocompatibility complex, class	3.13	3.05
40	425955	AW620035	Hs.778679	a disintegrin and metalloproteinase doma	3.13	2.95
	446519	AI070543	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.12	2.55
	406704	M21655	Hs.329	myosin, heavy polypeptide 7, cardiac mus	3.12	5.54
	443885	H91806	Hs.15284	ESTs	3.08	3.55
	418203	X54542	Hs.83758	ODC28 protein kinase 2	3.08	2.20
45	417540	U03057	Hs.82353	protein C receptor, endothelial (EPCR)	3.05	3.21
	447232	AW493834	Hs.327	interleukin 10 receptor, alpha	3.05	3.36
	409103	AF251237	Hs.112208	XAGE-1 protein	3.04	2.07
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.04	2.24
	421834	BE543206	Hs.288771	DKF ZP586A0522 protein	3.03	1.91
50	446565	BE292347	Hs.11538	long-chain fatty acid coenzyme A ligase	3.01	3.43
	425295	AA431366	Hs.37251	ESTs	3.01	3.07
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	2.99	2.55
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide (IT13 com	2.98	5.98
	418958	NM_000078	Hs.85536	cholesterol ester transfer protein, plas	2.97	2.68
55	438914	N53852	Hs.10727	ESTs	2.97	1.99
	418391	NM_003281	Hs.84673	tropinon 1, skeletal, slow	2.96	2.68
	410506	M69957	Hs.89575	CD798 antigen (immunoglobulin-associated	2.96	3.94
	445623	NM_003079	Hs.84443	chemokine (C-C motif) receptor 5	2.96	4.02
	452947	NM_003155	Hs.25590	stannocalcin 1	2.95	3.24
60	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.95	2.73
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	2.94	2.36
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	2.93	2.17
	424528	AW078971	Hs.236054	ESTs, Weakly similar to KIAA1204 protein	2.93	2.70
	408633	AW963372	Hs.46677	PRC2000 protein	2.92	2.16
65	443195	BE148235	Hs.130063	Homo sapiens cDNA FLJ14201 fa, clone NT	2.92	2.92
	425234	AW152225	Hs.165093	ESTs, Weakly similar to 380022 hypothel	2.90	2.99
	437802	AA175995	Hs.122510	ESTs	2.90	3.71
	417771	AA804688	Hs.82947	retinoic acid receptor responder (Izaro	2.90	3.56
	430000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	2.90	2.60
	414555	N58589	Hs.75422	phospholipase A2, group IIA (platelets,	2.87	2.07
70	421958	AA365185	Hs.109918	ras homology gene family, member H	2.87	3.48
	420224	M64371	Hs.86023	CD19 antigen	2.86	4.77
	434883	AW381538	Hs.19807	hypothetical protein MGC12959	2.85	5.44
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	2.84	2.55
	427527	AI809657	Hs.153261	immunoglobulin heavy constant mu	2.84	4.16
75	446231	NM_002163	Hs.144513	interferon consensus sequence binding pr	2.83	3.97
	408838	AI696335	Hs.40369	ESTs	2.82	1.82
	429124	AW505086	Hs.196914	minor histocompatibility antigen H-2	2.82	4.21
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.79	4.00
	425386	AA328384	Hs.186180	immunoglobulin kappa constant	2.78	2.79
80	414290	AI568801	Hs.77721	ESTs	2.78	1.19
	418255	AW135405	Hs.37251	ESTs	2.76	3.27
	451952	AL120173	Hs.301663	ESTs	2.75	1.74
	424865	AF011333	Hs.153563	lymphocyte antigen 75	2.75	3.10

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409245	AA361037		RNA isopentenylpyrophosphate transferase	2.74	2.12
453920	A1133148	Hs.36602	I factor (complement)	2.74	3.08
443968	AA287702	Hs.10031	KIAA0955 protein	2.74	2.34
434094	AA305599	Hs.238205	hypothetical protein PR02013	2.73	1.67
436476	AA326108	Hs.13829	hHLH protein DEC2	2.72	1.70
428598	A2403068	Hs.98558	ESTs	2.72	2.06
417141	U27652		nuclear receptor subfamily 1, group H, m	2.70	2.55
427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.69	3.15
442485	BE302285	Hs.29724	hypothetical protein FLJ13187	2.69	1.99
425517	AA431552	Hs.288016	Homo sapiens cDNA:FLJ121243 fic; clone C	2.69	1.70
443998	AI620661	Hs.295276	ESTs	2.69	2.30
417542	J04129	Hs.82269	proteoglycan-associated endomembranous prote	2.68	3.23
414291	AJ296919	Hs.13040	protein-coupled receptor B6	2.68	3.01
440861	AL049951	Hs.22370	Homo sapiens mRNA, cDNA DKFZp564D0122 (l	2.66	2.51
432435	BE215886	Hs.282070	ESTs	2.65	3.28
430132	AA204686	Hs.234149	hypothetical protein FLJ20647	2.65	3.04
427792	ME3928	Hs.180841	tumor necrosis factor receptor superfamily	2.64	3.82
414696	AF002020	Hs.76918	Homo sapiens cDNA:FLJ100111 protein, NM_005159	2.64	1.94
425991	AW504614	Hs.287379	Homo sapiens alpha, car	2.64	2.51
401566			ESTs	2.63	3.74
444119	R41231	Hs.184261	ESTs, Weakly similar to T26586 hypotheti	2.63	2.13
425231	AA527161		ESTs	2.61	2.95
417427	ME5391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	2.61	1.90
437669	AI358105	Hs.123164	ESTs, Weakly similar to match to ESTs AA	2.60	4.45
413856	D13639	Hs.75596	cyclin D2	2.60	5.71
407928	NM_002262	Hs.41602	killer cell lectin-like receptor subunit	2.59	2.88
445247	BE514387	Hs.333993	c-Myc target, JPO1	2.58	2.77
447131	NM_004585	Hs.17466	retinoic acid receptor responder [tazarot	2.58	9.28
443021	AA368546	Hs.8904	lg superfamily protein	2.58	4.49
424779	AL046851	Hs.153053	CD37 antigen	2.58	3.88
425235	AA353113	Hs.112439	Homo sapiens cDNA: FLJ22743 fic, clone H	2.57	2.09
424265	AF113901	Hs.144287	heavy-chain of -split related with YRP	2.57	3.57
426780	BE242284	Hs.172199	adenylylate cyclase 7	2.57	1.86
452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.56	2.90
442954	AW575008	Hs.11355	thymopoietin	2.56	3.39
433646	AA403319	Hs.155189	ESTs	2.54	2.19
417289	D68962	Hs.61875	growth factor receptor-bound protein 10	2.53	4.56
422640	M37984	Hs.118845	troponin C, slow	2.53	5.08
448413	AJ745379	Hs.42911	ESTs	2.53	2.38
429536	AAB72016	Hs.208097	oncogene TC21	2.49	2.52
446272	BE268912	Hs.14601	hematopoietic cell-specific Lys substrate	2.52	3.46
424378	W28020	Hs.167998	neural cell adhesion molecule 1	2.52	2.91
410267	BE244044	Hs.61469	hypothetical protein	2.51	3.67
427609	AK006436	Hs.179791	hypothetical protein FLJ20429	2.51	3.11
424868	AF568170	Hs.96086	ESTs	2.51	2.30
418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.50	2.64
402899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.50	3.04
413441	AI925374	Hs.75367	Glc-like adaptor	2.49	2.37
414761	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.49	1.82
429493	AL134708	Hs.145998	ESTs	2.49	2.40
419631	AW188117		popeye protein 3	2.48	1.85
437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.48	2.32
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	2.47	4.17
420168	A1791655	Hs.95340	hypothetical protein	2.47	2.62
453987	AA323750	Hs.235026	Homo sapiens, clone IMAGE:4247529, mRNA,	2.47	2.49
429640	UR3508	Hs.2463	angiopoietin 1	2.47	2.57
437330	AL335944	Hs.50115	Homo sapiens mRNA, cDNA DKFZp75L1112 (l	2.46	2.42
426869	AF036564		CD2-like kinase 1	2.46	2.41
427674	NM_003528	Hs.2178	H2B histone family, member O	2.46	2.17
405547			NM_018633? Homo sapiens transporter 2, A	2.46	2.84
406678	U77534		gb Human clone 1A11 immunoglobulin varia	2.45	2.89
407013	U36637	Hs.83870	gb Human retinoblastoma, partial cds	2.45	3.40
428746	AW503820	Hs.192861	Sp-B transcription factor (Sp-1/PU.1 r	2.43	2.65
453963	AW408337	Hs.36972	CD7 antigen (p41)	2.39	4.01
427759	BE245578	Hs.2200	perforin 1 (pore forming protein)	2.39	4.56
443071	AL080021	Hs.65986	complement component 1, q subcomponent,	2.39	3.31
437211	AA382207	Hs.56959	ectopic viral integration site 29	2.38	3.15
440596	H13032	Hs.103378	hypothetical protein MGCI1034	2.37	3.68
452651	AI218918	Hs.30209	KIAA0854 protein	2.36	4.08
421563	NM_006403	Hs.105806	granulysin	2.34	3.25
421924	BE514514	Hs.109950	coactivin, actin-binding protein, 1A	2.33	3.38
443092	U91641		alpha2,8-sialyltransferase	2.32	3.53
425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	2.32	7.02
418117	A922013	Hs.83496	linker for activation of T cells	2.30	3.56
425795	A300479	Hs.159343	EDG-6 (endothelial differentiation, G-p	2.26	3.42
428111	S76517	Hs.2243	B lymphoid tyrosine kinase	2.25	3.69
439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	2.25	4.05
425722	AI659076	Hs.97031	hypothetical protein MGCI3047	2.25	3.44
436048	R18656		ESTs	2.24	3.23
432250	BE511654	Hs.28607	hypothetical protein A-211C6.1	2.23	3.08
441715	AI929453	Hs.342655	Homo sapiens cDNA FLJ13289 fic, clone OV	2.23	3.30
423397	NM_001838	Hs.1652	chomokine (C-C motif) receptor 7	2.22	3.25
449626	AA774247	Hs.301637	zinc finger protein Z58	2.21	3.14

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5	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, 5	2.18	3.41
	418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.15	3.62
	418185	AW958272	Hs.347326	intracellular adhesion molecule 2 (ICAM	2.09	5.21
	436420	AA443966	Hs.31595	ESTs	2.07	3.81
	418174	L20638	Hs.83656	Rho GTP dissociation inhibitor (GDI) bet	2.05	3.14
	420626	AF043722	Hs.59491	RAS guanyl releasing protein 2 (calcium	2.01	4.42
	428289	M26301	Hs.2253	complement component 2	2.00	3.33
	429683	AF148213	Hs.211604	a diastatin-like and metalloprotease (2.00	3.75
	421445	AA013069	Hs.104453	Homo sapiens, clone IMAGE-4054868, mRNA	1.96	3.68
	450300	AL041440	Hs.58210	ESTs, Highly similar to ITIH_HUMAN INTER	1.91	4.84
10	415445	AL043004	Hs.75337	KIAA0135 protein	1.91	3.41
	409817	BE295464	Hs.56607	Williams-Beuren syndrome chromosome regi	1.87	3.53
	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.86	3.55
	437140	AA810265	Hs.122915	ESTs	1.86	3.79
	437338	A950087	Hs.	gdox0502.1 NC1_CGAP_Kid12 Homo sapien	1.83	3.42
	425240	AA305495	Hs.1869	phosphoglucomutase 1	1.83	3.75
	406972	M32053	Hs.	gls Human H19 RNA gene, complete cds.	1.80	4.03
	430378	Z28672	Hs.2656	tumor necrosis factor receptor superfam	1.78	3.53
	431470	AL330147	Hs.140472	hypothetical protein DAF2p47D065	1.78	3.39
	418350	AF188625	Hs.189507	phospholipase A2, group IID	1.78	5.48
20	417852	AJ250562	Hs.82749	transmembrane 4 superfamily member 2	1.78	4.88
	414682	AL021154	Hs.16984	inhibitor of DNA binding 3, dominant neg	1.77	5.79
	444290	S59115	Hs.10335	ratular killer cell group 7 sequence	1.74	3.41
	427278	AL031428	Hs.174174	KIAA0501 protein	1.74	3.80
	418518	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	1.73	4.21
	420397	NM_007018	Hs.97437	centrosomal protein 1	1.73	3.21
	418678	NM_001327	Hs.167239	oncophetosis antigen (NY-ESO-1)	1.73	3.77
	459245	BE426283	Hs.319339	manic fringe (Drosophila) homolog	1.72	3.52
	425356	BE244879	Hs.155939	inositol polyphosphate 5-phosphatase, 14	1.71	3.55
	423984	AF163825	Hs.136713	pre-B lymphocyte gene 3	1.70	7.70
30	422355	AW003724	Hs.300697	coagulation factor VII, human proprotein	1.70	3.10
	451579	AW507321	Hs.26510	Human PAC clone RP3-15H1 from 22q11.2 q	1.68	4.16
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associ	1.68	5.76
	416819	U77735	Hs.80205	pim-2 oncogene	1.67	3.17
	409598	AW020478	Hs.279780	NY-REN-16 antigen	1.67	3.74
	447532	AK000674	Hs.16791	hypothetical protein FLJ26057	1.66	3.62
	429666	AW500131	Hs.171763	CD22 antigen	1.65	4.67
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	1.65	3.43
	416371	R34657	Hs.80558	uncoupling protein 2 (mitochondrial, pro	1.64	3.66
	430468	AA352723	Hs.241471	RN68	1.62	3.08
40	424661	M26651	Hs.151531	protein phosphatase 3 (formerly 2B), cat	1.61	3.37
	453027	A1879341	Hs.539	ribosomal protein S29	1.61	11.60
	410068	A1633888	Hs.58435	FTY-binding protein (FYT-120130)	1.60	3.28
	404446	NM_013385	Hs.7189	pleckstrin homology, Sec7 and coiled-coil	1.59	3.14
	453657	V02327	Hs.286162	ADOL7 protein	1.59	3.12
	418102	R58958	Hs.26508	hypothetical protein MGC15880	1.58	3.55
	424614	S54486	Hs.151242	serine (or cysteine) proteinase inhibito	1.58	3.07
	406791	AJ220684	Hs.347839	hemoglobin, alpha 2	1.55	5.06
	421703	A336513	Hs.1416	Fr fragment of IgE, low affinity II, rec	1.53	3.59
	421859	AA356620	Hs.108947	KIAA0050 gene product	1.52	3.41
50	416783	AA206196	Hs.78889	monocyte to macrophage differentiation-a	1.52	3.28
	456086	AL161999	Hs.77324	eukaryotic translation termination facto	1.47	3.34
	425783	AJ026740	Hs.1948	ribosomal protein S21	1.46	4.95
	407682	AL038568	Hs.3807	PYD domain-containing ion transport reg	1.46	3.46
	409169	F00991	Hs.50889	(clone PMHLC2-24) myosin light chain 2	1.45	3.25
	436824	AF218942	Hs.24889	formin 2	1.45	3.11
	413989	X14034	Hs.75648	phospholipase C, gamma 2 (phosphatidyl	1.45	3.33
	425530	U24578	Hs.274625	complement component 4A	1.44	4.37
	429528	S55736	Hs.238552	ESTs, Weakly similar to hypothetical pro	1.44	3.65
	418219	AA731836	Hs.137319	ESTs	1.43	4.01
60	429671	AW794126	Hs.195453	ribosomal protein S27 (metalloprotein) m	1.41	4.23
	418473	AA434335	Hs.309493	nuclear body protein Sp140	1.41	4.29
	423766	AA333199	Hs.300141	ribosomal protein L39	1.40	3.22
	430150	L05148	Hs.234569	zeta-chain (TCR) associated protein kina	1.39	3.29
	416370	N90470	Hs.203697	CD38 antigen (p45)	1.36	3.08
	408758	AK652306	Hs.77039	ATP synthase, H transporting, mitochondr	1.32	3.29
	446700	NM_006157	Hs.21602	net (elav)-like 1	1.31	3.85
	444674	BE562200	Hs.244	amino-terminal enhancers of split	1.30	3.10
	407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	1.30	3.91
	427349	AA360154	Hs.177415	Finkel-Biskamp-Reilly murine sarcoma vira	1.28	3.59
70	419032	VR11330	Hs.598717	ESTs, Highly similar to JAK3B [H] sapien	1.28	3.21
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.27	4.00
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.24	3.25
	406623	X68392	Hs.	ribosomal protein L26	1.24	3.31
	437895	AB014568	Hs.5898	KIAA0658 protein	1.21	3.33
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing le	1.18	3.35

TABLE 538:

Phy: Unique Eos probe/seq identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Phy: CAT Number Accession

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[illegible]

TABLE S3C:

of

Unique number corresponding to an Eos probeset

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Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. 'Dunham, et al.' refers to the publication entitled 'The DNA sequence of human chromosome 22' Dunham, et al. (1999) *Nature* 402:489-495.

Strand: indicates DNA strand from which exons were predicted

NI_position: indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NI_position
405545	1054740	Plus	118677-118607, 119091-119290, 121626-12182
401556	846900	Minus	96277-96420, 96799-97160
405547	1054740	Plus	124381-124520, 124914-125050

TABLE 54A: ABOUT 161 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT LATER METASTASIZED RELATIVE TO PRIMARY MELANOMAS THAT DID NOT METASTASIZE LATER.

Table 54A lists about 161 genes upregulated in primary melanomas from tumors that later metastasized relative to primary melanomas that did not metastasize later. These genes were selected from 59680 probesets on the Ecoli/Myotest Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Ecol/Myotest probe set identifier number

ExAczn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of AIs for primary melanomas that later metastasized divided by the 80th percentile of AIs for primary melanomas that did not metastasize later

R2: 90th percentile of AIs for primary melanomas that later metastasized divided by the 90th percentile of AIs for primary melanomas that did not metastasize later, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

Pkey	ExAczn	UnigeneID	Unigene Title	R1	R2
445866	AW032814	Hs.86149	phosphoserine 3-phosphate-binding prot	7.15	3.41
413916	W45813	Hs.75515	apolipoprotein C-III	5.93	6.55
414807	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-1N	5.64	2.98
415668	AW957684	Hs.305814	hypothetical protein FLJ21869	5.03	4.56
440274	R24595	Hs.71722	scrapie responsive protein 1	4.96	4.83
417542	J04129	Hs.82269	prostaglandin-associated endometrial prote	4.96	7.07
427882	AA640987	Hs.193767	ESTs	4.68	4.58
452744	A1267652	Hs.246107	Homo sapiens mRNA; cDNA DKFp434E082 (tr	4.29	3.06
407907	AF52225	Hs.41270	procollagen-llysine, 2-oxoglutarate 5-dio	3.94	3.86
424410	W79027	Hs.271162	ESTs	3.67	3.19
429083	Y05297	Hs.227817	BCL2-related protein A1	3.46	2.49
407951	W77762	Hs.75015	antigen identified by monoclonal antibody	3.31	3.06
428330	L25254	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.27	2.12
440099	AL020958	Hs.6599	DKF2P564G002 protein	3.22	2.68
428001	H97428	Hs.210907	ESTs, Moderately similar to Transforming	3.20	1.85
451099	R52796	Hs.25954	interleukin 13 receptor, alpha 2	3.18	4.61
442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.13	2.11
433543	AW970066	Hs.287426	MEGF 10 protein	3.10	3.31
412262	W05406		seven in absentia (Drosophila) homolog 1	3.06	3.94
438328	A1492261	Hs.32450	ESTs	3.05	3.09
409780	AA302840		gb-EST10634 Adipose tissue, white 1 Homo	3.01	2.65
453912	AL121031		SWI5NF related, matrix associated, acti	2.94	1.86
415626	AA180256	Hs.216473	Homo sapiens cDNA FLJ14872 fs, clone PL	2.91	3.70
407744	AB020629	Hs.39095	ATP-binding cassette, sub-family A (ABC1	2.88	2.53
453935	A1633770	Hs.42572	ESTs	2.88	2.00
452689	F33868	Hs.284176	transferrin	2.84	6.47
448550	AA353125	Hs.184721	ESTs	2.83	4.74
409417	AA155247	Hs.104679	serine (or cysteine) proteinase inhibitor	2.82	2.43
438698	A1819863	Hs.105243	ESTs	2.81	2.08
403191	A1165880	Hs.188809	ESTs	2.80	2.69
408418	AW963897	Hs.44743	KIAA1436 protein	2.79	1.75
450157	AW961516	Hs.50178	ESTs	2.77	3.40
402380	AA640891	Hs.102406	ESTs	2.77	4.28
443172	AW662664	Hs.199081	p300/CBP-associated factor	2.75	2.88
450629	AW891986		histone deacetylase 2	2.72	2.24
407857	AS28445	Hs.92254	serpin/thrombin-inhibitor 2	2.72	1.53
421097	A1260112	Hs.126232	Homo sapiens cDNA FLJ13266 fs, clone OV	2.68	2.59
436280	A1690734		Homo sapiens cDNA: FLJ25562 fs, clone H	2.67	2.79
407650	Y10515		gb H sapiens mRNA for CD68 T7 protein,	2.65	1.98
427871	AW952405	Hs.59622	Homo sapiens, clone IMAGE:5967281, mRNA,	2.64	1.76
427899	AA826286	Hs.332053	serpin amyloid A1	2.59	3.01
442793	AJ017798		ESTs, Weakly similar to T147_HUMAN CARGO	2.58	1.60
446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.57	1.91
444381	BE387335	Hs.237113	ESTs, Weakly similar to S64054 hypotheti	2.57	2.13
458247	R144439	Hs.209194	ESTs	2.56	2.61
451668	Z13498	Hs.325444	carboxylic acid protein 1	2.52	2.74
433980	AA137152	Hs.280449	phosphoserine aminotransferase	2.51	1.88
412719	AW016610	Hs.815	ESTs	2.50	1.68
441789	DS2059	Hs.7972	KIAA0871 protein	2.50	3.11
438485			Target	2.50	3.15
453464	A1884911	Hs.32599	receptor (calcitonin) activity modifying	2.48	3.33
417821	BE245149	Hs.82643	protein tyrosine kinase 9	2.48	1.66
450202	AW959756	Hs.34145	ESTs, Weakly similar to A49647 GTP-bind	2.47	2.79
436825	AW341123	Hs.100735	ESTs	2.47	2.55
424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.42	2.28
432426	AW973152	Hs.31050	ESTs	2.42	1.76
409095	AW337272	Hs.293656	ESTs, Moderately similar to S72461 proba	2.41	2.41
403752			NM_007537 Homo sapiens mitogen-activate	2.41	2.87

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404689	AA669253	Target Exon
439195	H85590	RNA, U2 small nuclear
433582	AW854339	gb:vw28008.s1 Morbit Fetal Cochlea Homo
438461	AW075485	hypothetical protein FLJ11937
432878	BE385490	phosphoserine aminotransferase
416567	BE297139	Pitn
428666	AL080180	replication protein A2 (320D)
413645	AA130992	Homo sapiens mRNA, cDNA DKFZ434A202 (fr
421262	AA286914	gb:u05622.s1 Stratagene cdon (937204)
434418	AF134707	ESTs
413204	BE071603	a disintegrin and metalloproteinase doma
449720	AA311152	gb:CV3-010510-161299-032.R03 BT0510 Homo
451838	AW005866	hypothetical protein FLJ21582
419943	AW968322	ESTs
459711	BE385001	low molecular mass ubiquitinone-binding pr
429449	AF032203	intracellular repeat containing 3
429493	AL134708	aristolochin-like homeobox 3
422283	AW411307	ESTs
441989	AA305207	ODC45 (cell division cycle 45, S.cerevis
419352	AB750008	protein kinase, cAMP-dependent, regulato
427353	AB029018	ESTs
418522	AA605038	KIAA1095 protein
433468	AA832055	Homo sapiens cDNA: FLJ21950 fis, clone H
452782	AA028166	ESTs, Weakly similar to ALU1_HUMAN ALU S
443910	AW051711	ESTs
408632	AW085690	ESTs
407283	TS1008	ESTs, Weakly similar to Z195_HUMAN ZINC
437376	AA749400	gb:y556008.s1 Stratagene ovary (537217)
450712	AF721130	ESTs
421362	AA000050	ESTs, Weakly similar to ALU2_HUMAN !!!
445183	AB007877	hypothetical protein FLJ26043
438501	Z44110	KIAA0171 gene product
432882	NAL_013257	phosphoinositide 3-phosphate-binding pro
414900	AW453420	serumglycocalcortisol regulated kinase-II
427704	AW971063	ESTs
404942	AW947184	ESTs
452254	AA594386	splicing factor, arginine/serine-rich 9
418965	AA022238	ESTs, Moderately similar to 08022 hypot
443357	AW016773	ESTs
412432	AA126311	splicing factor, arginine/serine-rich 11
406567	AA907980	low molecular mass ubiquitinone-binding pr
433179	AW352945	ESTs
408243	Y00787	ESTs
435294	T84084	interferon 8
449656	AA002008	Homo sapiens cDNA FLJ11723 fs, clone HE
412649	NAL_002208	ESTs
445162	AB011131	vitrogen, alpha 7
419356	AB56166	picollo (presynaptic cytomatrix protein)
424283	M77840	hypothetical protein FLJ22316
414694	NAL_015382	L1 cell adhesion molecule (pyrocephalus
415825	Y18024	VSPC002 protein
409105	AW467539	insulin I, I, S-isophosphate 3-kinase B
444784	D12485	ESTs
404149	D12485	oclononucleotide pyrophosphatase/phosphodi
408387		C0002509:gb:051885:uHNP_055668.1 (s
420871	AA702972	Target Exon
457597	BE091833	ESTs
416751	BE385014	gb:IL2-8T0731-2-250400-076-F04 BT0731 Homo
412347	AW910025	phosphatidate-3-kinase, regulatory su
413211	AW967107	ubiquitin-cytochrome c inducible hinge p
459317	BRCA1b	hypothetical protein MGCA365
425625	AA368883	Eos Control
433603	AW749865	ESTs
433698	AL047879	ESTs, Weakly similar to G00222 hypot
424389	AA339786	ESTs, Weakly similar to ALU2_HUMAN ALU S
426672	AW270555	lymphocyte-specific protein 1
415977	AL037622	hypothetical protein
404780		methionine aminopeptidase; eIF-2-associ
436476	AA326108	Target Exon
428284	AA355762	bHLH protein DEC2
448597	AA486794	NM_004545:Homo sapiens NADH dehydrogenas
428186	BE265388	ESTs, Weakly similar to 15.7kd protein I
447752	M73700	mitochondrial ribosomal protein L20
447455	H08335	lactoferrin
453281	AW6280	Homo sapiens mRNA for FLJ00068 protein,
413142	M81740	ESTs, Weakly similar to A25704 synapsin
407194	AA621844	ornithine decarboxylase 1
444107	T46839	gb:u54407.s1 Scaevola, Jutea, Jutea, M2HF8,
406197	AA32224	UDP glycosyltransferase 2 family, polype
405711	N25514	ribosomal protein L6
414608	BE396215	myosin, light polypeptide 6, alkali, smc
		ATP synthase, H transporting, mitochondr

2.39	1.97
2.37	2.54
2.37	2.27
2.36	2.81
2.35	2.91
2.35	2.28
2.33	1.97
2.32	2.92
2.31	2.63
2.31	1.85
2.31	2.21
2.31	1.46
2.30	1.78
2.28	2.05
2.28	2.39
2.27	2.39
2.26	1.97
2.26	2.77
2.25	1.83
2.26	1.78
2.25	1.84
2.25	1.47
2.24	2.42
2.24	1.76
2.24	2.34
2.24	1.79
2.22	1.52
2.22	1.31
2.22	2.44
2.22	1.62
2.22	2.36
2.20	1.84
2.20	1.76
2.19	1.59
2.18	1.89
2.17	1.86
2.17	1.86
2.17	1.64
2.16	1.61
2.16	1.79
2.16	2.32
2.15	2.73
2.08	2.85
2.07	4.77
2.05	3.12
1.97	2.89
1.94	3.60
1.93	2.76
1.93	2.66
1.92	3.39
1.89	3.10
1.88	4.25
1.87	2.66
1.87	2.96
1.85	2.80
1.84	2.93
1.82	2.96
1.76	3.12
1.75	3.12
1.70	3.20
1.67	3.65
1.66	2.89
1.61	7.34
1.59	2.67
1.56	2.76
1.55	2.76
1.53	2.95
1.51	3.39
1.47	2.65
1.43	2.77
1.41	3.04
1.38	2.90
1.37	2.84
1.36	3.29
1.35	2.70
1.35	3.03
1.34	2.69
1.33	2.96
1.32	2.70
1.26	3.27
1.26	2.72
1.25	7.10
1.24	2.72

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401846			NM_000988 Homo sapiens ribosomal protein	1.24	2.82
432982	AA531058	Hs.182246	truncated calcium binding protein	1.23	3.10
428578	BE391797	Hs.343588	ribosomal protein S12	1.23	2.74
400199			Eos Control	1.21	3.98
400079			Eos Control	1.20	2.99
412623	R28898	Hs.74170	metallothionein 1E (function)	1.19	2.63
406713	U02629	Hs.77365	myosin, light polypeptide 6, alkali, smoo	1.19	4.15
406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smoo	1.18	4.75
424922	AA530409	Hs.234518	ribosomal protein L23	1.17	2.74
431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	1.17	3.15
436398	H87136	Hs.5174	ribosomal protein S17	1.16	3.22
432205	AB005083	Hs.125291	ESTs	1.15	2.76
428519	AI581134	Hs.181357	laminin receptor 1 (67kD, ribosomal prot	1.09	2.56
401254			Target Exon	1.00	3.08
405752			Target Exon	1.00	2.87
445772	A1733941	Hs.145493	ESTs, Weakly similar to ALU7, HUMAN ALUS	1.00	2.70
445916	AA542831	Hs.31016	putative DNA binding protein	1.00	2.62
451411	AA017492	Hs.135655	EST	1.00	2.62
419568	BE501921	Hs.270471	ESTs	1.00	2.82
448610	NM_006157	Hs.21602	nei (chicken)-like 1	1.00	3.30

TABLE 54B:

Pkey:

CAT number:

Accession:

Unique Eos probest identifier number
Gene cluster number
Genbank accession number

Pkey	CAT number	Accession
412262	4362_1	AK050501 AB91258 AI681134 AU146134 AB03300 AA917325 AA923663 BF895068 AB004442 AI67464 A284186 AA354272 AA292952 AA351910 T90303 AB862070 U070056 AA119916 BF446537 BE502007 BE502949 AB98102 AA285853 AV718529 AV719917 BF724133 BA438668 AB930400 BF394503 AV712224 BE654117 AC227754 AA445020 AB479147 AC261770 AV138872 AB459891 AC339265 AC332474 AA185112 BE771804 BF94569 AA455093 AC372651 AV138855 BF769996 R17298 AU138740 BF908607 BE57435 AV470012 AC227778 AA452099 AV921959 AA435418 T74315 F12666 AA022923 T99028 AC258066 W26406 BE338620 AV070076 AA101321 R41382 H144745 AA25304 R54810 R24704 RA4804 R41278 AA302840 T93016 T92950 AU184937 AA07751
409760	865166_1	BM47224 B956849 B96735 AW9302 B962894 B963604 AA549765 AB926034 AQA1551 AW437354 AB26702 AB008105 AB914849 AB514983 AA531327 AA516996 AB262962 AB508991 BF728943 AB593312 W35325 AA025922 BA460536 AB388442 AB538429 BF347777 W01360 N94710 HB7967
456629	207_22	AV1995 AB95004749 AB080872 R15559 BE177623 AB4883520 AW345343 A246167 T07082 AW805679 W96278 AA135796 W36155 AV959418 AB7901688 BE003037 AW801621 AW285742 AW385714 AW604757 W87409 AW604738 AW3385751 AV45907891 AB001747 BE003029 BE003183 AA847112 AW505045 AW804703 AV055777 BE164590 BE003030 AC062791 AV460475 AV056529 AW604738 H44337 AC178646 AV1990438 AV071237 AC236883 AC236639 AA091945 AW345454 AA053629 AA702504 AV061938 AV061948 AV508941 AA054372 T06399
40		AB165866 BE244066 BE060535 AW861913 AA551773 AW658460 AV437026 AW754352 AW889955 AV380408 AB074428 BE067491 ABW81939 AA248197 AV381373 AV177325 AW068194 AA35217 BE067498 BE083742 BE067470 AW894935 BE062529 AC248111 BE179917 BE002200 AW679506 AV392889 ABW94560 AW361360 ABW94206 AW863533 C00699 AW361372 BE068539 ABW86120 BE075323 AB392749 AV001420 AB595314 BE063790 AW658656 AW645500 BE171153 AW676046 BE350419 AB060191 AV030704 AB060171 AV068979 AV0734240 AA045556 AB588883 AB369364 AW05960 AW601421 AW360793 BE065524 BE083901 AW339947 AV361871 AV925435 AW664582 AV077775 AW583849 BE180465 AW585501 BE180454 A1371163 AA78231 AV174991 BE011720 AV877778 BE078780 ABW87795 T19900 AW856365 AW950909
45		BE011715 BE167842 BE0117 BE011724 AW363638 AV079658 AV078862 AW694887 BE023255 AV0369211 AW042266 AA510312 A9041771 AV0510318 AV059360 AB012596 AV050123 AW080033 AT062111 AV052582 AW393713 AV060593 AV176663 AW84264 AV042389 ABW42095 AV242349 AV002074 AW062592 AV176664 AW751592 BE087703 AB070439 BE090696 BE172115 BE070730 AW068556 AW33557 AB096262 BE070295 AV176241 BE077552 BE160370 BE160288 AW835656 AW605770 AW835678 AW605758 AW605758 ABW67778 A907484 BE138211 AW605769 AV995917 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA090510 AW044417 BE173367 AV0998078 AB124870 BE163472 ABW814283 AC279512 ABW82927 A1294296 BE1608132 AW10287 AV176676 AV067612 BE172639 ABW83222 AA326269 BE090908 BE172630 BE178214 BE063291 AV102026 AV099545 BE131255 BE171775 BE185787 AA552890 AB174840 AW0999112 BE181391 BE172734 BE178021 BE172738 BE173324 AW602494 AU036722 R38192 R60995 H53271 H41052 AU039717 R37795 AV999992 AA767189 AW044272 H06808 AB768399 AA767764 AB078888 H44202 BE22792 N03959 W613955 H05615 A5135353 BE501168 F10945 AW118215 A910480 BE172361 F01414 T880718 AC215165 BE7220 AW047481
436280	36296_1	AC022515 AC225161 BE071206 AA600434 AA730787 AB435407 D79304 D79906 AW961628 AB17068 BE044373 AC322458 AA587927 AC385869 BA492783 AW021853 R79299 N73208 AU106622 N24609 AV192569 AB4707818 AB690734 R79189 A153900 AV599329 A1129344 BE33011 BE337891 BF784655 H84048
442793	417830_2	BC741747 BC741822 AB017798 AB953594 AA450565 A1245087
411690	5396_1	AC027091 BF15493 BF768430 BC037830 BE175161 BG000114 BG897711 AA745391 AA665959 AA592525 B104953 BE304446 BG010136 BC038074 BF091358 BF752561 T56013 BC003629 BF091330 BE091337 BF091340 BA483330 AA174450 A75471 W26276 BF037837
65		AF086037 HB9360 HB9546 AA133992 AV069539 AC503635 BE071615 BE071613 BE071603 BE071587 BE071607 BE071615 BE071636 AV175934 BE065460 A052778 BG057892 AW016773 AM52373 AM52393 BE091833 BE091874 BE091871
70		BF190141 BE195988 AC937311 AU151256 AW341542 AW274231 AV463698 AW454447 AA436368 AW183056 AW007171 AV027027 A075098 AL520351 AA606892 ABW189425 AB427541 AB056561 AA023996 AA077899 ABW473512 AV226520 AA728919 A012416 A02518 AB425998 A5359154 A1500812 AC894311 A040740 BE167841 AW151374 BE16754 BE091830 AC299181 BC232716297 V95060 AA574412 A1506697 V95059 R51303 R09158 R59113 T48473 T50923 AA122065 AW06643 R03836 R06567
424389	1059_4	BC191078 AW961118 W77994 AC339871 AW045129 BC181820 BE16719 A125483 A161017 W73951 AC250771 AA912611 AA339786 BE335286 BE36282 BE17636 BE477718 W04963 BE16628 BE716625 BE166371 BF171644 BE171663 BF171642
75	0.0	AC322244 AW27890 AW093461 AW937014 AA535373 A1318525 A1246215 AA951591 A270640

TABLE 54C:

Ref:

Strand:

Nr_position:

Unique number corresponding to an Eos probest
Sequence source. The T digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

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5	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	1.78	3.54
	437865	AA156781		metallothionein 1E (functional)	1.77	2.97
	427751	AF000152		conserved gene amplified in osteosarcoma	1.75	6.89
	400442			DGZP2585G1722 protein	1.74	3.60
	450898	NM_001928	Hs.155597	D component of complement (adipon)	1.74	4.95
10	414477	U41035	Hs.75228	amplified in osteosarcoma	1.71	4.45
	432870	AW974124		gb:EST385227 MAGE: resequences, MAGM Homo	1.68	2.86
	455642	AW451523	Hs.109752	putative c-Myc-responsive	1.68	3.09
	455694	AW015302	Hs.105542	polyphosphoric cDNA: FLJ23271 fls, clone H	1.66	2.63
	430449	AS352723	Hs.241471	RNBS	1.65	2.84
15	401029			v-myc avian myelocytomatous viral rdnt	1.65	2.88
	402742			NM_002508 Homo sapiens nidogen (enactin)	1.64	3.37
	425559			Rho GTPase activating protein 1	1.63	3.07
	413271	NM_000319	Hs.83390	polyphosphoric cDNA: FLJ23271 fls, clone H	1.62	3.11
	406851	AA609834		major histocompatibility complex, class	1.62	2.86
20	450912	AW939251	Hs.25647	v-los FBI murine osteosarcoma viral onco	1.60	3.94
	447029	AL137381	Hs.17170	Homo sapiens mRNA, cDNA: DKFZp434C016 f1	1.60	3.75
	417739	ZC0995		gb:GIC102121 normalized infant brain cDNA	1.59	2.86
	452950	AA428123	Hs.302766	lysine 3-monooxygenase/hydrophalan 5-mo	1.58	2.95
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	1.58	4.11
25	444182	AW160432	Hs.296459	craniofacial development protein 1	1.57	2.98
	407815	AW373680	Hs.133603	hypothetical protein FLJ20277	1.57	3.88
	452887	AT02223	Hs.107253	hypothetical protein DKFZp761F241	1.56	2.88
	416819	U77735	Hs.80205	pim-2 oncogene	1.56	3.59
	414583	AA362907	Hs.76494	protein arginine-rich end leucine-rich r	1.56	4.28
30	426104	AL204418	Hs.190089	ESTs	1.55	3.47
	441591	AF055992	Hs.183	Duffy blood group	1.52	4.28
	446406	AF533681		Arg/Abi-interacting protein ArgBP2	1.49	2.87
	427343	AI880044	Hs.176977	protein kinase C binding protein 2	1.49	2.68
	415550	L13720	Hs.78501	growth arrest specific 6	1.47	4.62
35	411961	AA78432	Hs.72955	hypermetastatic in cancer 1	1.46	3.48
	406423			ENSP00002046202.DJ83M2.2 (similar to AC	1.42	3.19
	404642			NM_003105 Homo sapiens sortilin-related	1.41	2.97
	452650	AW270150	Hs.254516	NM_021965 Homo sapiens phosphoglucomuta	1.40	3.02
	432994	AW167668	Hs.279772	ESTs	1.40	2.66
40	404300			brain specific protein	1.37	5.52
	422033	AW245805	Hs.110923	NM_015669 Homo sapiens protocadherin be	1.37	3.03
	413752	AW411479	Hs.848	claudin 5 (transmembrane protein deleted	1.35	3.15
	425367	BE271188	Hs.155976	FK-506-binding protein 4 (5R.D)	1.34	3.09
	415198	AW009480	Hs.943	protein tyrosine phosphatase, receptor 1	1.32	3.29
45	406908	Z25437		natural killer cell transcript 4	1.32	2.89
	423959	AA333025		gb:H4.sapiens protein-tyrosine kinase gen	1.31	2.89
	408135	AA313248	Hs.42957	gb:EST371122 Embryo, 8 week I Homo sapien	1.31	2.88
	427523	BE242779	Hs.179526	methyltransferase-like 1	1.29	3.81
	415512	Y16270	Hs.78482	upregulated by 1,25-dihydroxyvitamin D-3	1.29	3.25
50	413531	AL036958	Hs.75416	paralemnin	1.29	2.85
	415908	AL037327	Hs.91586	DAZ associated protein 2	1.28	3.06
	424814	X54486	Hs.151242	transmembrane 3 superfamily member 1	1.27	2.90
	422934	BE244189	Hs.122482	serine (or cysteine) proteinase inhibito	1.26	2.90
	450935	BE514743		hypothetical protein	1.25	3.41
55	416630	H63932	Hs.174051	tumor suppressor deleted in oral cancer	1.25	3.63
	416950	AL046788	Hs.80552	small nuclear ribonucleoprotein 700D pol	1.24	2.93
	412558	AW962019		dermatopontin	1.22	2.81
	419593	W73092	Hs.58282	gb:EST374092 MAGE resequences, MAGG Homo	1.21	3.02
	403470			ESTs	1.19	2.84
60	402239			Target Exon	1.14	2.82
	400559			Fingertsh predicted: CYTOCHROME P450 4F5 (1.12	3.50
	412695	AW964439		Target Exon	1.00	2.90
	427072	H38046	Hs.293981	gb:PM3-HN0011-220300-002-c5 HN0011 Homo	1.00	2.84
	430439	AL133551		ESTs	1.00	2.89
65	418163	NM_001772	Hs.83731	DKFZP4340601 protein	1.00	1.99
				CD35 antigen (gp57)	1.00	2.93
70	TABLE 55B:					
	PrKey:	CAT Number	Accession	Unique Eos probe/seq identifier number		
	CAT number:			Gene cluster number		
	Accession:			Genbank accession numbers		
75	405636	U_9	L12064	L12063 L12065 L12066 L12068 L12072 L12082 L12081 L12062 L12080		
	439540	713_2	BC017171	BC021195 NM_000126 AF100572 AL137377 Z70758 BM474865 BG154806 AA124376 BG157203 BG764420 BG175028 BG824418		
			BM05810	AA120387 BG770228 BG666740 BG513323 BG759980 BG359998 BM048895 BE381070 BE313689 BE879144 NM005834 AW245847		
			AT170171	BF196861 BE356897 AA463876 AL375927 AA548810 AA948193 AA490916 AA159893 AA58188 AI240408 AI191843 AI31029 AW765399		
			AI351195	AW337894 AW061050 BE465591 BE524699 AR184308 AA172107 AW51027 AV151143 BF198825 BCB19063 BM458474 BE903557		
80			BE127115	BM443200 BE300263 BE300706 BE711097 BE390202 BG253394 BF795648 BF398930 BM475542 AW246215 BE501897 BE903610		
			BE561530	BE560532 BE903782 BE732947 BE227204 BG671305 BE262642 BE391848 BE382475 BC008258 BE454791 BI459099 BE31391 BE259420		
			BE28105	AW245422 AA123847 AA914818 HM0534 BE301004 AA31791 AA43581 BF793112 AL577303 AA372265 BE749665 BF743630 BE879296		
			AI359493	AA015598 AH95920 AW24500 F72021 AW151405 AW517572 AA773495 BG259594 BE391163 BE521529 AA421728 BG767231 BM462953		
			BC100524	W52648 AA113434 BE785431 B0941981 B0833368 BC253168 BG725940 BF369129 BF381332 BE735941 BE783738 B091658 W72152		
			W58732	W58569 BG365999 AD26705 H19721 W17051 W77958 B2267010 AA844319 W71413 W727214 N85194 BE734033 BG154049 AA931099		
			FI3645	AI41394 AK025758 BG189077 BE349455 AA812018 AA740241 A027722 AI150355 AA886395 AA937672 BE220225 AA84082 AA581814		
			AQ24384	AA809493 AA481029 AA825718 A1347866 AA431670 AA814436 AI251109 R07704 AA76506 AA742593 AA918359 AA37550 AA491103		

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TABLE 56A: ABOUT 277 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO BENIGN NEVI

Table 56A lists about 277 genes upregulated in melanoma metastases relative to benign nevi. Genes were selected from 59680 proteomes on the Eos/Alphatome: Hu03 Genechip array. Gene expression data for each probeet obtained from this analysis was expressed as average intensity [A], a normalized value reflecting the relative level of mRNA expression.

5	Play:	Unique Eos probeet identifier number			
	ExAccor:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
10	Unigene Title:	Unigene gene title			
	R1:	70th percentile of melanoma metastasis AIs divided by the maximum of benign nevi AIs			
	R2:	70th percentile of melanoma metastasis AIs divided by the maximum of benign nevi AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator			

	RfKey	ExAccor	UnigeneID	Unigene Title	R1	R2
	422424	A1165431	Hs.255638	prostate differentiation factor	13.73	17.18
15	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	11.67	13.25
	407846	AA426202	Hs.40403	Cbip330-interacting transactivator, wit	9.35	8.75
	444381	BE307335	Hs.263713	ESTs, Weakly similar to S64054 hypohel	8.63	6.22
	417800	BE241595	Hs.22948	selectin L (lymphocyte adhesion molecu	8.21	8.55
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	7.13	5.04
20	447210	AF035269	Hs.17752	phosphotyrosine-specific phospholipas	6.79	7.12
	417693	AW959741	Hs.40368	adaptor-related protein complex 1, sigma	6.55	5.94
	422500	X72555	Hs.289114	tenascin (tenascin C, cytotoxicin)	6.43	3.46
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.43	5.44
	451736	AW060356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.31	6.08
25	418870	AF147204	Hs.89414	chemokine (CX-C motif), receptor 4 (fus	6.20	6.04
	417308	AA534009	Hs.163487	interferon stimulated gene (20kD)	6.03	4.72
	417308	H80720	Hs.81892	KIAA0101 gene product	6.01	7.07
	448569	BE302657	Hs.21486	signal transducer and activator of trans	5.99	8.88
	439310	AF086120	Hs.102793	ESTs	5.95	6.53
30	452838	U65011	Hs.30713	preferentially expressed antigen in meta	5.95	3.77
	422241	Y00022	Hs.170121	protein tyrosine phosphatase, receptor I	5.76	6.37
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	5.76	3.14
	409274	NM_003930	Hs.52644	SKAP55 homologue	5.65	5.01
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	5.58	3.50
35	442711	AF151072	Hs.86465	hypohel	5.45	5.84
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	5.42	5.75
	412918	BE563957		activated RNA polymerase II transcriptio	5.35	4.94
	426125	AA330371	Hs.182579	leucine aminopeptidase	5.33	5.34
	446621	AB012113	Hs.16530	small inducible cytokine subfamily A (cy	5.33	4.98
40	431183	NM_008685	Hs.265856	KOEL (Lys-Asp-Glu-Leu) endoplasmic retic	5.30	6.25
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.16	5.33
	426600	NM_003378	Hs.171014	VGF nerve growth factor inducible	5.05	6.07
	415444	BE247295	Hs.78452	solute carrier family 20 (phosphate tran	5.03	5.17
	436701	AW583032		ESTs, Moderately similar to T88855 cetin	5.03	4.17
45	406648	AA503730	Hs.277477	major histocompatibility complex, class	4.99	5.08
	410850	AW362667	Hs.302738	Homo sapiens cDNA: FLJ12425; iso. clone C	4.98	4.71
	418299	AA278530	Hs.83968	integrin, beta 2 (integrin CD18 (p95), ly	4.98	4.08
	432469	AL080604		CD4-100 protein	4.97	4.70
	404854			Target Ecor	4.85	4.07
50	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.82	4.90
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.81	3.45
	408958	T99607	Hs.45346	signal recognition particle 54kD	4.76	2.34
	433949	AU077146	Hs.30327	heat shock 105kD	4.76	6.32
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	4.77	6.57
55	440245	AK001913	Hs.7100	hypohelical protein	4.74	3.83
	412228	AF053785	Hs.73792	complement component (3d)protein Barni	4.74	4.53
	417834	BE172266	Hs.25812	tumor rejection antigen (p95)	4.73	4.70
	451003	AF058696	Hs.25812	Nijmegen breakage syndrome 1 (nitkin)	4.67	4.60
	424571	BE379766		polymerase (RNA) II (DNA directed) polyp	4.62	3.50
60	434203	BE262677	Hs.283558	hypohelical protein PRO1855	4.61	5.67
	452268	NM_003512	Hs.28777	H2A histone family, member L	4.60	3.79
	421311	NT1646	Hs.26369	hypohelical protein PRO2032	4.60	3.58
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	4.60	4.68
	425706	AW406678	Hs.122559	hypohelical protein FLJ22570	4.59	3.83
65	450293	N36764	Hs.171118	hypohelical protein FLJ40025	4.57	5.40
	405836	AW514801	Hs.156110	immunoglobulin kappa constant	4.57	3.63
	413441	AI929374	Hs.75367	Src-like adaptor	4.53	4.77
	431129	AL137751	Hs.263671	Homo sapiens mRNA: cDNA DKF2p434081f2	4.48	4.89
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	4.47	4.17
70	411060	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN	4.47	4.33
	417501	AL041219	Hs.82222	sera domain, immunoglobulin domain (Ig)	4.45	3.32
	437763	AA489369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.43	4.43
	448883	BE614989	Hs.7903	hypohelical protein FLJ14153	4.42	3.91
	417274	N92836	Hs.61648	RAD23 (S. pombe) homolog	4.41	4.09
75	419265	D01867	Hs.89865	KIAA0162 protein	4.40	3.56
	418321	D63477	Hs.84067	KIAA0143 protein	4.38	3.00
	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibit	4.37	4.26
	428450	NM_014791	Hs.164329	KIAA0175 gene product	4.36	4.90
	428297	AA226291	Hs.183563	serine (or cysteine) proteinase inhibit	4.30	3.57
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	4.36	4.07
80	409598	NM_014018	Hs.55097	mitochondrial ribosomal protein S28	4.35	3.29
	424243	BE093589	Hs.38178	hypohelical protein FLJ23468	4.34	5.80
	407047	X55965		gcb.H.sapiens SOD-2 gene for manganese su	4.33	3.51

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433991	NM_002250	Hs.10062	potassium intermediate/small conductance
452322	BE566343	Hs.28988	glutathione (thioltransferase)
420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ001111 protein,
449722	EE280074	Hs.23660	cyclin E1
430310	AF123052	Hs.44332	ubiquitin
427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase
417933	X02308	Hs.82962	thymidylate synthetase
432828	AB042326	Hs.287402	chondroin 4-sulfotransferase
452336	AL030380	Hs.24766	(threonine domain-containing
440266	AA086909	Hs.19525	hypothetical protein FLJ27294
407951	W77162	Hs.79015	antigen identified by monoclonal antibody
429337	Z46223	Hs.176663	Fr. fragment of IgG, low affinity IIIb, r
428789	AW361666	Hs.49500	KIAA0745 protein
449626	AA177427	Hs.301637	zinc finger protein 258
422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr
415726	T89844	Hs.78712	ammodendrolase, delta-, synthase 1
444207	U552004		cathepsin D (lysosomal aspartyl protease)
415993	AA381133	Hs.80684	high-mobility group (nonhistone chromos
438718	AL040038	Hs.6375	uncharacterized hypothalamus protein HT0
437802	AA75935	Hs.122910	ESTs
446392	AF142419	Hs.15020	homolog of mouse quaking (QK) (KH domain
430461	AA382108	Hs.54463	N-myc (and STAT) interactor
427247	AW504223	Hs.174103	integrin, alpha L (antigen CD11A (p18),
414359	M62194	Hs.75529	cadherin 11, type 2, OB-cadherin (osteob
450071	AA018283	Hs.24359	Homo sapiens cDNA FLJ11174 f3, clone PL
452882	AW572990	Hs.195270	kilasin transportcarrier
414522	AW514544	Hs.76325	immunoglobulin J chain
407756	AA118021	Hs.38260	ubiquitin specific protease 18
405506			Target Exon
417497	AW402482	Hs.82212	CD53 antigen
413715	AW851121	Hs.75407	Homo sapiens cDNA: FLJ22139 f3, clone H
421508	NM_004833	Hs.105115	absent in melanoma 2
446701	AF055581	Hs.13131	lymphocyte adaptor protein
443071	AL080021	Hs.8596	complement component 1, q subcomponent,
417615	BE544641	Hs.82314	hypothetical phospholipidtransferase 1
444371	BE540274	Hs.239	bedford box M1
450515	AW304226		biphenyl hydrolase-like (serine hydrolas
446506	AI213118	Hs.15159	chemokine-like factor, alternatively spl
410368	BE379794	Hs.199651	hypothetical protein
443710	AI580136	Hs.5851	Homo sapiens cDNA: FLJ22345 f3, clone C
406837	R70292	Hs.156110	immunoglobulin kappa constant
419381	AB023420	Hs.90093	heat shock 70kD protein 4
420474			NM_004075Homo sapiens cathepsin S (CTSS
454080	AI199711	Hs.576	luciferase, alpha-L-, tissue
406284	NM_014937	Hs.52463	KIAA0956 protein
426358	AI245368	Hs.98558	ESTs
423484	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac
414829	AA321568	Hs.17436	pleckstrin
427235	AW023355	Hs.5541	ATPase, Ca transporting, ubiquitous
433867	AK000596	Hs.3618	Hippocalin-like 1
432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)
416310	AA814100	Hs.86693	ESTs
403688	AA504445	Hs.320597	immunoglobulin heavy constant gamma 3 (G
438746	AB85815	Hs.184727	Human melanoma-associated antigen p87 (p
427527	AI802057	Hs.153261	immunoglobulin heavy constant mu
442455	BE592285	Hs.25724	hypothetical protein FLJ13187
423266	NM_002104	Hs.3366	granzyme K (serine protease, granzyme 3;
435000	AB317760	Hs.155111	hypothetical protein FLJ14420
436810	AA353044	Hs.5321	ARF3 (pcdn-related protein 3, yeast) ho
422545	X02761	Hs.287820	fibronectin 1
439142	AL136877	Hs.50758	SMC4 (structural maintenance of chromos
424026	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase
416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp
448410	AK000227	Hs.21126	hypothetical protein FLJ20020
423842	BE297635	Hs.3069	heat shock 70kD protein 9B (hsc70b) 2)
425234	AW512225	Hs.165809	ESTs, weakly similar to D8022 hypothetical
443623	AA345519	Hs.9541	complement component 1, q subcomponent,
426480	NM_001621	Hs.170087	aryl hydrocarbon receptor
443958	BE241880	Hs.10029	cathepsin C
407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 f3, clone OV
412677	Z22668	Hs.74076	CD163 antigen
414050	NM_004766	Hs.75724	coatamer protein complex, subunit beta 2
442904	AW575008	Hs.11355	thymopoietin
421633	AF121880	Hs.106280	sorting nexin 10
413936	AF113676	Hs.297651	serine (or cysteine) proteinase inhibitor
428797	AA486205	Hs.193700	Homo sapiens mRNA: cDNA DKF259B03324 f1
408515	AI289507	Hs.299883	hypothetical protein FLJ23399
409442	AA310162	Hs.169248	cyclochrome c
456373	BE241726	Hs.897651	homomapsin-binding 4 domain, subfamily A
430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)
418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic
452139	AA059969	BE16331	Homo sapiens cDNA: FLJ21482 f3, clone C
430478	NM_014349	Hs.241535	apolipoprotein L 3

4.33	4.23
4.32	2.68
4.32	4.54
4.31	3.73
4.30	5.74
4.28	4.80
4.28	3.59
4.25	4.15
4.24	3.15
4.23	4.12
4.22	4.64
4.20	4.62
4.20	4.92
4.19	3.17
4.18	8.91
4.16	4.21
4.16	1.89
4.14	3.30
4.14	3.04
4.12	5.13
4.12	3.87
4.11	4.96
4.11	6.37
4.10	4.16
4.10	2.35
4.10	4.10
4.09	6.07
4.09	5.03
4.08	3.71
4.07	8.61
4.05	4.05
4.05	4.61
4.02	4.56
4.00	8.91
3.99	4.15
3.96	4.28
3.85	4.56
3.81	4.06
3.80	6.84
3.77	6.44
3.76	4.00
3.75	4.67
3.74	6.22
3.69	4.36
3.68	5.18
3.67	4.12
3.65	4.45
3.63	4.84
3.59	4.46
3.54	5.31
3.49	4.57
3.48	4.33
3.47	6.87
3.44	10.42
3.41	
3.40	4.50
3.40	4.22
3.40	5.03
3.39	7.32
3.36	4.47
3.34	5.02
3.34	4.24
3.32	4.29
3.32	4.64
3.24	13.58
3.23	4.20
3.16	5.05
3.15	5.32
3.14	5.03
3.13	4.65
3.13	4.34
3.12	4.99
3.11	5.47
3.10	4.30
3.10	4.03
3.07	4.00
3.07	4.38
3.04	5.53
3.03	4.97
3.01	4.87
2.98	4.44

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	436237	AW408158	Hs.318893	ESTs, Weakly similar to A47562 B-cell gr	2.95	7.45
	406782	AA430373		gblzw/2011.151 Soams ovary tumor NMIOT H	2.93	8.40
	450455	AL117424	Hs.25035	chloride intracellular channel 4	2.90	5.08
5	422530	AW972305	Hs.118110	bone marrow stromal cell antigen 2	2.87	7.07
	429440	AK911131	Hs.23886	ESTs, Weakly similar to ALUT, HUMAN ALU S	2.87	4.26
	410231	AA314163	Hs.61153	proteosome (prosome, macrophage) 26S subu	2.82	5.53
	419956	AL137939	Hs.40096	cadherin 19, type 2	2.80	4.26
	416511	NM_005762	Hs.76256	Lysosomal-associated multispanning membr	2.79	5.55
	421712	AK000140	Hs.1017139	hypothetical protein	2.79	6.29
10	429132	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	2.78	4.74
	448517	AA082750	Hs.42194	hypothetical protein FLJ25456 similar to	2.78	4.69
	427792	M53926	Hs.180641	tumor necrosis factor receptor superfam	2.77	5.18
	426872	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrate	2.75	5.00
	422173	BE365268	Hs.25810	phorbol-like protein MD5010 (CEM15)	2.75	4.33
15	445566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	2.72	4.19
	429402	AF116571	Hs.201671	SRY (sex determining region Y)-box 13	2.72	5.15
	421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1 b	2.71	4.67
	425762	BE244076	Hs.159578	AT-toxin transcription factor ARN	2.71	4.61
20	429412	NM_005235	Hs.2407	POU domain, class 2, associating factor	2.69	4.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.68	4.89
	425124	U258389	Hs.250697	phosphatidylethanol glycan, class F	2.68	4.25
	424572	X12784	Hs.119129	collagen, type IV, alpha 1	2.67	5.00
	417389	BE260564	Hs.82045	midline leucine growth-promoting factor	2.65	9.54
	445784	U253155	Hs.146065	ESTs	2.65	4.11
25	410341	AW495965	Hs.42915	ARF2 (acrin-related protein 2, yeast) ho	2.64	4.50
	425633	BE242587	Hs.118651	hematopoietically expressed homodimer	2.63	4.17
	424667	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.62	5.80
	410106	AA297977	Hs.57907	small inducible cytokine subfamily A (Cy	2.61	5.57
30	424779	AL046851	Hs.153053	CD37 antigen	2.60	5.72
	420224	MB4371	Hs.09023	CD18 antigen	2.60	4.02
	421924	BE514514	Hs.109566	coronin, actin-binding protein, 1A	2.57	4.83
	426143	BE379836		proteasome (prosome, macrophage) subunit,	2.56	4.50
	421563	NM_006433	Hs.105006	granulysin	2.56	5.35
35	425593	AA278521	Hs.1938	proteoglycan 1, secretory granule	2.55	4.32
	428165	AI028984	Hs.105703	beta1 phosphotyrosine	2.54	4.78
	417022	NM_014737	Hs.80905	Fas association (Fas/GSIAF-5) domain fam	2.54	4.09
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.53	4.41
	429600	AA333375	Hs.223014	antizyme inhibitor	2.50	5.68
40	407281	M34516	Hs.107526	gp.Human orosin light chain protein 14.1	2.50	4.06
	421739	AB004650	Hs.107526	UDP-Gal 4-epimerase-like 1,4- galactosyl	2.46	4.35
	412619	T25829	Hs.24046	FK506 binding protein precursor	2.45	4.66
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.44	4.91
	434883	AW361538	Hs.19807	hypothetical protein MGC12959	2.41	4.03
45	420340	NM_000234	Hs.57087	CD32 antigen, beta polypeptide (T1T) com	2.41	4.00
	446206	AL137257	Hs.23458	homo sapiens cDNA: FLJ20155 fs, clone L	2.41	4.77
	417370	T26651	Hs.82030	tylophanyl-rRNA synthetase	2.41	4.04
	402223			Eos Control	2.39	5.47
50	431626	AL077025	Hs.265827	interferon, alpha-inducible protein (chi	2.38	7.67
	414822	A1752666	Hs.76669	nicotinamide N-methyltransferase	2.38	5.32
	415149	X12451	Hs.76056	cathepsin L	2.37	8.07
	435096	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.37	5.23
	454380	AB020713	Hs.56868	KIAA0550 protein	2.35	4.57
	427407	BE268449	Hs.177766	ADP-ribosyltransferase (NAD, poly (ADP-r	2.31	4.46
55	445029	N29898	Hs.22891	solute carrier family 7 (cationic) amino	2.24	4.08
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.23	4.02
	423397	NM_001836	Hs.1652	chemokine (C-C motif) receptor 7	2.23	4.09
	416232	AW502676	Hs.79050	expresin 1 (CD44, yeast, homolog)	2.16	4.57
	436692	AW243158	Hs.5267	DKFZP554A2416 protein	2.17	4.13
60	420842	A1083668	Hs.50601	hypothetical protein MGC10986	2.14	5.14
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	2.13	4.43
	429542	268264	Hs.211579	melanoma cell adhesion molecule (MCAM) f	2.11	5.42
	416446	L13210	Hs.79336	lectin, galactoside-binding, soluble 3	2.10	6.36
	416714	AF283770	Hs.79630	CD79A antigen (immunoglobulin-associated	2.10	4.06
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.09	4.67
65	414045	NM_002951	Hs.75722	tylophanyl-rRNA synthetase	2.07	4.32
	424251	AA310753	Hs.42461	ESTs, Weakly similar to S65567 alpha-1-C-	2.07	4.04
	441211	AW946155	Hs.7750	hypothetical protein AL133006	2.06	4.64
	434692	H06586	Hs.34	DnaJ (Hsp40) homolog, subfamily A, membe	2.05	4.33
70	425263	AI082743	Hs.94653	Homo sapiens, Similar to complement comp	2.04	13.36
	426393	AA351615	Hs.50740	Homo sapiens cDNA: FLJ22772 fs, clone H	2.03	4.53
	413313	NM_002047	Hs.283108	glycyl-tRNA synthetase	2.02	4.13
	452700	AI856390	Hs.289540	five-span transmembrane protein MB3	2.00	4.04
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.99	4.35
75	424415	NM_0015975	Hs.146580	endostatin 2, (gamma, neuronal)	1.98	4.32
	429451	BE409861	Hs.202833	heme oxygenase (hemoxygen) 1	1.95	5.60
	416967	BE516731	Hs.80545	interferon regulatory factor 1	1.95	5.38
	414945	BE076358	Hs.77967	lymphocyte antigen 6 complex, locus E	1.93	4.69
	419817	X02394	Hs.1217	adenosine deaminase	1.91	4.32
	445411	AL137255	Hs.12946	CD14 antigen	1.91	4.51
80	413945	NM_000591	Hs.75827	CD14 antigen	1.90	6.03
	429116	AV660012	Hs.195437	hypothetical protein FLJ10788	1.90	4.08
	413317	U53225	Hs.75283	sorting nexin 1	1.89	4.06
	427239	BE270447		ubiquitin carrier protein	1.87	5.98

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TABLE 56B:
Pkey:
CAT number:
Accession:

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428398	A1249368	Hs 98558	ESTs	6.57	3.80
408889	AW361666	Hs 48500	KIAA0746 protein	6.48	4.93
417022	NM_014737	Hs 80595	Ras association (RalGDS/AF-6) domain fam	6.38	3.65
405644	AW960707	Hs 148323	ESTs	6.35	5.84
412326	R07566	Hs 72817	small inducible cytokine A3 (homologous	6.30	7.18
457211	AW972655	Hs 32369	ESTs, Weakly similar to SS1797 vasodilat	6.25	7.21
420591	AW504814	Hs 287379	Human sapiens cDNA for FLJ00111 protein,	6.25	5.36
422227	AA321549	Hs 2248	small inducible cytokine subfamily B (Cy	6.18	6.01
432828	AB042325	Hs 207402	chondroin-4-sulfotransferase	6.12	6.51
449078	AK001256	Hs 22975	KIAA1576 protein	6.05	8.55
436856	AI469355	Hs 127310	ESTs	6.00	5.54
433659	U3678	Hs 156110	immunoglobulin kappa constant	5.92	7.18
424247	K14008	Hs 224754	lysaxase (lysoz. amyloidosis)	5.89	4.07
409417	AA156247	Hs 104879	serine (or cysteine) proteinase inhibito	5.85	6.07
431574	AW572659	Hs 261373	hypothetical protein dJ43A014.3	5.74	6.03
458079	U196870	Hs 54277	DNA segment on chromosome X (unique) 992	5.72	5.92
440274	R24555	Hs 7122	scrape responsive protein 1	5.69	3.22
429412	NM_006235	Hs 2407	POU domain, class 2, associating factor	5.59	5.17
432656	NM_002104	Hs 3066	granzyme K (serine protease, granzyme 3)	5.68	3.35
436315	BE390513	Hs 27935	hypothetical protein MGC4837	5.67	4.56
452923	H80409	Hs 40527	ESTs	5.63	5.50
426559	AB001914	Hs 170414	perox. basic amino acid cleaving system	5.60	3.09
406663	U24683		immunoglobulin heavy constant mu	5.54	9.68
416975	NM_004131	Hs 1051	granzyme B (granzyme 2, cytotoxic T-lymp	5.52	6.42
408360	AF123050	Hs 44432	diubiquitin	5.51	4.49
412599	AA278530	Hs 83368	integrin, beta 2 (anigen CD18 gp95), ly	5.43	4.50
429500	X78565	Hs 289114	heretractation (tenascin C, cytotactin)	5.42	3.54
446341	AL040763	Hs 310735	ESTs, Moderately similar to ALU7_HUMAN A	5.41	5.29
425234	AW152225	Hs 163509	ESTs, Weakly similar to I30202 hypothi	5.40	4.35
434203	BE265677	Hs 283558	hypothetical protein PRD1655	5.38	4.16
420338	AA825595	Hs 85269	Human sapiens, clone MGC-17393, mRNA, com	5.37	5.77
430580	AA806105	Hs 300659	immunoglobulin heavy constant gamma 3 (G	5.31	5.32
428604	AK000713	Hs 193736	hypothetical protein FLJ20705	5.29	4.80
447335	AA75258	Hs 6127	Human sapiens cDNA: FLJ23020 fs, clone L	5.29	3.61
410491	AA463131	Hs 54001	Human sapiens clone 25218 mRNA sequence	5.27	3.55
410361	BE391804	Hs 62661	guanylate binding protein 1, interferon-	5.26	6.00
412561	NM_002286	Hs 74011	lymphocyte-activation gene 3	5.26	5.04
450293	N36754	Hs 171118	hypothetical protein FLJ00026	5.23	3.60
400750			Target Exon	5.18	3.62
417933	X02308	Hs 82962	thymidylate synthetase	5.14	3.33
413385	M34455	Hs 840	indoleamine-pyrole 2,3 dioxygenase	5.12	5.36
445784	AI251155	Hs 146055	ESTs	5.12	4.06
420502	AF760877	Hs 392326	regulator of G-protein signalling 20	5.06	7.68
421508	NM_004833	Hs 105115	abovet in melanoma 2	5.03	5.59
434826	AF155661	Hs 22265	pyruvate dehydrogenase phosphatase	4.96	6.25
402474			NM_004793: Homo sapiens cathepsin S (CTSS	4.96	5.13
409417	X72475		Target	4.90	3.93
420137	AA306478	Hs 95327	CD33 antigen, delta polypeptide (T13 co	4.88	6.81
408264	NM_014937	Hs 52463	KIAA0955 protein	4.88	3.18
418460	M26315	Hs 85258	CD8 antigen, alpha polypeptide (p32)	4.87	4.20
418506	AA084248	Hs 85339	G protein-coupled receptor 39	4.85	5.86
409142	AI136877	Hs 50758	SMCA (structural maintenance of chromoso	4.83	5.94
425088	AA663372	Hs 169395	hypothetical protein FLJ12915	4.82	5.19
405506			Target Exon	4.74	4.09
408612	AW979187	Hs 283591	melanoma differentiation associated prot	4.74	3.72
430338	N46564	Hs 165395	hypothetical protein FLJ12015	4.73	3.50
439963	AW247529	Hs 6193	platelet-activating factor acetylhydrola	4.72	3.66
421379	Y15221	Hs 103982	small inducible cytokine subfamily B (Cy	4.71	5.16
427217	BE465754	Hs 17778	neuropilin 2	4.70	4.52
422309	U79745	Hs 114924	solute carrier family 16 (monocarboxylic	4.69	3.51
413670	AB000115	Hs 75470	hypothetical protein, expressed in ovine	4.68	3.69
419956	AL137939	Hs 40096	cathepsin 19, type 2	4.68	5.83
429903	AL134197	Hs 93597	cyclin dependent kinase 5, regulatory su	4.68	5.29
449217	AA278536	Hs 23262	ribonuclease, RNase A family, h6	4.66	3.84
449722	BE260074	Hs 22960	cyclin B1	4.64	4.29
424006	AF054815	Hs 137548	CD84 antigen (leukocyte antigen)	4.62	4.54
407846	AA426202	Hs 40403	Obp300-interacting transactivator, wit	4.62	6.78
414821	M63835	Hs 77424	Fc fragment of IgG, high affinity Ia, re	4.59	5.81
406673	KC4996	Hs 196263	major histocompatibility complex, class	4.57	5.60
431520	AA126109	Hs 264981	Z 5-oligoadenylate synthetase 2 (HS-11	4.56	4.44
441224	AU076964	Hs 7753	calumenin	4.56	3.75
442739	NM_007274	Hs 8679	cytosolic acyl coenzyme A thioester hydr	4.56	3.22
444731	BE540274	Hs 239	forkhead box M1	4.53	5.28
442719	AA033827	Hs 21858	trichostatin repeat containing 3	4.48	4.08
420301	AA767526	Hs 22000	paired box gene 5 (beta cell lineage specifi	4.47	5.61
430294	A538226	Hs 32976	guanine nucleotide binding protein 4	4.43	4.11
428513	BE220806	Hs 184659	Human sapiens clone 23785 mRNA sequence	4.41	4.43
445006	NM_004403	Hs 13330	deafness, autosomal dominant 5	4.39	3.99
432485	N00965	Hs 276770	CDWS2 antigen (CDMP111-1 antigen)	4.38	5.50
428242	H55709	Hs 2250	leukemia inhibitory factor (cholinergic	4.37	3.25
421633	AF121860	Hs 106260	sorting nexin 10	4.36	6.23
414829	AA321568	Hs 77436	pleckstrin	4.35	2.91
417166	AA431323	Hs 42746	ESTs	4.35	4.08

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448410	AK000227	Hs.21126	hypothetical protein FLJ20220	4.34	5.35
419381	AB023420	Hs.90053	heat shock 70kD protein 4	4.34	3.72
411305	BE241596	Hs.69547	myelin basic protein	4.32	4.18
425289	AW133442	Hs.155530	interferon, gamma-inducible protein 16	4.28	2.44
451099	RS2795	Hs.29564	interleukin 13 receptor, alpha 2	4.27	4.48
432642	BE297635	Hs.3069	heat shock 70kD protein 96 (mortalin) 2	4.25	2.69
422882	AF019225	Hs.114309	apolipoprotein L	4.25	3.75
433667	AK000596	Hs.3618	hippocalcin-like 1	4.23	5.13
415817	UB9967	Hs.78967	protein tyrosine phosphatase, receptor-I	4.20	2.15
438619	AB032773	Hs.169294	TUJ2B1-TY protein	4.19	3.32
426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific, silver (mouse homolog) like	4.16	5.14
420208	BE276055	Hs.95972	Protein kinase C-binding protein NELL2	4.16	5.08
416602	NM_061559	Hs.73386	ESTs	4.15	2.38
430770	AA765694	Hs.122296	ESTs	4.15	3.67
424541	AW382551	Hs.180559	ESTs, Weakly similar to A56194 thromboxane	4.15	3.98
427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.14	3.51
456700	AW961251	Hs.127628	guanine nucleotide binding protein (G protein) heavy constant gamma 3 (G	4.14	4.42
420868	AA529445	Hs.300587	small inducible cytokine B subfamily (Cy	4.12	6.43
420931	AF044197	Hs.100431	small inducible cytokine subfamily A (Cy	4.11	8.73
410016	AA297977	Hs.57907	chemokine (C-C motif) receptor 1	4.11	4.48
452638	NM_001295	Hs.301921	serine (or cysteine) proteinase inhibitor	4.10	4.78
444963	AW384082	Hs.104579	hypothetical protein FLJ14428	4.07	2.76
435080	AI831760	Hs.155111	hypothetical protein	4.06	3.49
442711	AF151073	Hs.8645	cadherin 19, type 2	4.06	2.42
423605	AF047826	Hs.129887	small inducible cytokine subfamily A (Cy	4.05	3.29
460328	T97490	Hs.56002	hypothetical protein	4.02	7.60
421712	AK000140	Hs.107130	CDCA5 (cell division cycle 45, S.cerevisiae	4.00	3.87
422283	AW411307	Hs.114311	Homo sapiens cDNA FLJ21020 ts, clone C	4.00	5.87
409415	AA579258	Hs.6083	ESTs	3.99	5.45
412719	AW016910	Hs.816	serologically defined colon cancer antigen	3.96	4.51
431719	AA335688	Hs.96553	hypothetical protein	3.95	5.47
420319	AW406289	Hs.6194	chondroitin sulfate proteoglycan BIEH4b	3.91	4.58
438380	T06430	Hs.83384	S100 calcium-binding protein, beta (neur	3.94	4.42
418064	BE387287	Hs.111377	ESTs	3.93	5.56
422866	AF063935	Hs.111377	ESTs, Moderately similar to S65657 alpha	3.90	5.70
410500	AW575742	Hs.47650	ESTs	3.76	4.86
410326	AI388909	Hs.47650	CD37 antigen	3.70	8.72
427199	AL046851	Hs.153053	Utrichin-like protein FAT10777 - distal	3.69	6.38
442414	AF072069	Hs.67846	leukocyte immunoglobulin-like receptor, RAB5 interacting, kinesin-like (rabkin	3.65	5.40
412140	AA219691	Hs.73525	MAGE-like 2	3.64	5.82
424153	AA451737	Hs.141496	endothelin 3	3.64	5.52
421956	AI.035250	Hs.1438	lymphocyte cytosolic protein 2 (SP-2 doma	3.60	5.56
429732	U20158	Hs.2438	phorbol-in-like protein MDS019 (CEM15	3.59	4.35
421273	BE385828	Hs.250619	granulyan	3.49	7.38
421563	NM_006433	Hs.105806	baculoviral IAP repeat-containing 7 (liv	3.49	6.13
453837	AL138387	Hs.250126	ADAM-like disintegrin protease, decayin	3.48	4.23
424326	NM_014479	Hs.145236	integrin, alpha L (antigen CD11A (p180),	3.47	5.38
427247	AW504221	Hs.174103	ESTs	3.45	4.59
408838	AI695535	Hs.40369	CD100/2500/gp154/245/49eHNP_034610 1) hea	3.42	5.01
402829	X07871	Hs.89476	truncation (p50), sheep red blood cell	3.42	8.14
418918	AK000790	Hs.248385	hypothetical protein FLJ20783	3.40	4.36
429714	BE561801	Hs.2484	T-cell leukemialymphoma 1A	3.36	4.84
414324	Y14768	Hs.890	lymphotaxin beta (TNF superfamily, memb	3.35	4.45
421958	AA357185	Hs.109918	ras homolog gene family, member H	3.35	4.28
428231	AA334009	Hs.134847	interferon stimulated gene (ISG) 3	3.34	4.18
424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31	8.00
451736	AW008036	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.29	4.50
412790	NM_014767	Hs.74593	KIAA0275 gene product	3.28	5.42
404654	X08650	Hs.2438	Target Eson	3.28	4.28
430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.26	4.41
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	3.24	4.35
422846	BE313934	Hs.1583	myeloid cytosolic factor 1 (XND), chr	3.24	4.90
440655	AK03476	Hs.265331	hypothetical protein FLJ04955	3.20	2.21
440704	M69241	Hs.162	insulin-like growth factor binding prote	3.20	4.72
411088	BE247593	Hs.145053	ESTs	3.18	4.20
447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	3.18	4.89
413190	AA151882	Hs.40298	nitric oxide synthase complex 1, alpha 1	3.15	2.27
430017	AA283172	Hs.35	protein tyrosine phosphatase, non-recept	3.15	4.28
406837	R70292	Hs.156110	immunoglobulin kappa constant	3.12	4.09
409103	AF251237	Hs.112208	XAGE-1 protein	3.04	4.04
425706	AW406678	Hs.122559	hypothetical protein FLJ22570	3.04	4.28
447656	NM_033726	Hs.151026	src kinase-associated phosphoprotein of	3.03	3.03
427792	M63826	Hs.180841	tumor necrosis factor receptor superfam	3.01	4.82
402994	AF123659	Hs.33005	NM_002463? Homo sapiens myxovirus (infl	2.99	5.74
443276	AF123659	Hs.33005	truncation (p50), sheep red blood cell	2.97	5.07
449523	NM_000079	Hs.54443	chemokine (C-C motif) receptor 5	2.96	4.15
435237	AWA08158	Hs.318893	ESTs, Weakly similar to A47582 B cell g	2.96	5.81
436521	X57809	Hs.8997	immunoglobulin lambda locus	2.93	7.88
447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazarus	2.91	13.22
425322	J05068	Hs.2012	transcobalamin I (cyanin B12 binding pr	2.90	8.37

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448275	BE514434	Hs.20830	kinesin-like 2	2.87	4.15
423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	2.86	5.53
406782	AA403073		gb:zv2011.s1 Soares ovary tumor NbhOT H	2.81	4.60
414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	2.80	5.89
412819	T25829	Hs.24048	PC505 binding protein precursor	2.78	4.90
423886	BE159028	Hs.279704	chromatin accessibility complex 1	2.76	4.21
428380	NM_004271	Hs.184018	MD-1, RP105-associated	2.76	5.15
408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.76	4.30
416511	NM_005762	Hs.73536	Lysosomal-associated multiprotein membr	2.75	4.13
423530	AW072305	Hs.118110	bone marrow stromal cell antigen 2	2.74	5.05
428746	AW503820	Hs.192861	Sp1-G transcription factor (Sp1-1PU1 1 r	2.73	9.20
435953	AW408337	Hs.36972	CD7 antigen (p41)	2.72	4.38
407241	MA516		gb:human omega light chain protein 14.1	2.68	4.07
431669	AS29105	Hs.123164	ESTs, Weakly similar to match to ESTs AA	2.66	4.71
453779	N35187	Hs.43388	28kD interferon responsive protein	2.65	4.31
423874	WS4322	Hs.279651	melanoma inhibitory activity	2.64	4.15
410129	DE244074	Hs.58831	regulator of Fas-induced apoptosis	2.62	7.36
417508	AJF9076	Hs.94761	cytosolic phosphoglycylated alanine-rich C	2.62	4.43
418739	AA310964	Hs.88012	SHP2 interacting transmembrane adaptor	2.61	5.42
424625	AF207069	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-dio	2.60	9.69
417370	T28651	Hs.82630	tryptophanyl-tRNA synthetase	2.60	5.17
411358	RA7479	Hs.94761	KIAA1691 protein	2.59	4.01
425357	BE271188	Hs.165975	protein tyrosine phosphatase, receptor t	2.58	13.24
426470	AA528794	Hs.128644	ESTs	2.54	4.52
425535	AB007937	Hs.158287	KIAA0468 gene product	2.52	11.31
431629	AJ077325	Hs.265827	interferon, alpha-inducible protein (p10	2.50	7.80
423722	AB090976	Hs.97031	hypothetical protein MGC13047	2.49	4.25
428291	BE514505	Hs.289092	Homo sapiens cDNA: FLJ22303 fls, clone H	2.49	4.04
416426	AA180256	Hs.210473	Homo sapiens cDNA: FLJ14872 fls, clone PL	2.48	4.08
441959	AW194364	Hs.94814	ESTs, Weakly similar to FIG1 MOUSE FIG-1	2.48	5.15
416714	CA23770	Hs.79630	CD79a, antigen (immunoglobulin-associated	2.48	4.68
431186	NM_012249	Hs.250697	ras-like protein	2.46	6.04
417389	BE269964	Hs.82045	midkine (neurile growth-promoting factor	2.45	5.34
424481	R19453	Hs.1767	proteolipid protein 1 (Pelizaeus-Merzbac	2.43	6.57
425437	AW658917	Hs.184326	CD176 protein	2.42	4.96
427634	AJ389745	Hs.18449	hypothetical protein MGC10820	2.39	8.46
420842	AI083668	Hs.50601	hypothetical protein MGC10986	2.38	5.90
428289	M26301	Hs.2753	complement component 2	2.38	5.32
417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.37	6.99
413270	DE365206	Hs.853	interferon-epsilon protein, 15 kDa	2.34	4.88
433671	AW138797	Hs.132906	19kA2 protein	2.34	4.81
432403	AA550815	Hs.124840	ESTs	2.34	4.99
427759	BE245578	Hs.2200	perlefin 1 (pore forming protein)	2.32	4.55
419870	AW403911	Hs.256175	phosphoprotein associated with GEMs	2.30	4.22
421445	AA913659	Hs.104433	Homo sapiens, clone IMAGE-4054958, mRNA	2.30	6.18
401591			Target Exon	2.29	7.01
481708	AI306536	Hs.60975	ESTs	2.26	4.50
452700	AB595990	Hs.288940	five-span transmembrane protein MB3	2.24	4.90
424818	L29472	Hs.1802	major histocompatibility complex, class	2.22	5.40
409208	Y00093		integrin, alpha X (antigen CD11C (p150),	2.21	4.74
436456	AW292677	Hs.248122	G protein-coupled receptor 24	2.19	4.61
419741	NM_007019	Hs.53002	ubiquitin carrier protein E2-C	2.17	7.43
415446	L13210	Hs.79339	lectin, galactoside-binding, soluble, 3	2.16	5.58
438555	AJ222089	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	2.13	4.26
407260	L09095		gb:hm: sapiens mRNA fragment	2.13	4.00
448243	AW369771		integrin, beta 8	2.10	4.03
437638	AB560807		gb:wg:002.1 NCL CGAP_K612 Homo sapien	2.07	4.45
425802	DB7119	Hs.155418	GS3955 protein	2.06	4.36
414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	2.05	4.66
400261			Eos Control	2.04	4.22
423468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TfT3	2.02	4.23
416867	BE618731	Hs.80645	interferon regulatory factor 1	1.99	4.45
420626	AF043722	Hs.99491	RAS guanyl releasing protein 2 (calcium	1.99	4.42
424622	AF083811	Hs.7345	MD1 (mitotic arrest deficient, yeast, h	1.98	4.55
452923	BE276018	Hs.288940	five-span transmembrane protein MB3	1.96	4.54
452244	L03530	Hs.176674	ESTs	1.95	4.23
427239	BE270447		ubiquitin carrier protein	1.94	4.93
418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	1.94	5.28
431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	1.93	4.17
444090	S69115	Hs.10306	notch-like cell group 7 sequence	1.93	5.06
424067			Target Exon	1.92	6.16
426890	AA383167	Hs.41294	ESTs	1.91	4.23
453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	1.91	4.01
401914			Target Exon	1.87	4.76
448499	BE613280	Hs.77550	hypothetical protein MGC1780	1.87	1.17
439627	BE621702	Hs.29076	hypothetical protein FLJ21841	1.85	6.59
425923	NM_005026	Hs.162808	phosphoinositide-3-kinase, catalytic, de	1.85	4.03
416819	U77735	Hs.80205	prn-2 oncogene	1.84	4.57
425069	AA687465	Hs.230194	potassium voltage-gated channel, shaker-	1.84	5.40
430378	T25572	Hs.2556	tumor necrosis factor receptor superfam	1.78	4.02
439568	AW161481	Hs.111577	integral membrane protein 3	1.76	5.25
410423	AA402432	Hs.63489	protein tyrosine phosphatase, non-recept	1.75	4.30
434224	AA380731	Hs.84	interleukin 2 receptor, gamma (severe c	1.74	4.91

413066	AW004051	Ha_285814	sprouty (Drosophila) homolog 4	1.71	6.00
431048	BE387620	Ha_23489	lactate dehydrogenase B	1.70	3.34
410068	AW53388	Ha_58435	FYH-binding protein (FYB-120130)	1.69	4.04
437696	Z83844	Ha_5780	hydraconin protein dJ37E-10	1.66	5.96
423884	AF153825	Ha_135713	pre-B lymphocyte tyrosine-3	1.64	2.30
426666	AW005131	Ha_171763	CD22 antigen	1.63	3.33
409098	Z25437		glt-H2apases protein-tyrosine kinase gen	1.62	7.19
440087	W29895	Ha_7718	hydraconin protein FLJ22678	1.61	4.33
421859	AA355520	Ha_108967	KIA0222 gene product	1.59	4.30
415198	AW005480	Ha_943	nasal viller cell transcript 4	1.56	1.12
406827	AA871409		gltap264.51 NCI CGAP Lu5 Homo sapiens	1.55	4.29
413699	X14034	Ha_75648	phosphatase C, gamma 2 (phosphatidylethanolamine-specific)	1.53	4.63
458066	AL161999	Ha_77324	neuronic translation termination factor	1.52	4.11
433202	D6047	Ha_250679	EST_1, highly similar to CTXAR RAT, CORTED	1.52	4.36
440906	Z25424		glt-H2apases protein-tyrosine/threonine kin	1.50	8.67
443889	D28423		glt-Human mRNA for pre-mRNA splicing fac	1.49	5.07
437193	BE90832	Ha_134729	FX1D domain containing on transport reg	1.48	4.50
440174	AA091724	Ha_180258	hydraconin protein FLJ21096	1.46	4.91
448143	AF039704	Ha_20478	ceroid lipofuscinosis, neuronal 2, late	1.43	4.26
451524	AK001466	Ha_25516	hydraconin protein FLJ10604	1.43	4.74
417287	AB31878	Ha_285714	HLA559 protein	1.41	4.01
435665	AW903880		ATPase, H+ transporting, lysosomal (vacuo	1.38	1.07
420343			Target Ester	1.36	8.89
407239	AA076350	Ha_67846	Isotachylin immunoglobulin-like receptor,	1.32	4.57
436655	AW407157	Ha_8997	Immunoglobulin lambda kappa locus	1.30	4.00
422634	BE234189	Ha_122492	hydraconin protein	1.30	4.37
425960	BE270707	Ha_8563	similar to APOEC1	1.26	4.48

TABLE S7B:			
Play:	Unique Ent. probeid identifier number		
Ref:	Gene cluster number		
Accession:	Genbank accession numbers		

Play	CAT Number	Accession
438619	318214_1	AW_015876 AW023773 AW76551 AW047577 AW167523 AW467338 BF000570 AB184966 H2451 AL043306 BF476138 BF593363 AA132787
		AL17248 AB06795 AA151317 T59529 AW093544 AW032331 N7951 AT769860 AB1458 AW20506 AB00679 A04173 AL459902 BE327641
		AB06852 AF254736 AC020433 AT744145 AT73281 AA027842 LS2583 AL52492 BF947764 BF34077 BF478700 BG99356 NS3455 N21027
		AL15676 N35991 AA682453 AA678243 AA149374 AL12582 T15981 H99988 N40717 H959402 AC20751 BF790328 AT142005 T95793 H92400
		BS6632 HT218 HT1231 AC020433 AW040688 BS4266 F1422
		AA054108 BC019055 AA187684 BG655226 BM02232 AT23311 AA263481 AC239831 BM021463 AL434333 AJ31577 AL129580 AW262782
		AA132758 BC223515 AA14342 AW055636 AB89725 AA975268 BM021207 AB090074 AC217842 NB0581 AB179119 AB002259
		AC028414 A074114 AA165536 BF051677 AW194318 AA191700 W9430 AB1042984 AC090571 AC043486 AW020058 B149103 B149071 B149121 RA1226
		BM3633 F0425 C02343 AA115926 BA15222
		AA045946 AW69616 AA185222 AL050110 AW155742 AT229494 BF453447 AB059452 AB358424 AB358424 AB071421 BM491497
		AB94413 AA994700 AB91264 N73548 AB020055 AW211652 W24196 W24182 AT19718 BA004658 AW010120 AW15394 T79755 AA68043
		AT070339
		AA430373 AB968771
		AK074047 A14342 AW014280 BM145128 B28267 AW206231 AA189041 H93197 AW594063 BG232696 AW236606 AW081031 AA1765843 BM14437
		AA289341 AB182483 AB96370 AB371691 AB196330 BA247526 BM148789 BF85364 BF891946
		BF156513 AA1479726 BE022314 AL134933 BE000305 BE006312 BE006296 AA04582 AW544656 AA234175 AA043096 BE006033 B237669
		BE006157 BF326759 BF347959
		U1454 AA48211 H76801
		BF051188 AC02552 T8281 A020501 T23235 RG0506 RG7840 AW9611 A013349 W37181 AA1180029 AW025562 AB088777 AA85975 BF172457
		BF701514 A141346 AB050434 AB09062 AB87135 AA150685 AB67273 AB093807 AB150339 AB126688 AA048892 AC35094 AA396442
		AW028416 A59007 BF159902 N01208 AA203144 AA148964 H00032 R07040 BF86660 AB096677 BF1971573 AW96761 A3031819 AA251875
		AB085898 AB15225 AB44499 A020071 A123322 AW150299 AW270905 A1406420 H63488 T2448

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5	400860	8757499	Minus	151830-152104,152643-152744
	402994	2996643	Minus	4727-4969
	401591	9966977	Minus	55410-55835
	404687	3282162	Plus	1415-2071
	401614	5395230	Plus	62537-62645,63153-63308
	403043	7768753	Minus	314423-316252

TABLE 58A. ABOUT 183 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE

Table 58A lists about 183 genes upregulated in melanoma metastases from patients with limited disease relative to melanoma metastases from patients with progressive disease. Genes were selected from 59680 probesets on the Affymetrix Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Key: Unique Exon: Exon number, Genbank accession number
 Exon#: Exon number
 UnigenID: Unigen number
 Unigen Title: Unigen gene title
 R1: 90th percentile of AIs for metastases from patients with limited disease divided by 90th percentile of AIs for metastases from patients with progressive disease
 R2: 90th percentile of AIs for metastases from patients with limited disease divided by 90th percentile of AIs for metastases from patients with progressive disease, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

	Probe	Exon	UnigenID	Unigen Title	R1	R2
25	419568	AW557684	Hs.306814	hypothetical protein FLJ21899	12.74	12.92
	447414	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	7.66	5.88
	412859	AW753865	Hs.74376	olfactomedin related ER localized protein	7.23	5.76
	430154	AW683698	Hs.234726	serine (or cysteine) proteinase inhibitor	6.91	14.26
30	414430	A346201	Hs.75118	ubiquitin carboxyl-terminal esterase L1	6.86	7.10
	426485	X59135	Hs.156110	immunoglobulin kappa constant	6.85	6.81
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	6.73	11.21
	430822	AIJ050371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	5.53	4.63
35	414626	AA190266	Hs.210473	Homo sapiens cDNA FLJ14872, clone PL	5.48	7.06
	423858	AL137326	Hs.133483	Homo sapiens mRNA; cDNA DKFZ434B0650 (f	5.27	5.94
	433658	LC0678	Hs.156110	immunoglobulin kappa constant	4.78	3.07
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	4.68	3.27
40	413816	N48613	Hs.75515	apoptosis protein C-8	4.62	4.62
	407825	NM_005162	Hs.40202	lymphoid-restricted membrane protein	4.55	3.12
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.31	4.15
	409060	A015687	Hs.50130	necdin (mouse) homolog	4.23	3.44
45	401194			Target Exon	3.89	3.19
	447471	AF039843	Hs.185676	spodoptera (Drosophila) homolog 2	3.68	2.43
	419628	H67546	Hs.49768	ESTs	3.66	4.16
	414863	AW131473	Hs.106105	rat guanine nucleotide dissociation stim	3.63	2.81
50	402315	NM_004920	Hs.128316	apoptosis-associated tyrosine kinase	3.47	3.06
	424745			NM_005113 Homo sapiens serpinH4 synth	3.47	3.43
	425283	NM_003837	Hs.169138	lysine oxidase (L-lysine oxidase)	3.42	1.96
	442117	AW664964	Hs.128859	ESTs; hypothetical protein for IMAGE-447	3.41	2.89
55	411763	AW862589		gb CVO-CT0387-18300-167-a07 CT0387 Homo	3.37	6.31
	402307			C180005037.g0922165069P_060080.1) h	3.34	3.74
	424775	AB014540	Hs.153026	SWAP70 protein	3.30	2.00
	424036	AA770688		H2A histone family, member L	3.30	3.16
60	453464	A1804911	Hs.32699	receptor (calcitonin) activity modifying	3.30	5.58
	401739			NM_005622 Homo sapiens SA (rat hyperten	3.30	3.23
	440274	R24585	Hs.7122	scapic responsive protein 1	3.27	2.47
	413388	D21262	Hs.75337	nucleolar and coiled-body phosphoprotein	3.26	2.61
65	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ12425 fs, clone C	3.26	2.58
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ne	3.14	4.04
	426655	Z11894	Hs.156110	gb Hsapiens rearranged mRNA for immunog	3.13	2.38
	453807	AL080235	Hs.35961	DNF2P86E1621 protein	3.13	4.27
70	404405			Target Exon	3.11	4.69
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.11	2.10
	443247	BE514387	Hs.333893	c-Myc target JP01	3.10	2.26
	403417	X72495		Target	3.08	2.32
75	401512			NM_014080 Homo sapiens dual oxidase-like	3.07	2.87
	423242	AL039402	Hs.125783	DEME-6 protein	3.06	2.78
	417501	AL041219	Hs.82222	sera domain, immunoglobulin domain (Ig)	3.06	2.81
	451952	A122172	Hs.301663	ESTs	3.05	2.65
80	427419	NM_000200	Hs.177888	histatin 3	3.05	4.24
	406663	U24683		immunoglobulin heavy constant mu	3.05	4.55
	442104	L20971	Hs.188	phosphodiesterase c 4B, cAMP-specific (dun	3.03	1.90
	451983	AA785776	Hs.122863	ESTs	3.02	1.71
85	421097	A180112	Hs.125522	Homo sapiens cDNA FLJ13266 fs, clone OV	3.01	3.11
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	3.00	3.47
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	3.00	2.22
	400237			NM_007057 Homo sapiens angio-associated	2.98	2.43
90	414063	H06904	Hs.75736	apoptoprotein D	2.97	3.76
	426153	AF057189	Hs.182771	vitelliform macular dystrophy (Best disc	2.94	2.38
	414781	D50917	Hs.77293	KIAA0127 gene product	2.94	2.88
	445823	AA178563	Hs.145519	FKS087 protein	2.92	1.98
95	404439			ENS0000000222 Mitochondrial 28S rlos	2.92	2.57
	421218	NM_004049	Hs.72912	cyclophilin P450, subfamily I (aromatic c	2.90	2.47
	402350	AA046896	Hs.86269	Homo sapiens, clone MGC-17339, mRNA, com	2.90	3.87
	424855	AW204725	Hs.25560	ESTs	2.89	2.61
100	436700	AI693690	Hs.301406	hypothetical protein PP3501	2.88	3.63

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451131	A267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain
427157	U51166	Hs.173824	thymine-DNA glycosylase
402273			Target Exon
414135	NM_004419	Hs.2128	dual specificity phosphatase 5
435643	AW910965	Hs.287425	MEGF10 protein
451979	P06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX)
405642	AJ245210		gb:Human sapiens mRNA for immunoglobulin
407360	X13075		gb:Human Zs12 mRNA for kappa-immunoglobulin
405441			Target Exon
450916	BE271927	Hs.87385	ESTs
435675	AA694059	Hs.266820	ESTs
426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial)
441623	AA315605		desmoglein 2
413336	AI639306	Hs.256178	hypothetical protein FLJ122637
408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA
437740	AA810265	Hs.122515	ESTs
426322	J05088	Hs.2012	transcobalamin I (vitamin B12 binding pr
411652	AAS28140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti
428422	AI557280	Hs.184270	capping protein (actin filament) muscle
426793	X98987	Hs.172350	HR (histone cell cycle regulation defec
401454			NM_014226*Homo sapiens renal tumor anti
450825	AW341123	Hs.120275	ESTs
407705	AB023130	Hs.37892	KIAA0522 protein
416782	L35035	Hs.75986	ribicose 5-phosphate isomerase A (ribicose 5
449151	AI632331	Hs.196038	ESTs
433454	N52481		gb:cb12g12.s1 Soares_fetal_jung_NJHL19W
401009			Target Exon
427227	AF103803	Hs.283690	hypothetical protein
405268			ENSP00000223174*KIAA0783 PROTEIN.
410265	AA741357		nidogen (enadin)
435905	AW997484	Hs.5903	KIAA0456 protein
436378	Z26572	Hs.2596	tumor necrosis factor receptor superfamily
457423	AK000942	Hs.265018	hypothetical protein FLJ20635
448752	AA593867	Hs.300842	KIAA1605 protein
414931	AK000342	Hs.77546	Homo sapiens mRNA; cDNA DKFZp761M0223 (f
441285	AA927670	Hs.131704	ESTs
439352	BE614347	Hs.169615	hypothetical protein FLJ20989
421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran
406678	UT7534		gb:Human clone IA111 Immunoglobulin varia
430276	AI673074	Hs.116557	ESTs, Weakly similar to T22914 hypotheti
425970	AK001500	Hs.165186	hypothetical protein FLJ13852
407363	AF035032	Hs.8997	gb:Human sapiens clone MCA11 myosin-react
408367	AK001178	Hs.44424	homolog of rat orphan transporter v7-3
420103	AA382259	Hs.95197	aldelyde dehydrogenase 1 family, member
418635	L11329	Hs.1183	dual specificity phosphatase 2
451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ADC1
430354	AA954810	Hs.239784	human homolog of Drosophila Scribble
405701			ENSP0000004964*Adenovirus (Scindens).
433427			cholesterolphosphatransferase 1
401965	AI816449	Hs.171889	CGH-148 protein
417866	AW067903	Hs.82772	collagen, type XI, alpha 1
428142	NM_001308	Hs.2246	carboxypeptidase N, polypeptide 1, 50kD
422103	AA984330	Hs.111676	protein kinase H11, small stress protein
425746	NM_001701	Hs.156440	zinc acid Coenzyme A: amino acid N-acyl
404855			NM_018943*Homo sapiens tubulin, alpha-1
401127			Target Exon
406161			Target Exon
421654	AW163267	Hs.106489	suppressor of var1 (S. cerevisiae) 3-like
406632	AB005638		gb:Human sapiens mRNA for HRV Fab N31-VH,
447940	D66982	Hs.20060	KIAA0229 protein
411773	NM_006799	Hs.72026	protease, serine, 21 (bestatin)
413211	AW957107	Hs.109292	hypothetical protein MGCA365
425722	AI659076	Hs.97031	hypothetical protein MGCI3047
437044	AL035864	Hs.69517	differentially expressed in Fanconi's an
436420	AA443966	Hs.31595	ESTs
414809	AA24699	Hs.77358	transferrin receptor (gp90, CD71)
423400	AI571364	Hs.126382	Homo sapiens mRNA; cDNA DKFZp76111224 (f
427923	AW274357	Hs.301406	hypothetical protein PP3501
406652	AW150304	Hs.277477	major histocompatibility complex, class
433624	AF216942	Hs.24889	formin 2
406552	NM_014638	Hs.5216	HSPC028 protein
408204	AA454501	Hs.43666	protein tyrosine phosphatase type IVA, m
402728			C1002541*gi4758590*rat(NP_004249.1) im
420932	AW374605	Hs.116607	ESTs, Weakly similar to T21697 hypotheti
435559	AN028620	Hs.263614	ESTs
400278			ENSP00000043264:Dolichyl-diphosphoketos
425751	T19239	Hs.1940	crystallin, alpha B
402737	L08096	Hs.99999	CD70; tumor necrosis factor (ligand) s
410006	AW732308	Hs.57763	ribosomal translation initiation factor
454429	BE272437	Hs.301406	hypothetical protein PP3501
426321	BE046490	Hs.180677	zinc-finger protein 162
402897			NM_022068*Homo sapiens sialoadhesin (SN
423639	AB037826	Hs.130411	KIAA1405 protein

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5	448848	AF131851	Hs.22241	hypothetical protein	1.65	4.27
	414420	AA043424	Hs.76095	immediate early response 3	1.60	3.02
	440747	AW972226	Hs.137840	ESTs, Moderately similar to SIX4_HUMAN H	1.56	3.28
	465635	AK003954	Hs.25237	mesenchymal stem cell protein DCS075	1.55	3.73
	402252			NM_004551* Homo sapiens: ubiquitin specifi	1.55	3.26
10	411825	AK000334	Hs.300463	hypothetical protein FLJ20327	1.55	3.18
	414328	Z21566	Hs.300463	acetylase 2, mitochondrial	1.52	4.03
	400263			Eos Control	1.51	3.42
	421552	AF026692	Hs.105700	secreted ficolin-related protein 4	1.50	3.19
	436673	AF120191	Hs.5268	hypothetical protein FLJ10479	1.49	3.33
15	404739			Target Exon	1.49	3.10
	433344	BE387725	Hs.343411	DEAD(H) (Asp-Glu-Ala-Asp) like box polyep	1.46	3.42
	421695	AF035306	Hs.108959	Homo sapiens clone Z21771 mRNA sequence	1.44	3.15
	425240	AA388405	Hs.1869	phosphoglucomutase 1	1.44	3.04
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	1.43	3.71
20	434642	W25739	Hs.73165	chromobox homolog 5 (Drosophila HP1 alpha	1.42	3.07
	404406			Target Exon	1.42	3.87
	433320	D00547	Hs.250879	ESTs, Highly similar to CTXN RAT CORTEXI	1.41	3.80
	447697	W52125		tubulin alpha 1	1.40	4.45
	415780	U75989	Hs.78846	heat shock 27KD protein 2	1.40	3.28
25	447216	R75812	Hs.165248	p13NTR-associated cell death executor, o	1.39	3.77
	401772			NM_014520 Homo sapiens MYB binding prote	1.39	3.67
	413031	BE515951	Hs.75150	phosphohistidine kinase, muscle	1.38	3.31
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	1.37	3.17
	428011	BE367514	Hs.181418	KIAA0152 gene product	1.37	3.05
30	445880	AF167512	Hs.12912	shRNA (S. pyrae) homolog	1.35	3.11
	436703	AW089614	Hs.145818	RNA binding motif protein, X chromosome	1.34	3.05
	438277	AL022326	Hs.6139	synaptotagmin 1	1.34	3.09
	451481	AA300228	Hs.256866	hypothetical protein DKFZP434K1923	1.32	3.23
	421818	AW692976	Hs.50058	NM_024858 Homo sapiens NADH dehydrogenas	1.31	3.01
35	412968	AW502508	Hs.75102	staphylococcal synthetase	1.28	3.58
	452378	AA025655	Hs.19597	KIAA1854 protein	1.25	3.08
	447455	H08335	Hs.6750	Homo sapiens mRNA for FLJ00058 protein,	1.24	3.45
	422212			KIAA0430 gene product	1.21	3.03
	428773	BE258238	Hs.193163	bridging integrator 1	1.20	3.20
40	450087	U79458	Hs.231840	WW domain binding protein 2	1.18	3.03
	418289	AW403103	Hs.83951	Hermansky-Pudlak syndrome	1.17	3.32
	405752			Target Exon	1.00	3.40
	422836	AL037365	Hs.194093	AKAP-binding sperm protein roppurin	1.00	3.00

TABLE 58B:

Play: Unique Eos probe/identifer number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

45	Play	CAT Number	Accession
	400275	16707_1	NM_006513 BC009309 X01257 BC000716 BM450041 B1771139 AW10955 AW120415 AW141719 AW21081 BE40928 AW141397 AW122238
			BC256188 BC368217 AW143398 AW133780 AW133074 BC531086 BE256825 BE454320 AW140344 AW76120 AW12842 AW143343 BE273054
			BG473378 BE288163 B072260 BE167354 AW140124 BE277005 BG746716 BE164969 AW161287 AV762084 BC696945 AW16817487 A313975
			AW749196 BE341428 BM011248 AW098465 AW238868 BG400951 BG284599 AW1004031 AA378483 A04914 AL513323 AL540818 AW1537282
60			AL572817 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW140308 B1262249 BG284713 AA659594 A0935882 AW658546
			AA652206 AS680744 AA654357 AW146982 AW127447 AW157450 BC603509 AW878624 AB18522 AA703707 BE452673 AL515504
			AW156882 AA631254 AA208521 AB088022 AA648454 AW108691 BF382616 AA648464 BC261351 AW035994 BG442820 AA532698 W56955 AW182900
			W313340 AW407364 C17924 C18528 AU299318 BF154399 BG319570 BF764242 BF764209 AC820202 T06029 BF47193 F72685 AL58849 B133075
			BF743602 BE518230 BE28139 BF036434 BE562718 BG74381 AA659833 AA297649 AA010945 BG405552 BE289205 T32823 BG015619 AW181585
65			AL517118 AL538396 AW069881 AL581975 AW152041 W26586 BE161609 A068306 BC257663 BT782656 ABA44580 AA055570 BE161906 C17428
			AQ42744 H03345 HB5743 BF752508 AW057940 B081399 AW075179 AA039536 H08712 W55445 AL515438 W337117 HB5514 T85373 W33369
			AWR62589 AW60959
			NM_033445 BC001153 AB85781 BF794032 AA476620 AA810506 AA810905 AI291244 AB850597 AJ397078 AJ335620 BF7396 J344589 AJ303377
			AF447566 AW771833 BE456261 AC004068 AD54452 A1648505 A1918342 AG28670 AA88580 AL51029 AA886344 A186419 BC325906 BM045465
70	400237	9484_1	BC011422 AW106572 NM_010187 BC020044 BC008809 AL542809 AL522027 AL517616 AL539615 AL555640 AL548094 AL528959 AL555071 BB85185
			B1002907 AU120890 BE257146 AW707985 B011155 DG575776 BE302895 BE271499 BE389232 AL533354 BC39814 BG829179 BE348687
			BE73814 BG1746912 BG425149 AL047913 BE290277 BG1160056 AW410799 BG478074 BG471558 BF813185 AA016192 BG334833 BE383857
			AQ218784 AL517615 B102267 BE675719 AW161032 AW410600 AW144268 A215124 AW257235 AW141438 BE205773 AA33920 A0572200
			AA669173 AS684056 AA742466 AW052003 BE58669 B789274 AC103312 A028567 F28193 BE92573 AL035407 AA603722 AA19246
75			AW405597 BF445723 AA411804 AA774757 BG152509 AL032444 BF056147 AB789460 AA107194 D0610 AL032357 W56781 A301243 AB88048
			AL501917 AL542808 BE300552 AA143563 AL567123 AA553412 AA547999 AW262487 AW027349 AW469544 BE300553 A1687352 BG222716
			AW146823 AA647176 AA72493 AB88782 AL530431 A1583915 AW158328 BB857710 C00178 AW130066 A1312650 AW071671 AW17658 BF616236
			BF154592 BE221500 W48855 T54102 AB08100 AW100155 AA561278 AL581055 BE596475 BM013215 AC109977 AW38177 AA381776 AA38176 AA381486
			BF915382 BE457391 AA330239 BF4711939 BF37403 BG740295 AL567952 AL517817 BE325059 BF032720
80	406642	0	AJ425210 AJ245212 AJ245211 AJ245213
	441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706565 BE708678 AA723159 BE153169 BE706729 BE706558 BE153162 BE706706 AW371853
			AU271846 BE153241 A021032 A021031 A021030 AW002300 BE219837 BE501576 BE501724 A1742222 AA023594 AA58424 AA05373
			AJ28894 AB84563 AA040325 N02562 A05802 AW241694 AA038448 A067201 A081839 AA576391 A081784 AW185932 W37445 AA512994
			AZ77548 HB9551 AB959714 HB9385 AA315805 AW595796 EC014584 BC014581 AW780125 AB72414 BE32815 AW069197 BF103106 AW127758
85			AW146823 AA345675 BE375779 H028241 D25318 BF450013 BE794688 BF110262 AA528775 W53757 BE041544 AW66504 AM126522 DM126522
			AW122760 BE718200 AW867496 AA149420 BE705307 BE530396 BE748765 A1373653 R705979 BF79185 BF591364 BG495595 B019458 BE705702
			BC495559 BF244333 BC494800
			N02481 AW074508 AA553478 AW974058 AW75294
			BC402852 B054066 AA150252 AL036760 AA454480 AK033256 W58776 W03372 N31248 A052219 A1367635 W65374 N88510 R58194 B152464
90	433464	101599_1	AF497111 BF340043 A126298 AC979398 A1056640 AA124241 A042150 AW144993 AA003148 A181180 A419420 A1356058 BF6183243 AC49330 A131248
	410295	2817_1	W76547 BF47710 AW059153 BF994549 AW682626 AA054518 B03710 AW147491 AW147491 AC032146 AW062239 AW062273 A124546 A336371

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Table S5A lists about 201 genes upregulated in melanoma metastases from patients with progressive disease relative to melanoma metastases from patients with limited disease. Genes were selected from 59680 probesets on the EuzalAffymetrix Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Probe Unique Euzal probe set identifier number
Accession Accession number, Genbank accession number
UnigeneID Unigene number
Unigene Title Unigene gene title
R1: 90th percentile of AIs for metastases from patients with progressive disease divided by the 90th percentile of AIs for metastases from patients with limited disease
R2: 90th percentile of AIs for metastases from patients with progressive disease divided by the 90th percentile of AIs for metastases from patients with limited disease, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

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Probe	Accession	UnigeneID	Unigene Title	R1	R2
422168	AW32914	HS.121408	S100 calcium-binding protein A7 (psorias)	8.58	13.77
448965	AW32914	HS.86149	phosphoinositide 3-kinase-binding protein	7.43	5.91
440099	AL080058	HS.6909	DKFZP564C202 protein	7.07	4.56
431211	M86849	HS.323733	gap junction protein, beta 2, 290d (conn)	6.91	3.51
422059	AW468397	HS.100000	S100 calcium-binding protein A6 (calgran)	6.90	6.44
418067	AI127558	HS.83393	cystatin EMI	6.62	10.34
422166	W72424	HS.112405	S100 calcium-binding protein A9 (calgran)	6.47	13.26
409632	W74001	HS.55279	serine (or cysteine) proteinase inhibitor	6.25	3.41
401780			NM_005537 Homo sapiens keratin 16 (foca)	6.10	4.24
431751	NM_005846	HS.331555	serine protease inhibitor, Kazal type, 5	5.97	6.60
422511	AU076442	HS.117938	collagen, type XVII, alpha 1	5.89	3.57
412636	NM_004415		desmoplakin (DPI, DPL)	5.82	3.51
417124	BE122762	HS.26338	ESTs	5.16	3.16
432665	NM_001042	HS.2633	desmoglein 1	5.03	3.57
421733	AL119671	HS.1420	fibroblast growth factor receptor 3 (ach)	4.84	4.15
421922	AA305159	HS.113019	Itih45	4.79	4.59
407366	AF028942	HS.17518	g0 Homo sapiens cig33 mRNA, partial sequ	4.33	2.37
422493	AL134708	HS.145698	ESTs	4.28	4.79
456525	AW468397	HS.100000	S100 calcium-binding protein A8 (calgran)	4.23	4.82
409010	AU648675		Homo sapiens, similar to RIKEN cDNA 1700	4.23	3.69
410748	BE363816	HS.12532	chromosome 1 open reading frame 21	4.11	2.33
409760	AA302840		g0:EST10034 Adipose tissue, white 1 Homo	4.05	3.65
424670	W61215	HS.116651	epithelial Na ⁺ channel 1	4.02	4.07
417366	BE185289	HS.1076	small proline-rich protein 1B (cornelin)	3.97	4.71
418663	AK001100	HS.41690	desmocollin 3	3.95	5.08
402075			ENSP00000251056 Plasma membrane calcium	3.93	5.85
422330	L22524	HS.22556	matrix metalloproteinase 7 (matrilysin,	3.90	3.19
427809	ME2630	HS.183978	lipoprotein lipase	3.87	3.21
413859	AW992356	HS.8364	Homo sapiens pyruvate dehydrogenase kinase	3.85	5.75
431048	R50253	HS.249129	cell death-inducing DFFA-like effector a	3.80	3.10
431369	BE184456	HS.251754	secretory leukocyte protease inhibitor (3.79	3.36
427485	AA243499	HS.104800	hypothetical protein FLJ10134	3.67	3.35
429652	AB010446	HS.225948	small inducible cytokine subfamily A (C)	3.65	4.14
418686	Z36830	HS.87268	annexin A8	3.65	3.62
448429	D17408	HS.21223	calponin 1, basic, smooth muscle	3.64	3.18
422963	MT9141	HS.13234	ESTs	3.60	4.10
428874	W32133	HS.194366	transferrin (prealbumin, amyloidosis t	3.58	3.97
401785			NM_002275 Homo sapiens keratin 15 (KRT1	3.58	5.05
454117	BE410100	HS.40368	receptor related protein complex 1, alpha	3.56	1.92
419329	AY007220	HS.289908	S100-type calcium binding protein A14	3.54	5.62
424012	AW368377	HS.137569	tumor protein 63 kDa with strong homolog	3.53	4.70
417515	L24203	HS.82237	ataxia telangiectasia group D-associated	3.52	8.33
430376	AW292053	HS.12532	chromosome 1 open reading frame 21	3.51	2.32
454229	AW957744	HS.276469	liver and prostate rich protein	3.50	3.12
401781			Target Exon	3.45	3.57
409000	L11690	HS.196889	bullous pemphigoid antigen 1 (230/240kD)	3.45	5.07
431567	N51357	HS.260855	Homo sapiens cDNA: FLJ21410 fis, clone C	3.44	5.03
419648	T73661	HS.91677	thyroid hormone responsive SPOT14 (rat)	3.42	7.72
414708	A226323	HS.97411	hypothetical protein M201235	3.41	2.65
442315	AA173992	HS.7956	ESTs, Moderately similar to ZNF1_HUMAN Z	3.41	5.03
442498	U54017	HS.8364	Homo sapiens pyruvate dehydrogenase kinase	3.32	2.86
410883	DK3767	HS.65742	CCL17 chemokine (TARC) (SCYA17)	3.28	3.18
418026	BE379727	HS.83213	liver and adipose binding protein 4, adipocyte	3.26	3.10
453309	AU91809	HS.32949	desferin, beta 1	3.24	3.64
420763	AI659838	HS.59923	lectin, galactose-binding, soluble, 7	3.21	3.64
409601	AF237621	HS.80828	keratin 1 (epidermolytic hyperkeratosis)	3.19	4.37
413163	Y00818	HS.75216	protein tyrosine phosphatase, receptor 1	3.15	3.16
452101	T60298	HS.10844	Homo sapiens cDNA: FLJ114475 fis, clone MA	3.15	3.60
412633	AF001691	HS.74304	periphrin	3.15	3.98
407839	AA045144	HS.161566	ESTs	3.15	4.11
427318	AF186081	HS.175783	zinc transporter	3.11	3.53
427899	AA826286	HS.332053	serum amyloid A1	3.10	3.53
421948	L42583	HS.334309	keratin 6A	3.08	2.75
452744	AU267652	HS.246107	Homo sapiens mRNA, cDNA DKFZP454C082 (f)	3.05	2.59
410001	AB041036	HS.57771	kallikrein 11	3.04	3.02
413435	X51405	HS.75360	carboxypeptidase E	2.40	3.00
428500	AB15395	HS.184641	fatty acid desaturase 2	2.98	5.22
410099	AA081630		KIAA0036 gene product	2.97	2.85
437679	NM_014214	HS.5753	inositol (myo)-1-(or 4)-monophosphatase 2	2.93	3.45
413835	A272721	HS.249193	fatty acid hydroxylase	2.53	4.78

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446068	AL049801	Hs 13649	Novel human gene mapping to chromosome 13	2.89	2.93
450680	AF131784	Hs 25318	Homo sapiens clone Z5194 mRNA sequence	2.88	3.14
478398	AF249368	Hs 98558	ESTs	2.80	2.05
474433	BE270266	Hs 82128	5T4 oncotelet lipophilic glycosphingolipid	2.86	2.12
427919	AA173942	Hs 325416	Homo sapiens mRNA: cDNA Z0564H1916 (t	2.98	2.98
412676	NM_000165	Hs 74471	gap junction protein, alpha 1, 43kD (con	2.83	2.82
426955	A035647	Hs 189959	putative receptor (family a group 5)	2.83	2.37
446989	AF001898	Hs 16740	hypothetical protein FLJ11036	2.82	2.73
428471	X07348	Hs 104530	stathmin	2.79	3.15
416305	AL076628	Hs 79187	coxsackie virus and adenovirus receptor	2.79	2.72
433147	AF091434	Hs 43080	platelet derived growth factor C	2.77	1.70
412326	R07956	Hs 73817	small inducible cytokine A3 (homologous	2.76	2.18
425787	AA353867	Hs 155029	ESTs	2.75	2.42
450172	NM_005864	Hs 24587	signal transduction proteins (SH3 contain	2.75	2.36
421773	W69233	Hs 112457	ESTs	2.73	5.59
408536	AW381532	Hs 135108	ESTs	2.73	5.17
437143	AW204056	Hs 6917	ESTs	2.72	1.84
452862	AW070865	Hs 9687	ADAMTS2 (a disintegrin-like and metallo	2.70	1.82
418394	AF132818	Hs 84728	Kruppel-like factor 5 (intestinal)	2.69	4.62
410325	AB023154	Hs 62264	KIAA0037 protein	2.69	2.32
447184	AF028941	Hs 17518	viperin, similar to inflammatory respon	2.69	3.74
444984	H15474	Hs 132058	lally acid dehydratase 1	2.67	2.36
434727	H43374	Hs 78950	Homo sapiens mRNA for KIAA1671 protein,	2.65	1.78
420876	AA918425	Hs 177744	ESTs	2.64	7.26
428106	AB678765	Hs 21812	ESTs	2.64	2.51
411917	AF052107	Hs 90737	Homo sapiens clone Z3629 mRNA sequence	2.64	2.66
409509	AL036923	Hs 322710	ESTs	2.62	2.09
426354	NM_004010	Hs 169470	dystrophin (muscular dystrophy, Duchenne	2.62	2.68
432503	AA551196	Hs 188952	ESTs	2.62	4.64
403341	AB963376	Hs 12532	chromosome 1 open reading frame 21	2.62	1.74
421116	T19132	Hs 101850	retinol-binding protein 1, cellular	2.62	2.62
456247	R09746	Hs 10927	glycyl(27010)1 Scores fetal liver spleen	2.61	3.43
414217	AI309258	Hs 278986	Homo sapiens cDNA: FLJ23165 fs, clone L	2.60	3.84
438706	AW672627	Hs 59761	ESTs, Weakly similar to DAPI_HUMAN DEATH	2.58	3.40
440859	AF134160	Hs 7327	cladin 1	2.57	3.59
459710	AF101596	Hs 121592	ESTs	2.57	3.59
430937	XS3463	Hs 2704	glutathione peroxidase 2 (gastric/intestin	2.56	3.35
433882	U90441	Hs 3622	procollagen-proline, 2-oxoglutarate 4-di	2.51	3.75
427666	AF91495	Hs 160142	catinulide-like sh1n protein (CLSP)	2.51	3.02
431103	ME7399	Hs 44	pleiotrophin (heparin binding growth fac	2.51	3.53
449550	AA353125	Hs 184721	ESTs	2.43	4.22
424675	NM_005512	Hs 151641	glycoprotein A repetitions predominant	2.40	6.22
442800	H30871	Hs 8071	KIAA0735 gene product, synaptic vesicle	2.38	3.14
427122	AW057736	Hs 323910	HER2 receptor tyrosine kinase (erb-b2,	2.36	3.59
429039	NM_004065	Hs 94561	autotransferase family, cytosolic, 26,	2.36	2.91
412477	AA150864	Hs 29955	microsomal glutathione S-transferase 1	2.34	4.15
450693	AW450461	Hs 203965	ESTs	2.32	3.93
405430			Target Exon	2.29	3.20
423017	AW178761	Hs 227948	serine (or cysteine) proteinase inhibitor	2.24	4.40
422158	L10343	Hs 112341	protease inhibitor 3, skin-derived (SKAL	2.23	4.67
421314	BE440002	Hs 180324	Homo sapiens, clone IMAGE:4183312, mRNA,	2.23	4.22
422083	NM_001141	Hs 111255	arachidonate 15-lipoxygenase, second typ	2.22	5.71
442503	AF147076	Hs 158653	p63-responsive gene 5	2.21	4.86
416007	M13509	Hs 83169	matrix metalloproteinase 1 (interstitial	2.19	3.90
442572	AI001922	Hs 135121	hypothetical protein FLJ22415	2.16	2.87
413278	BE965305	Hs 833	interferon stimulated protein, 15 kDa	2.13	3.27
414521	D88124	Hs 76387	neuroblastoma, overexpression of hemaggl	2.06	2.09
428899	AA744610	Hs 194431	palladin	2.08	3.76
417079	U65590	Hs 81134	interleukin 1 receptor antagonist	2.06	3.09
439496	BE616501	Hs 32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.05	2.88
450423	AA486735	Hs 31869	slit/roshetin	2.02	3.74
444105	AW185057		ESTs	2.01	3.05
430410	AF099144	Hs 347533	trypsin beta 1	2.01	3.71
409453	AB85516	Hs 95612	ESTs	2.01	4.34
428655	U40959	Hs 211552	myosin, light polypeptide kinase	2.00	5.28
432374	W68615	Hs 301885	Homo sapiens cDNA FLJ11346 fs, clone PL	1.99	3.59
447990	BE048821	Hs 70144	small inducible cytokine subfamily A (Cy	1.92	4.16
451541	BE279383	Hs 26557	plekophillin 3	1.89	3.90
425206	NM_002153	Hs 155109	hydromyosin (17-beta) dehydrogenase 2	1.89	3.29
410197	NM_005518	Hs 59889	3-hydroxy-3-methylglutaryl Coenzyme A sy	1.84	3.32
401760			Target Exon	1.84	3.32
427579	AA366143	Hs 179669	hypothetical protein FLJ20637	1.83	4.69
424263	M77840	Hs 1757	L1 cell adhesion molecule (hydrocephalus	1.83	2.96
452206	AA224782	Hs 31895	hypothetical protein MG04093	1.82	3.70
420074	AA253425	Hs 190074	ESTs	1.81	2.90
429299	AB20463	Hs 347408	hypothetical protein MG13102	1.79	3.65
427540	R12014	Hs 20976	ESTs	1.77	2.92
429259	AA420450	Hs 232911	Plekophillin	1.76	3.65
422106	DM4239	Hs 111722	Fc fragment of IgG binding protein	1.69	1.75
453506	AA425414	Hs 33267	nuclear factor YB	1.74	3.07
436895	AF037335	Hs 5338	carbonic anhydrase XII	1.73	3.22
408551	AA605784		major histocompatibility complex, class	1.73	3.96
444726	NM_006147		interferon regulatory factor 6	1.71	3.65

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40910	10331_1	AL575207 AA1561714 BM0148781 BG542863 BG771232 AA429722 AJ375111 AJ070155 AA716695 BG003427 AA810811 AA427640 AA128610 AA059411 AT786263 AG494075 A1572127 AA209992 BF36083 AB40675 AA878813 BH48614 BG70885 AA128605 AV702879 AA731146 AB580336 AK032224 AA919169 AT158175 AA76350 BG701414 BF057094 AV135598 AA062983 BA496361 AT185077 AA933879 AK024545 AA193289 AA045194 BG026396 BG556883 BF343565 AA195423 AW237417 R99285 DG1992 BE86637 BF358770 AA194235 N51319 AA383499 NB3065 BG548812 BF127888 BC775448
5	409760 865166_1 410099 16732_1	AA302840 T19316 192505 AA184987 AD77551 AA055674 AA955247 AV751598 AA290526 RS3043 AA331387 AA056148 BB917678 BG181935 BG911971 BG820167 AT114254 AA348720 AA364503 BG714279 AA098320 A0811774 H24222 AV772178 BF875175 AA081630 BG000834 AA343890 AL563737 BG029705 WS2682 AA139558 BE551237 AA033724 BF109320 AG5706 AB029902 AB467736 AA693457 AB07593 AB487631 AT167419 AA051980 AA091758 BE702778 AA484549 T23811 BE270437 AA715027 AT917004 AA167714 BF735975 AA084618 AB18634 T31586 AA436630 AD36472 AA706191 AA423304 A204899 AB041169 AA211402 AA087081 AA788593 T23236 AT767935 AA747914 T03534 AA059843 AL119527 BE327037 AW501982 AW993370 AW901977 AW902071 W60500 NT79505 GC2685 107725 BG702059 BE702172 T06571 BE761121 BE767117 BE767113 R10710 R02146
10	456247 2142387_1 412477 8669_2	AD201117 AB57837 AD218371 BM051400 AA049664 AB198508 AA007738 AW571545 AW650042 AA039943 AA347280 AA150878 BF197070 A257984 BF594181 BF196968 AA43152 AA338921 AD200364 A280191 AB562531 AB74938 AB342447 AA020350 A2181295 AT148621 NS4781 AT338121 A1281153 NS1899 A087072 AA354788 AW069054 AA246309 BG529629 AD340135 BF083036 A167365 AW819567 AA256848 A1467868 AW148701 AA033720 BE407885 AW015456 AA937149 AA708546 AW741718 AA082598 H53334 AA036924 AW738230 A153322 A155088 AW50043 A901682 AV705506 R01153 AA125514 H62757 A1533893 A0695242 AA18720 N09864 A568933 A915737 AB015891 A183538 A48956 N68575 H82824 H6037 A1247247 T35664 BF593863 A1749637 AA085491 AA91294 AA087452 A037326 A663312 A6623674 AA625648 A629656 AA575535 A1168758 AA654572 A1085786 AA494396 AA091209 AA948663 AA929954 AA927952 T87001 AA282810 AA625296 AA0802267 AV364129 BF744400 AA194110 AA282839 AA119437 AA040284 AD250750 R37035 A1525586 WD1244 AW185957 AT123917 AT12926 AA609784 R97304
20	444105 549788_1 408851 0_0 444726 3503_2	BG285809 BE040673 BG432524 BE157554 DG679880 AU144784 AT45383 AU159045 A939350 AV293658 AW371408 BE556107 A1338042 AA188320 A558246 BE073290 AA297623 AA156532 A017342 A1190754 A1190644 A184302 AA355751 BE857018 A0307420 A1318157 AA034327 AA065658 AW747339 AA537786 A345741 A301433 AB073468 A1173388 BF718731 AB1343 AA374055 BF01575 A1549633 A084954 AW945405 AA945366 AA051073 BE57370 A511327 AA705753 BE154578 AW849414 A095359 A105759 A1140849 T57412 A088965 AW104547 A1912495 A1883874 AT744241 BE717113 BE717108 BE715554 AB72527 AD292457 C00338 AH05559 A167577 AA045413 BF84313 BE141599 AA545895 AW178095 BE140919 BE140909 AW178107 AW178094 AW845383 BF349527 AW845838 AA054581 A1878541 A1677720 AA05478 4472_16
30	454194 171445_1 402799 0_0 413559 159681_1 454478 4723_16	AA065648 AA065648 BE15547 BE15567 AW795251 AW798102 AW805749 AW805872 BF965060 AW794380 BF380448 AW794466 AW794538

35	TABLE 59C: Play: Ref:	Unique number corresponding to an Eos probe(s) Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
40	Strand: Nucleotide position	Indicates DNA strand from which exons were predicted. Indicates nucleotide positions of predicted exons.

40	Play	Ref	Strand	Nucleotide position
40	401780	7249190	Minus	28397-26617,28920-29045,29135-29296,2941
40	402075	8117407	Plus	128707-128933,122804-12291,124019-12416
40	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
45	401781	7249190	Minus	83155-83435,83531-83656,83740-83991,8423
45	406433	9256507	Plus	58704-58865
45	401760	9256599	Plus	83126-83250,83320-83540,94719-95287
45	403903	7710571	Plus	101165-102597
45	404457	8077530	Minus	28651-28853

50	TABLE 60A: ABOUT 53 GENES UPREGULATED IN BENIGN NEVIL RELATIVE TO NORMAL TISSUES	
50	Table 50A lists about 53 genes upregulated in benign nevus relative to normal tissues. These genes were selected from 5980 probesets on the Eos/Arraymax Hu30 Genechip array Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.	
55	Play: ExAccn: UnigeneID Unigene Title	Unique Eos probe set identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title
60	R1: R2:	average of benign nevus AIs divided by the 50th percentile of normal tissue AIs average of benign nevus AIs divided by 50th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

65	Play	ExAccn	UnigeneID	Unigene Title	R1	R2
65	403077	NM_001912	Hs.301865	dopachrome tautomerase (dopachrome delta	8.09	5.62
65	403601	AF237021	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	8.37	13.47
65	403686	NM_001942	Hs.2933	desmoglein 1	7.26	4.78
65	406964	M21305		FGFES predicted novel secreted protein	6.50	3.73
65	425555	NM_000372	Hs.2053	tyrosinase (oculocutaneous albinism IA)	6.40	7.35
70	425852	AB010445	Hs.225948	small inducible cytokine subfamily A (C)	6.23	8.85
70	430822	AJ301371	Hs.248017	glyoxylate-3-phosphate dehydrogenase	5.49	4.32
70	420208	BE277605	Hs.95972	silver (mouse homolog) like	5.45	9.84
70	413860	NM_000427	Hs.251680	lecithin	3.88	3.00
70	421773	V699333	Hs.112457	ESTs	3.80	9.04
70	438380	T08430	Hs.5194	chondroitin sulfate proteoglycan BEHABD	3.74	4.23
75	431089	BE041395	Hs.95972	ESTs, weakly similar to unknown protein	3.21	2.34
75	420798	V93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis)	3.08	3.20
75	442503	AF147078	Hs.150853	p53-responsive gene 5	2.88	5.01
75	435451			glyoxylate-3-phosphate dehydrogenase-like 3	2.86	2.85
75	432440			ESTs	2.86	1.90
75	402525	A1591147	Hs.61232	NM_002599: Homo sapiens POU domain, clus	2.78	2.72
80	413171	AA318325	Hs.75219	tyrosinase-related protein 1	2.65	5.58
80	439496	BE615501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	2.55	3.18
80	427656	AB870435	Hs.1569	LMH homeobox protein 2	2.45	2.38

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453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	2.34	3.76
420763	A059838	Hs.99923	lectin, galactoside-binding, soluble, 7	2.33	2.43
422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.28	2.00
427666	A1791495	Hs.180142	calmodulin-like protein (CLP)	2.28	2.50
459702	A1204965	Hs.180142	gh anti-303.11 Striatogenes cortex brain S1	2.25	1.85
451668	Z43948	Hs.326444	cartilage acidic protein 1	2.23	2.42
431703	AA514264	Hs.4437	triosephosphate isomerase 1	2.15	2.20
453511	AL031224	Hs.33102	AP-2 beta transcription factor	2.13	2.20
401780			NM_005557 Homo sapiens keratin 16 (foca	2.13	2.02
416640	BE262478	Hs.79404	neuron-specific protein	2.11	2.02
444105	AW189097		ESTs	2.11	1.46
428748	AW593206	Hs.98785	Kap37 protein	2.09	1.52
418667	A1127959	Hs.83393	cyclin E1	2.09	2.12
417017	AA578954	Hs.180842	ribosomal protein L13	2.08	2.52
401781			Target Exon	2.02	2.03
407178	AA195651		AP-2 beta transcription factor	1.88	2.17
452308	A167950	Hs.61297	ESTs	1.84	2.38
425446	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.83	3.26
402880			Target Exon	1.69	2.10
434276	AF123659	Hs.53005	leucine zipper, putative tumor suppressor	1.59	2.20
401583			NM_006311 Homo sapiens nuclear receptor	1.86	2.02
424016	AL080188	Hs.137556	Homo sapiens mRNA, cDNA DKF-2K43A132 (fr	1.65	2.05
432800	BE391046	Hs.278952	AIN-1 protein	1.61	2.83
400328	X87344		transporter 2, ATP-binding cassette, sub	1.57	2.27
412580	AA113262	Hs.17901	Homo sapiens, clone IMAGE3937015, mRNA	1.55	2.42
435292	N20514	Hs.172965	ESTs	1.53	2.21
405561	A030037	Hs.64120	hypothetical protein MGCL13016	1.52	2.01
427723	AW274357	Hs.301406	hypothetical protein PP3501	1.47	2.71
477963	BE519911	Hs.115803	hypothetical protein	1.40	2.10
454478	AW085749		superoxide dismutase 2, mitochondrial	1.39	2.36
427286	A057346		phosphorylase aminotransferase	1.24	2.82
430513	AJ012008	Hs.241586	GSC protein	2.20	2.18
411388	X72925	Hs.69752	desmocollin 1	1.00	2.43

35	TABLE 60B:	
	Pkey:	Unique Eos probe/identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

40	Pkey	CAT Number	Accession
	431089	12941_2	BG040189 AW053489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	459702	538529_1	BG02709 BE166299 A1204965 AW969908 AAS28756 AW440776 B1043564
	444105	649788_1	AW189097 A123917 A123926
45	407178	63307_1	AW235123 AA195651
	427289	1820_2	AW1796521 AW1796102 AW085749 AW066872 BF585060 AW794330 BF380445 AW794466 AW794638
			BC007350 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA478353 AW327973 AW402425 A189360 AA685504
			AW612968 AA635644 A1751211 B20000 AL394506 AA747849 BF154826 BF477185 AA649647 B191135 A1750216 T35363 B03678 AW079375
			AW612240 AAS25485 AA15380 BG70573 AW370651 B20000 BG762422 B2074607 B06852 A102671 AW181715
			AV703420 H52047 AA485882 R56186 H50385 R56913 B1061497 B1018403 BF376945 T75578 BF933325 BF933283 BG502266 AW685504 A1683004
			B1018121 A14953 BF933343 BF932871 B108334 R14102 BF897622 T50816 BG698803 BF340083 Z20199

50	TABLE 60C:	
	Pkey:	Unique number corresponding to an Eos probe/
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
	Strand:	sequence of human chromosome 22" Dunham, et al (1999) <i>Nature</i> 402:489-495
	N_positon:	Indicates DNA strand from which exons were predicted.
		Indicates nucleotide positions of predicted exons.

60	Pkey	Ref	Strand	N_positon
	405451	7622517	Minus	145943-146227
	425225	5930048	Minus	19748-20683
	407180	7245190	Minus	28397-28517,28920-29045,29135-29296,2941
	401781	7245190	Minus	83215-83435,83531-83556,83740-83901,8423
	402880	992661	Minus	41555-41865
65	401963	3126783	Plus	51382-51521

70	TABLE 61A: ABOUT 72 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO PRIMARY MELANOMAS	
	Table 61A lists about 72 genes upregulated in benign nevi relative to primary melanomas. Genes were selected from 99680 probesets on the Eos/ArrayMetric Hu30 Connectiv array.	
	Gene expression data for each probe/identifier obtained from this analysis was expressed as average intensity (R1), a normalized value reflecting the relative level of mRNA expression	
	Probe:	Unique Eos probe/identifier number
	Ex/Accession:	Exemplar Accession number, Genbank accession number
	Unigene number:	Unigene number
	Unigene Title:	Unigene gene title
75	R1	average of benign nevi AIs divided by the 90th percentile of primary melanoma AIs
	R2	average of benign nevi AIs divided by the 90th percentile of primary melanoma AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

80	Pkey	Ex/Accession	UnigeneID	Unigene Title	R1	R2
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.80	2.50
	424897	D63216	Hs.153684	litzke-related protein	3.40	2.69
	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	2.90	3.25
	431089	BE041395		ESTs, Weakly similar to unknown protein	2.82	1.56

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450334	AW450979		gb U41813.ata-a-12.0.U1.s1 NC1_CGAP_Su	2.73	3.00
417017	AA976064	Hs.180842	ribosomal protein L13	2.71	3.73
420880			Target Exon	2.56	3.55
422656	AB70435	Hs.1569	UIM homeobox protein 2	2.45	3.38
425451	AY008165	Hs.169946	GATA-binding protein 3 (T-cell receptor	2.41	1.91
423467	AK000214	Hs.129014	hypothetical protein FLJ20007	2.32	2.24
424797	AA622394	Hs.153177	ribosomal protein S28	2.29	2.53
459702	AI204595		gb AF03033.1.S1 Slc alginate chitin brain S1	2.25	2.19
426644	U01306		FCGIES: predicted novel secreted protein	2.24	1.65
428748	AW593206	Hs.98785	Kap3 protein	2.09	1.43
402525			NM_002699: Homo sapiens POU domain, clas	2.06	2.03
415923	R81864	Hs.205103	ESTs	2.05	1.87
412432	AA126311	Hs.6879	ESTs	2.05	2.05
421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	2.03	2.20
414876	AW950925	Hs.524	crystallin, mu	2.02	2.30
432006	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	2.02	2.39
424010	AL280188	Hs.137556	Homo sapiens mRNA, cDNA DKFZp434A132 (fr	1.35	2.72
453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	1.95	2.66
452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.88	2.85
410545	U52324	Hs.64310	interleukin 11 receptor, alpha	1.85	3.07
430495			ENSP000002247 16' GTP-binding protein SAR	1.84	2.09
405972	M32053		gb Human H19 RNA gene, complete cds.	1.83	1.14
405266			Target Exon	1.75	2.38
414309	AK000639	Hs.75584	DKFZP568A011 protein	1.73	2.80
416250	AA581385	Hs.73452	hypothetical protein MGCG10791	1.72	2.27
451840	AI198251	Hs.27191	hypothetical protein from clone 24756	1.70	2.99
441134	W29092	Hs.346590	cellular retinoic acid-binding protein 1	1.58	2.37
401963			NM_006311: Homo sapiens nuclear receptor	1.66	2.38
430547	U01212	Hs.248153	olfactory marker protein	1.65	2.00
413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine-g	1.63	2.18
406387			Target Exon	1.57	2.14
405776			cytochrome c-1	1.55	2.23
410677	NM_003278	Hs.55424	tetranectin (plasminogen-binding protein	1.53	3.25
406807	AA057605	Hs.163520	ribosomal protein S9	1.53	2.67
420438	AW436251	Hs.1311	CD13c antigen, c polypeptide	1.52	2.99
422089	AA523172	Hs.103135	ESTs, Weakly similar to SFRI_HUMAN SPLUC	1.52	2.66
456898	NM_001928	Hs.155597	D component of complement (adipon)	1.48	2.57
402412			Target Exon	1.48	2.42
427795	BE266268	Hs.180842	ribosomal protein L13	1.48	3.48
452547	AA335295	Hs.74120	acipotes specific 2	1.47	3.89
414323	NM_014759	Hs.334888	KIAA0273 gene product	1.46	3.14
425831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	1.45	2.09
457090	AL268243	Hs.186520	ribosomal protein S9	1.40	2.56
445431	AF137368	Hs.12701	plasmidogen	1.39	2.00
445636	AW106401		ribosomal protein L29	1.38	2.08
414582	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.37	3.32
406845	AI567284	Hs.119598	ribosomal protein L3	1.37	2.04
456808	AF60337	Hs.189520	ribosomal protein S9	1.35	3.32
403986			Target Exon	1.34	2.09
402218			NM_022165: Homo sapiens Lin-7b protein (1.31	2.16
400649			Target Exon	1.29	2.07
425447	AI807481	Hs.276581	fibroblast growth factor receptor 2 (bac	1.28	2.40
403211			NM_005400: Homo sapiens protein kinase C	1.26	2.13
452678	AI243131	Hs.164651	ESTs, Weakly similar to TLX_HUMAN PROTE	1.26	2.14
406589	D60310	Hs.79333	cyclin I	1.26	2.37
447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.25	2.39
404406			Target Exon	1.24	2.09
428594	AW167668	Hs.279772	brain specific protein	1.23	2.28
406757	T65957	Hs.77039	ATP synthase, H transporting, mitochondr	1.21	2.01
425843	AL137008	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434H0322 (l	1.20	2.07
409726	AA475341	Hs.724	thyroid hormone receptor, alpha (avian e	1.17	2.62
436398	H87136	Hs.5174	ribosomal protein S17	1.17	2.42
444674	BE562200	Hs.244	amino-terminal enhancer of split	1.16	2.02
424250			Target Exon	1.16	2.08
425758	AA552326	Hs.77039	ATP synthase, H transporting, mitochondr	1.13	2.03
412423	U46455	Hs.252189	syndecan 4 (amphiphysin, tyrosocan)	1.13	2.23
407032	U73799		gb Human dynactin mRNA, partial cds.	1.10	2.01
402921			ENSP00000244047: Cadherin-like protein V	1.00	2.00

70 TABLE 61B:

Key: Unique Eos probe set identifier number
CAT number Gene cluster number
Accession Genbank accession numbers

75	Key	CAT Number	Accession
	AI31089	125941_2	BG940189 AW063469 AA715880 BF001091 BF880095 AA666102 AA621946 AA491825
	456034	685986_1	AA136553 AA136556 AW450979 AA084358 AA080054 AA0238038 AA092073 BE168845
	459702	335626_1	BC007205 BE168299 AG045495 BC165335 AA082908 AA023756 AA040776 B1043454
	445636	8561_5	BF339388 AI345516 EG391657 BE708957 BC0626034 BE261703 H56716 H65572 H53801 T43830 R50953 R59980 R30707 BE897553 AA090310
			AA090672

80 TABLE 61C:

Key: Unique number corresponding to an Eos probe set

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5	403532			NM_024638.Homo sapiens hypothetical prot	1.75	2.06
	402829			C1002500.gi754254refNP_034810.1) hea	1.72	2.20
	403828			CA000447.gi770557refNP_038851.1) Ki	1.72	2.04
	453837	AL138387	Hs.296126	baculoviral IAP repeat-containing 7 (Iv	1.68	2.40
	407826	AA129423	Hs.40330	calpain 3, (p4)	1.67	2.13
10	411253	AE632744	Hs.129501	ESTs	1.67	2.13
	405776			cytochrome c-1	1.66	2.36
	430540	AW245422		Homo sapiens cDNA: FLJ27105 fs, clone H	1.66	2.08
	415745	AB807524	Hs.13245	KIA04065 gene product	1.66	2.34
	401963			NM_005311.Homo sapiens nuclear receptor	1.66	2.97
15	402994			NM_002453.Homo sapiens myxovirus (influ	1.66	2.56
	406016			Target Exon	1.65	2.23
	429516	BE503443	Hs.112695	hypothetical protein DKFZB34M1819	1.65	2.30
	440437	AIB75076	Hs.75061	NM_021158.Homo sapiens protein kinase d	1.63	2.46
	440437	AI923201	Hs.182352	macrophage myristoylated alanine-rich C	1.61	2.28
20	403960			ESTs	1.59	2.07
	406266			ENSP00000174317.NM040303 (FRAGMENT)	1.59	2.41
	424481	R19453	Hs.1787	Target Exon	1.56	2.16
	403803			proteolipid protein 1 (Policzeus-Merzbac	1.55	3.14
	407038	X00237		CA001432.gi6009519refNP04A54941.1) (AB	1.54	2.04
25	424412	H15512	Hs.10043	gh-Human F variable segment 5' to antihi	1.53	2.09
	431836	AF178532	Hs.271411	hypothetical protein FLJ133074	1.53	2.45
	427923	AW274357	Hs.301406	beta-site APP-cleaving enzyme 2	1.52	2.76
	419348	BE041436	Hs.93379	hypothetical protein PP3501	1.52	3.04
	404780			eukaryotic translation initiation factor	1.51	3.42
30	434596	T59538		C20011077.gi7325219refNP_038859.1) k	1.50	2.16
	425060	AA587465	Hs.296184	gly556/12.1 Stratiopone ovary (G37217)	1.48	2.02
	435450	BE368001	Hs.21858	potassium voltage-gated channel, shaker-	1.47	4.05
	427289	AB073740		truncates de repeat containing 3	1.46	2.48
	428118	AB021225	Hs.159581	phosphoserine aminotransferase	1.44	4.46
35	432800	BE391046	Hs.279962	nucleoside phosphorylase 17 (membrane-in	1.43	2.32
	447763	BE619511	Hs.115803	AIM-1 protein	1.43	2.08
	443218	AI354669	Hs.187461	hypothetical protein	1.42	2.21
	451489	NM_005503	Hs.25468	ESTs, Weakly similar to C29143 proline-r	1.41	2.31
	450541	AW054121	Hs.279175	arimid beta (A1) precursor protein-bend	1.41	2.35
40	402318			ESTs	1.41	2.01
	402343			C7002129.gi3638957refNP04A36301.1) (ACQ	1.40	2.31
	447103	AW449602	Hs.241493	Target Exon	1.40	2.35
	431222	X56777	Hs.273790	natural killer-tumor recognition sequenc	1.40	2.11
	400263			zona pellucida glycoprotein 3A (sperm re	1.39	2.06
45	403866	BE278594	Hs.5912	Eos Control	1.38	2.09
	437912			Target Exon	1.38	2.09
	425020	AL110198	Hs.198017	F-box only protein 7	1.36	2.27
	401914			microphthalmia-associated transcription	1.36	2.77
	450395	BE048545	Hs.161757	Target Exon	1.33	2.43
50	425335	AB007937	Hs.158287	ESTs	1.29	2.01
	450355	AB010098	Hs.24007	KIA04068 gene product	1.29	2.94
	427560	AA405394	Hs.161851	connexin, actin-binding protein, 2B	1.26	2.84
	402450			ESTs	1.27	2.14
	406885	D28423		Target Exon	1.27	2.89
55	405368			Target Exon	1.26	3.19
	454429	BE273437	Hs.301406	gbz human mRNA for pre-mRNA splicing fac	1.26	2.45
	414580	BE368918		NM_022355.Homo sapiens putative dipeptid	1.25	2.06
	414080	BE248327	Hs.123164	hypothetical protein PP3501	1.23	2.07
	405617			gb01273386F1 NIH_MGC_20 Homo sapiens c	1.22	2.21
60	437026	AW976573		gltCRAP1E1957 Prostatic pre-B cell acut	1.22	2.01
	401008	H84083	Hs.25734	cofilin 1 (non-muscle)	1.21	2.19
	448143	AC038704	Hs.29478	ESTs	1.21	2.31
	416630	H60392	Hs.174051	Target Exon	1.20	2.09
	407239	AA076350	Hs.67846	ESTs, Weakly similar to BIN1G1 (H.sapiens	1.17	2.22
65	419045	T85653		cardiolipin phosphatidylcholine, neuronal 2, like	1.17	2.58
	443923	X60702	Hs.210	small nuclear ribonucleoprotein 70kD pol	1.16	2.34
	457585	AE040790	Hs.278283	leukocyte immunoglobulin-like receptor,	1.14	2.58
	452958	AA883929	Hs.40527	glyc060405.1) Soares fetal liver spleen	1.13	2.08
	403969			leukocyte tyrosine kinase	1.11	2.24
70	438878	BE485204	Hs.47448	G-protein-coupled receptor 27	1.08	2.04
	415929	AA724373	Hs.49344	ESTs	1.03	2.28
	404632			ENSP00000034663.Zinc finger protein 131	1.00	2.04
	452838	U65011	Hs.30743	ESTs	1.00	2.12
	447937	AL106716	Hs.20034	hypothetical protein FLJ11006	1.00	2.18
75				NM_022490.Homo sapiens hypothetical prot	1.00	2.19
				preferentially expressed antigen in meda	1.00	2.35
				Homo sapiens mRNA full length insert cDN	1.00	2.41
80						

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404632 979666 Plus 45095-45229

5	TABLE 63A: ABOUT 181 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO MELANOMA METASTASES				
	Table 63A lists about 181 genes upregulated in benign nevi relative to melanoma metastases. Genes were selected from 59680 probesets on the Eot/Alfmythrix Hu33 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression				
10	Probe:	Unique Eot probe set identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
15	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
20	R1	average of benign nevi AIs divided by the 90th percentile of melanoma metastasis AIs			
	R2	average of benign nevi AIs divided by the 50th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator			
25	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	401781			Target Exon	19.33 19.21
30	422511	AU076442	Hs.117538	collagen, type XVII, alpha 1	13.54 14.18
	401780			NM_005577*Homo sapiens keratin 16 (foca	12.97 13.63
35	409501	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	12.61 31.19
	412536	NM_004415		desmoplakin (DPL DPH)	11.73 6.91
40	422763	A0559836	Hs.99923	iodin, galactose-binding, soluble, 7	10.16 14.08
	429632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	8.48 6.79
45	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (sch	8.28 9.62
	430686	NM_001942	Hs.2633	desmoglein 1	7.26 5.64
50	429652	AB010445	Hs.225845	small inducible cytokine subfamily A (Cy	7.12 10.88
	425777	AA292958	Hs.163800	ESTs	7.01 6.59
55	406964	M21305		FGENES predicted novel secreted protein	6.50 8.82
	401785	AB041036	Hs.57771	NM_002275*Homo sapiens keratin 15 (KRT1	6.40 9.77
60	410001	L24203	Hs.87258	kallikrein 11	6.16 6.18
	417515	L24203	Hs.87258	stata1 telangiectasia group D-associated	5.73 16.57
65	419686	Z36830	Hs.87258	annexin A8	5.32 5.27
	430496	BE616501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	4.89 9.81
70	452240	AI591147	Hs.61232	ESTs	4.89 6.67
	425255			NM_002699*Homo sapiens POU domain, clas	4.74 4.80
75	431360	NM_000427	Hs.251680	loricrin	4.66 3.98
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	4.63 5.69
80	418067	AI127959	Hs.83363	cystatin EM	4.46 6.78
	424012	AI936377	Hs.137659	tumor protein 63 kDa with strong homolog	4.56 5.73
85	419863	AK001130	Hs.41680	desmocollin 3	4.44 5.23
	419329	AY007220	Hs.288998	S100-type calcium binding protein A14	4.24 6.49
90	430906	AI9872527	Hs.59161	ESTs, Weakly similar to DAPI_HUMAN DEATH	3.95 3.37
	421773	W69233	Hs.112457	ESTs	3.88 9.60
95	429536	AI981532	Hs.135188	ESTs	3.82 10.18
	416394	AF132918	Hs.84728	Kruppel-like factor 5 (inlesinal)	3.78 6.33
100	408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	3.77 4.92
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11345 fs, clone PL	3.70 5.30
105	424049	AB014524	Hs.138380	KIAA0024 protein	3.68 4.41
	421948	L25683	Hs.334309	keratin 6A	3.62 3.13
110	427656	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	3.59 4.40
	422168	AA588894	Hs.112408	S100 calcium-binding protein A7 (psoriasis	3.48 6.08
115	438896	AF037335	Hs.5336	carbonic anhydrase XII	3.42 3.28
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	3.26 3.89
120	401760			Target Exon	3.21 7.11
	431089	BE041395		ESTs, Weakly similar to unknown protein	3.21 5.78
125	434293	NM_004445	Hs.3796	Ephb6	3.14 3.11
	412432	AA126311	Hs.9879	ESTs	3.14 4.65
130	442503	AF147078	Hs.150853	p53-responsive gene 5	3.11 5.92
	414987	AA524394	Hs.294022	hypothetical protein FLN14950	3.07 4.89
135	427098	W93774	Hs.59936	keratin 10 (epidermolytic hyperkeratosis	2.99 3.09
	433339	AF019826	Hs.9036	glioblastoma overexpressed	2.96 2.75
140	414876	AI952005	Hs.904	crystallin, mu	2.94 3.82
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.87 3.42
145	424891	D63216	Hs.153684	hitzed-related protein	2.87 1.96
	460334	AI945979		gh UH H83-01a-12-GU1-1 NCL CGAP_Su	2.73 2.54
150	424364	AF028328	Hs.163834	ESTs, Weakly similar to G17153 atrophin-	2.72 2.92
	427318	AF186081	Hs.175783	zinc transporter	2.71 2.21
155	422887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	2.67 6.47
	425208	AI167560	Hs.61297	ESTs	2.67 4.61
160	427788	BE514982	Hs.38691	S100 calcium-binding protein A2	2.64 2.68
	431569	BE184455	Hs.251754	secondary leukocyte protease inhibitor (2.57 3.91
165	451541	BE279383	Hs.26557	plakophilin 3	2.49 5.47
	453317	NM_002277	Hs.41696	keratin, hair, acidic, 1	2.45 4.17
170	412633	AF001691	Hs.74364	porpalein	2.42 4.90
	417233	W62905	Hs.24395	small inducible cytokine subfamily B (Cy	2.41 2.66
175	424797	AA62394	Hs.153177	ribonuclease protein S28	2.39 2.67
	424010	AL080188	Hs.137556	Homo sapiens mRNA, cDNA DKFZP434A132 (fr	2.39 4.67
180	432421	H58985	Hs.37648	ESTs	2.39 2.34
	426451	A080165	Hs.169346	GATA binding protein 3 (T cell receptor	2.36 1.88
185	423467	AK003214	Hs.129014	hypothetical protein FLN20207	2.32 2.24
	432222	AI204995		g0 an0c0x.11 Stratagene schizo brain S1	2.31 1.99
190	430168	AI968343	Hs.145582	DKFZP434B173 protein	2.30 2.60
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	2.28 1.91

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	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.27	8.50
	446889	AK001898	Hs.16740	hypothetical protein FLJ11036	2.27	2.21
	429365	AA451798	Hs.99249	ESTs	2.25	2.54
	459702	AJ204965		gla-m3ctd3.r1 Stratagene schizo brain S1	2.25	2.35
5	428511	AF052892	Hs.98485	gap junction protein, beta 3, 3140 [com	2.23	2.17
	444946	AW135025	Hs.155457	hypothetical protein FLJ22003	2.23	3.23
	417017	AA876364	Hs.180842	abnormal protein L13	2.21	2.74
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.21	1.68
	430152	AB001325	Hs.234542	aquaporin 3	2.20	3.32
10	444726	NM_005147		interleukin regulatory factor 6	2.15	5.20
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.15	2.82
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	2.14	2.96
	419812	AF249745	Hs.8066	Rho guanine nucleotide exchange factor 1	2.14	2.25
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.12	2.99
15	444105	AW189097		ESTs	2.11	2.98
	428748	AW553205	Hs.98785	Ksp37 protein	2.09	1.51
	456826	AB71742	Hs.302428	wingless-type MMTV integration site fami	2.09	3.25
	413163	Y06815	Hs.15216	protein tyrosine phosphatase, receptor 1	2.09	4.97
20	410677	NM_003278	Hs.65424	serpinectin (glutathione-binding protein	2.06	5.68
	430285	AB17602	Hs.106440	ESTs	2.05	2.04
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.05	5.92
	451688	Z43948	Hs.285444	cartilage acidic protein 1	2.04	2.19
	441134	W25992	Hs.345550	cellular retinoic acid-binding protein 1	2.04	3.08
	433428	T29975	Hs.33104	Hunt1nglin interacting protein C	2.04	1.63
25	428831	U46689	Hs.159608	aldehyde dehydrogenase 3 family, member	2.03	3.92
	446727	AB011036	Hs.19332	KIAA523 protein	2.01	2.60
	431703	AA514264	Hs.4137	inosophosphate isomerase 1	2.01	2.65
	425254	AW452434	Hs.58006	ESTs, Weakly similar to ALLUS_HUMAN ALU S	1.99	4.04
	439525	AF084543	Hs.58611	ESTs	1.99	2.31
30	420390			Target Exon	1.99	2.75
	428717	X57348	Hs.184510	strafin	1.98	2.08
	413959	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.97	3.16
	425247	AA335295	Hs.74120	adipose specific 2	1.95	3.89
35	437679	NM_014214	Hs.5753	inositol(myo-)(or -)-monophosphatase 2	1.94	2.06
	44420450		Hs.292911	Platagophilin	1.92	3.93
	430337			Target Exon	1.92	2.97
	455797	BE091833		gbL12-ET0731-260400-076-F04 BT0731 Homo	1.91	3.46
	437202	AA326110		nuclear transcription factor Y, gamma	1.89	2.00
40	426150	NM_003558	Hs.167218	Bcl-1-like homeobox 2	1.86	2.60
	434574	AU24458	Hs.345070	ESTs	1.85	1.61
	444051	BE448061	Hs.37054	ephrin-A3	1.85	3.48
	424471	AA341329	Hs.311524	ESTs	1.84	2.62
	422105	D84239	Hs.111732	Fc fragment of IgG binding protein	1.83	4.69
	451721	NM_008946	Hs.26915	spectrin, beta, non-erythrocytic 2	1.82	2.00
45	451849	A1193261	Hs.27191	hypothetical protein from clone 24196	1.81	2.31
	429348	AJ242859	Hs.199731	Langerhans cell specific c-type lectin	1.79	3.07
	423523	AV299828	Hs.193580	ESTs	1.77	3.37
	432843	AA52699	Hs.152423	Homo sapiens cDNA: FLJ12724 fs, clone C	1.76	2.46
50	426528			CA000447?P1735573jseqUP_030885.1.1.KI	1.73	2.65
	412446	AJ768015		ESTs	1.68	3.16
	420033	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	1.67	2.22
	411274	NM_002776	Hs.69423	kallikrein 10	1.65	2.26
	401963			NM_005311Homo sapiens nuclear receptor	1.66	2.52
55	435016	AJ84219	Hs.130749	ESTs, Weakly similar to CB0222 hypothesis	1.65	2.20
	437897	AA770561	Hs.146170	hypothetical protein FLJ22959	1.64	3.21
	419648	T73561	Hs.91877	thyroid hormone responsive SPOT 14 (rat)	1.63	2.94
	410545	U32324	Hs.64310	interleukin 11 receptor, alpha	1.62	2.58
	429211	AF052893	Hs.158249	gap junction protein, beta 5 (connexin 3	1.62	3.92
60	456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.60	3.43
	423526	AB011086	Hs.129739	KIAA0514 gene product	1.60	2.18
	416305	AJ076628	Hs.79187	oxoesterase and adenosine receptor	1.59	2.47
	413966	AA133335	Hs.173704	ESTs, Moderately similar to AC39589 hom	1.59	2.99
	414217	AJ030928	Hs.273938	Homo sapiens cDNA: FLJ23165 fs, clone L	1.59	2.82
	429299	AJ520463	Hs.347408	hypothetical protein MGCL13102	1.57	2.54
65	432647	AJ307481	Hs.275581	fibroblast growth factor receptor 2 (bac	1.56	2.74
	429002	AJ268439	Hs.23440	junction plakoglobin	1.56	2.97
	430171	AF086289	Hs.234765	skin-specific protein	1.54	2.18
	422717	AJ557623	Hs.119475	cold inducible RNA-binding protein	1.51	2.19
	414323	NM_014759	Hs.334688	KIAA0273 gene product	1.51	3.73
70	423184	NM_204428	Hs.1624	ephrin-A1	1.50	2.18
	433101	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKF Zp568.203 (f	1.50	2.00
	424362	AL137646		Homo sapiens mRNA: cDNA DKF Zp568F0624 (f	1.48	2.04
	433662	W07162	Hs.150826	RAB25 RAB25, member RAS oncogene family	1.46	2.83
	445431	AF137386	Hs.12701	plasmalogin	1.46	2.00
75	426906	AF117646	Hs.156637	Cis-8-N (trans)-octopropyl retinoid tr	1.44	2.04
	425299	AF078037	Hs.324051	RelA-associated inhibitor	1.42	3.50
	445656	W22050	Hs.21299	ESTs, Weakly similar to AF151840 1 CGS 8	1.42	2.53
	444672	Z35636	Hs.116659	laminin, alpha 5	1.40	2.36
	441990	BE348821	Hs.20144	small inducible cytokine subfamily A (Cy	1.40	2.29
80	418452	BE001556	Hs.85266	integrin, beta 4	1.39	2.86
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	1.38	2.28
	416340	N13172	Hs.79226	fasciculation and elongation protein zet	1.38	2.24
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.38	2.14

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AW370992 RH2918 H10757 R10703 C21061 R27637 AB27230 AW151953 AA61655 AA22806 AA233950 BE85810 R30801 W32704 H39784
BE90279 BG697650 AW872265 B1818938 BF528291 AW953624 RS7461 BF969694
BC21735 A968212 AL120184 BT69949 BE710102 BE184363 BE119031 BG102238 BF093049 BF963218 BF961912 BF943013 AA936414 AA151245
BF920559 A458707 Z114145 BF908059 BF308051 BF930943 BE659424 BF906910 BF956232 BF952020 BF906134 B103530 BF900052 BF900057
BF900026 BF945158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 A163388
AA617829 BF947001 B035448 BE935876 AW890837 AW898804 BF967405 BF903433 BG704815
AF284241 AL137646 BG642551 A278089 A4423915 A1274095 BE838965 BE839174 BE839102 BF924520 B1913343 A2938809 AL134380 AW973289
AL534638 197116 AW851672 C02210 A1783486 AW024874
AW796921 AW798102 AW805745 AW855872 BF985060 AW794380 BF380449 AW794466 AW794538

14246 63467_1

424362 Z18_7

454478 4273_16

TABLE 63C.

Play:
Ref:
Unique number corresponding to an Eos probe(s)
Sequences in this column are Genbank identifier (G) numbers. "Dunham, et al" refers to the publication entitled "The DNA
sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand:
NT_position:
Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

Play Ref Strand NT_position

401781 7249190 Minus 83215-83435,83531-83556,83740-83901,8423

401780 7249190 Minus 28397-28617,28920-29045,29135-29296,2941

401785 7249190 Minus 165776-165996,166189-166314,166408-16656

422525 9800046 Minus 15748-22653

401760 9829699 Plus 83126-83250,85320-85540,94719-95287

402880 9926561 Minus 41555-41865

406387 9256180 Plus 116229-116371,117512-117651

403828 9839214 Plus 31755-32148

401963 3126783 Plus 51382-51521

404246 7406725 Plus 82477-82626,82721-82810,83071,8314

403986 8576059 Plus 90692-91238

402216 7697983 Plus 127677-127895

		TABLE 64A: ABOUT 829 GENES DOWNREGULATED IN PRIMARY MELANOMAS AND/OR MELANOMA METASTASES RELATIVE TO NORMAL SKIN	
		Table 64A lists about 829 genes downregulated in primary melanomas and/or melanoma metastases relative to normal skin. Genes were selected from 59680 probesets on the	
		EquiArray/mtm1.h33 Genechip array. Gene expression data for each probe(s) obtained from this analysis was expressed as average intensity (A), a normalized value reflecting the	
		relative level of mRNA expression.	
		Play: Unique Eos probe(s) identifier number	
		ExAco: Exemplar Accession number, Genbank accession number	
		UnigeneID: Unigene number	
		Unigene Title: Unigene gene title	
		R1 90th percentile of normal skin A/s divided by the 90th percentile of primary melanoma and melanoma metastasis A/s	
		R2 90th percentile of primary melanoma A/s divided by the 90th percentile of primary melanoma and melanoma metastasis A/s, where the 15th percentile of normal tissue	
		A/s was subtracted from both the numerator and denominator	

45	Play	ExAco	UnigeneID	Unigene Title	R1	R2
	420813	X15101	Hs.59649	prolactin-induced protein	27.72	20.12
	408551	AF015221	Hs.14642	mammaglobin 1	26.40	24.25
	431350	NM_009427	Hs.21680	keratin	26.16	20.45
	401781			Target Exon	19.68	19.56
50	412636	NM_004415		desmoplakin (DPL, DPl)	18.12	10.36
	429441	AJ224172	Hs.204036	lipophilin B (pateroglobin family member)	16.61	18.06
	118067	AJ127588	Hs.83363	cystatin E4	16.00	20.00
	429632	W74001	Hs.85279	serine (or cysteine) proteinase inhibitor	15.64	11.81
	409691	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	15.03	37.51
	401780			NM_005567 Homo sapiens keratin 16 (foca	14.20	14.86
	422158	AA585854	Hs.112108	S100 calcium-binding protein A7 (psorias	13.95	28.08
	420763	AB598936	Hs.99923	hecin, glycosylase-binding, soluble, 7	13.52	18.85
	422511	AJ075442	Hs.117938	collagen, type XVII, alpha 1	13.14	13.81
	428330	L22524	Hs.22556	matrix metalloproteinase 7 (matrilysin)	12.78	6.35
60	421733	AL115971	Hs.1420	Rhodolact growth factor receptor 3 (ach	12.78	12.78
	426824	W82624	Hs.173069	EST1	12.67	12.24
	453309	A791809	Hs.32549	defensin, beta 1	12.02	12.42
	446227	A781459	Hs.270114	EST5	11.79	12.32
	421948	L42683	Hs.334309	keratin 9A	11.58	9.02
65	423877	AJ931411	Hs.282477	EST5	11.18	11.30
	412947	AA534598	Hs.49696	EST5	11.04	11.07
	407230	AA157857	Hs.182265	keratin 19	10.79	11.40
	421296	NM_002666	Hs.103253	periplin	10.73	7.94
	410001	AB041036	Hs.57771	kallikrein 11	10.72	10.70
70	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	10.33	7.16
	447966	AJ340605	Hs.105687	EST5, Weakly similar to Homolog of rat Z	10.09	9.67
	401203			Target Exon	9.95	7.37
	452308	AL167560	Hs.61297	EST5	9.71	20.05
	425580	L11144	Hs.1907	galactin	9.66	8.41
75	433124	US1712	Hs.13775	hypothetical protein SM331	9.50	4.96
	420919	N57892	Hs.100322	carbonic anhydrase VI	9.41	6.34
	443162	T49561	Hs.5029	DNF ZFN34G332 protein	9.36	10.58
	427666	A791185	Hs.180142	cathepsin-like skin protein (CLSP)	9.19	11.73
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor	8.85	17.76
80	40536	AW381532	Hs.135188	EST5	8.82	26.43
	430686	NM_001942	Hs.2633	desmoglein 1	8.73	6.58
	436895	AF037335	Hs.5338	carbonic anhydrase XII	8.61	8.69
	418663	AJ001100	Hs.41690	desmoglein 3	8.61	9.15

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	429852	AB010445	Hs.229848	small inducible cytokine subfamily A (Cyt	8.51	13.13
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.44	9.61
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKF7p761G02121 (8.39	5.13
	442577	AA292989	Hs.163890	ESTs	8.34	7.92
5	437161	NM.008445	Hs.331555	serine protease inhibitor, Kazal type 5	8.16	10.08
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	8.04	7.55
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	7.68	7.88
	452240	A591147	Hs.61232	ESTs	7.63	9.39
	442757	A1739526	Hs.203445	ESTs	7.52	7.31
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.51	6.17
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	7.49	7.12
	407328	AA588857	Hs.279698	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35	7.20
	414217	AC306298	Hs.48028	Homo sapiens cDNA: FLJ123165 fs, clone L	7.16	8.39
	417240	NS7661	Hs.16740	EST	7.13	15.05
15	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fs, clone MA	7.13	7.28
	413842	NM.005764	Hs.271473	epithelial protein up-regulated in cancer	7.06	6.93
	426488	XG3350	Hs.4	alcohol dehydrogenase 1B (class I, beta)	7.03	7.85
	435994	AA149250	Hs.56105	ESTs	7.00	4.53
20	422963	M79141	Hs.13234	ESTs	6.99	5.30
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.97	20.68
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	446399	AK001698	Hs.16740	hypothetical protein FLJ11036	6.95	6.68
	427890	AA435761	Hs.16740	ESTs	6.94	6.68
25	432374	WS8815	Hs.301885	Homo sapiens cDNA FLJ11346 fs, clone PL	6.84	8.44
	429624	AA458648	Hs.59476	ESTs, Weakly similar to 1313184B alpha1	6.83	6.37
	415020	AA652097	Hs.25529	ras-related protein	6.81	8.96
	429640	L11690	Hs.198689	bulbosus pompholyx antigen 1 (2302/40kD)	6.80	7.58
	439496	BE16501	Hs.32343	Homo sapiens, Similar to RIKEN cDNA 1110	6.77	14.06
	431713	AK000388	Hs.267997	EHM2 gene	6.72	7.11
30	451253	H46299	Hs.26126	claudin 10	6.71	7.17
	414937	AA542494	Hs.294422	hypothetical protein FLJ114950	6.67	11.68
	400304	AF005082	Hs.113261	Homo sapiens skin-specific protein (p33	6.64	7.90
	480063	BE06548	Hs.42346	calcineurin-binding protein calcitactin-1	6.60	7.29
35	424364	AW383226	Hs.163534	ESTs, Weakly similar to G1703 atropin-	6.58	6.78
	421773	WS8223	Hs.113457	ESTs	6.55	19.99
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (pol	6.55	6.79
	411388	XT72925	Hs.659752	desmoglein 1	6.55	8.97
40	401785	AA157857	Hs.182265	NM_002275: Homo sapiens keratin 15 (KRT1	6.51	9.94
	406867	X99133	Hs.204238	keratin 19	6.50	6.20
	429504	X99133	Hs.204238	Ippocath-2 (proenzyme 24p3) (HGAL)	6.43	6.79
	426106	AA678765	Hs.21812	ESTs	6.41	7.69
	413172	M38180	Hs.38586	hydroxy-delta-5-steroid dehydrogenase, 3	6.39	7.09
	407395	AF005082	Hs.113261	gH Homo sapiens skin-specific protein (p33	6.39	7.71
45	422166	WT2424	Hs.112405	S100 calcium-binding protein A5 (calgran	6.36	9.23
	437176	AW176909	Hs.42346	calcineurin-binding protein calcitactin-1	6.30	5.45
	440383	AA884208	Hs.30494	ESTs	6.26	6.25
	418329	AY007220	Hs.288998	S100-type calcium binding protein A14	6.22	10.13
	416686	Z36830	Hs.87268	annexin A8	6.19	6.14
50	440115	AF398851	Hs.16740	hemoglobin, gamma G	6.18	4.28
	424049	AB014524	Hs.138380	KIAA0624 protein	6.18	6.91
	417366	BE185289	Hs.1076	small proline-rich protein 1B (pomifin)	6.17	7.42
	432543	AA355690	Hs.152423	Homo sapiens cDNA: FLJ12174 fs, clone C	6.16	6.86
	414449	AA557660	Hs.76152	decom	6.15	3.93
55	441188	AW292830	Hs.255609	ESTs	6.12	6.68
	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	6.12	5.33
	431319	AA783350	Hs.302222	ESTs	6.11	6.84
	444105	AW189097	Hs.101915	Homo sapiens mRNA; cDNA DKF7p34A202 (f	5.97	6.20
60	428358	AA932222	Hs.101915	Stargardt disease 3 (autosomal dominant)	5.94	5.15
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.71	5.83
	438706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	5.69	4.48
	428666	AC080192	Hs.189242	Homo sapiens mRNA; cDNA DKF7p34A202 (f	5.65	6.06
	410541	AA005503	Hs.64175	synlein-2 protein	5.62	5.84
	431926	AW972724	Hs.239483	gb-EST384816 MAGE resequences, MAGL Homo	5.61	5.75
65	430332	RS1790	Hs.239483	Human clone 23933 mRNA sequence	5.60	5.76
	444964	AW153205	Hs.154547	hypothetical protein FLJ22408	5.53	5.25
	430714	AA484757	Hs.287601	Homo sapiens cDNA FLJ13830 fs, clone TH	5.48	5.38
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	5.46	3.19
	414407	AA147026	Hs.76704	ESTs	5.43	5.29
70	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE-451935, mRNA se	5.40	5.40
	442315	AA172992	Hs.7956	ESTs, Moderately similar to ZN11_HUMAN Z	5.40	3.87
	416931	DM5371	Hs.80485	actinose most abundant gene transcript 1	5.39	9.12
	431048	RS0253	Hs.249129	cell death-inducing DFFA-like effector 1	5.39	6.06
	436909	AA646635	Hs.332879	EST	5.37	5.33
	411274	NM.002776	Hs.65423	histidine 10	5.37	5.97
75	418394	AF132818	Hs.84728	Kruppel-like factor 5 (musclelinal)	5.36	9.35
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	5.34	4.08
	430171	AF086289	Hs.234766	skin-specific protein	5.32	10.40
	452747	BE153855	Hs.61460	tyrosinase-like receptor 1 (NHR	5.31	5.01
	426451	AK001655	Hs.163846	CAT1A-binding protein 3 (T cell receptor	5.31	3.81
80	414602	AW630088	Hs.765550	Homo sapiens mRNA; cDNA DKF7p564B1264 (f	5.26	9.92
	424399	AA906687	Hs.101915	A905687-IL10T95-109199-019 BT095 Homo	5.25	15.94
	430071	AA355896	Hs.232068	transcription factor 8 (represses intei	5.20	5.01
	431416	AA532718	Hs.178694	ESTs	5.18	5.39

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5	420339	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.17	5.72
	446082	A12741.39	Hs.156452	ESTs	5.16	5.14
	430369	AW96847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETN	5.14	4.97
	434625	W01370	Hs.46824	ESTs	5.12	6.18
	420101	AJ049887		Homo sapiens mRNA; cDNA DKFZp564F112 (h	5.11	3.79
10	419548	T73661	Hs.91877	thyroid hormone responsive SPOT 14 (rat)	5.08	13.64
	438962	BE046594		gb h4t1c11 x1 NC1_CGAP_RDF2 Homo sapiens	5.08	4.09
	418912	AF249145	Hs.6066	Rho guanine nucleotide exchange factor (5.06	4.77
	420563	H77659	Hs.65450	reticulon 4	5.06	5.56
	432125	AW972657	Hs.183006	Homo sapiens cDNA FLJ12301.35, clone MA	5.05	6.32
15	445263	H57646	Hs.42586	KIAA1560 protein	5.03	5.22
	407839	AA045144	Hs.161566	ESTs	5.03	5.27
	434293	NM_004445	Hs.3795	EPH8	5.003	4.91
	427850	AA415756	Hs.161051	ESTs, Moderately similar to ALLU5_HUMAN A	4.99	15.04
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	4.94	8.14
20	445493	AB915771		metallothionein 1E (functional)	4.93	4.33
	429305	AA461798	Hs.99249	ESTs	4.90	5.19
	413533	AF001691	Hs.74304	peripodin	4.90	11.71
	448490	AS523897	Hs.271692	ESTs, Weakly similar to D8022 hypoteth	4.85	4.88
	408491	AD080063	Hs.7882	ESTs	4.80	4.39
25	430168	AW968343	Hs.145582	DKFZP434H1735 protein	4.80	6.05
	407102	AA007629		glycerol 3-phosphate dehydrogenase 1 (po	4.78	7.23
	421998	R74441		poly(A)-binding protein, nuclear 1	4.77	4.78
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	4.72	6.24
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	4.71	3.72
30	435622	WE7826	Hs.55412	ESTs, Weakly similar to K1CJ2_HUMAN KERAT	4.70	3.60
	455626	AW109099	Hs.1508	insulin-degrading enzyme	4.68	5.14
	456988	NM_001928	Hs.155597	D component of complement (adipisin)	4.68	15.83
	408239	AA053401		ESTs, Moderately similar to ALU7_HUMAN A	4.67	6.17
	418192	D17793	Hs.76183	aldo-keto reductase family 1, member C3	4.64	4.48
35	420827	AA078667	Hs.134667	ESTs	4.63	4.06
	413441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	4.63	4.48
	408741	M73720	Hs.546	carboxypeptidase A3 (mast cell)	4.63	3.19
	427316	AF166081	Hs.175783	zinc transporter	4.62	3.57
	453767	AB011792	Hs.35054	extracellular matrix protein 2, female o	4.62	5.14
40	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	4.61	6.80
	437233	D61448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	4.60	6.19
	446525	AW967069	Hs.211556	hypothetical protein MG5487	4.59	2.45
	402294			Target E-on	4.57	5.47
	424038	AF077374	Hs.139222	small proline-rich protein 3	4.57	5.12
45	420798	W53774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	4.57	4.76
	418021	M15881	Hs.1137	unomodulin (unomocidin, Tamm-Horsfall gly	4.54	4.49
	422068	AB079119	Hs.104520	Homo sapiens cDNA FLJ13594.6s, clone PL	4.54	4.32
	414789	AD26323	Hs.57411	Microtubuli-associated glycoprotein-2	4.53	3.64
	410132	NM_003480	Hs.300946	Eos Control	4.53	2.91
50	400109				4.52	3.94
	427242	M18728		gb.Human nonspecific crossreacting antiq	4.51	4.07
	431991	AW255550	Hs.272023	transferrin, acidic coiled-coil contain	4.50	4.16
	435952	A033292	Hs.116317	Homo sapiens cDNA FLJ12089.6s, clone HE	4.50	4.77
	447365	BE383676	Hs.334	Rho guanine nucleotide exchange factor (4.50	3.99
55	449785	AJ252335	Hs.288300	hypothetical protein FLJ23231	4.49	4.02
	424620	AA101043	Hs.151254	kallikrein 7 (chymotrypsin, stromal com	4.47	5.43
	423559	AW452948	Hs.257631	ESTs	4.47	3.10
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	4.45	3.17
	422313	AF045941	Hs.115166	scletin	4.45	5.07
60	416305	AJ278628	Hs.79187	coxsa-like virus and adenovirus receptor	4.44	5.25
	422114	AA533447	Hs.312689	ESTs	4.44	3.52
	441623	AW958544	Hs.112242	normal mucosa of esophagus specific 1	4.43	2.84
	424670	W61215	Hs.110551	epithelial V-like antigen 1	4.42	4.27
	414489	AK620677	Hs.73105	ESTs	4.41	3.77
65	413040	AA193338	Hs.12221	sodium calcium exchanger	4.36	4.58
	426974	AB002238	Hs.173035	KIAA0300 protein	4.35	4.97
	446249	AW855331	Hs.337124	ESTs	4.35	4.49
	451743	AW014266	Hs.23071	ESTs	4.34	4.52
	427919	AA173942	Hs.326416	Homo sapiens mRNA, cDNA DKFZp564H195 (f	4.31	3.94
70	422305	AB28242	Hs.291438	ESTs, Highly similar to AF194888 1 trans	4.31	4.20
	408104	AW912927	Hs.293968	ESTs	4.31	3.53
	447945	AJ228238	Hs.9670	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.30	3.72
	430349	AW068098	Hs.6834	ESTs	4.29	4.16
	433339	AF019286	Hs.8026	goblastoma overexpressed	4.29	3.94
75	427074	AA527435	Hs.178569	hepatocellular carcinoma antigen gene S2	4.28	4.97
	453574	AJ767947	Hs.50841	ESTs	4.25	3.66
	410677	NM_003278	Hs.65424	telomericin (plasminogen-binding protein	4.25	17.64
	424633	NM_003894	Hs.153405	period (Drosophila) homolog 2	4.22	3.13
	425448	T11884	Hs.293668	ESTs	4.21	4.09
80	410480	R87457	Hs.63364	cadherin 13, H-cadherin (heart)	4.19	2.76
	406805	AB660003	Hs.296031	ESTs	4.19	3.87
	438533	AA440266	Hs.170673	ESTs, Weakly similar to T24932 hypoteth	4.18	5.53
	451831	NM_0016174	Hs.460	activating transcription factor 3	4.18	7.74
	431211	NM6649	Hs.322733	gap junction protein, beta 2, 28kD (conn	4.17	2.83
	434936	AJ285970	Hs.183817	ESTs	4.17	4.39
	430361	A003395	Hs.239526	sterol C4-methyl oxidase-like	4.17	2.38
	446429	D17408	Hs.21223	caposin 1, basic, smooth muscle	4.16	5.15

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5	421978	AJ243652	Hs.110196	NICE-1 protein	4.15	8.07
	431735	AL038624	Hs.208752	ESTs, Weakly similar to ALU8_HUMAN ALU 5	4.14	4.92
	442544	AW467376	Hs.129640	ESTs	4.12	4.00
	451814	AA647992	Hs.130003	ESTs	4.11	4.58
	410023	AB011169	Hs.57929	sh (Drosophila) homolog 3	4.10	3.92
10	451721	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09	3.19
	426539	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	4.09	3.69
	430191	AI145860	Hs.186609	ESTs	4.07	4.49
	430433	AA476883	Hs.273766	ESTs	4.07	3.74
	425992	AA367069	Hs.100636	ESTs	4.06	4.37
15	428931	AA994979	Hs.98967	ATPase, H ⁺ -transporting, lysosomal, non	4.05	4.15
	425292	L20815	Hs.507	connexosome	4.04	11.00
	420845			ENSG00000224626:KIAA0444 PROTEIN (FRAGME	4.03	4.18
	439873	BE159253	Hs.300638	ESTs	4.03	3.86
	432305	M62402	Hs.274313	insulin-like growth factor binding prote	4.02	8.79
20	420789	AF670057	Hs.199882	ESTs	4.02	4.34
	453580	AA348626	Hs.5650	hypothetical protein FLJ23306	4.02	5.13
	428967	NM_003681	Hs.194679	WNT1 inducible signaling pathway protein	4.01	4.29
	429556	AW139399	Hs.98988	ESTs	4.01	4.69
	448585	AB020676	Hs.21543	KIAA0862 protein	4.01	4.52
25	403710			C6000160:gil12735793na[XP_011928.1] pr	4.00	3.31
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	3.98	6.61
	421465	AA243499	Hs.104800	hypothetical protein FLJ10134	3.98	3.79
	437611	AA897108		gla080806.s1 Soares_NFL_T_GBC_S1 Homo s	3.97	4.24
	426500	NM_014638	Hs.170156	KIAA0450 gene product	3.96	4.93
30	448710	TC6205	Hs.304184	ESTs	3.96	4.54
	408199	AA132637	Hs.15396	Homo sapiens, clone IMAGE:394099, mRNA,	3.95	5.57
	428340	AF261088	Hs.154721	acinarize 1, soluble	3.94	3.24
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl Coenzyme A sy	3.94	9.16
	456972	AA65547	Hs.2017	ribosomal protein L38	3.93	4.07
35	416381	AA682953	Hs.119237	ESTs	3.93	4.45
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	3.92	15.00
	456332	AA228357		gluc39405.r1 NCI_GCAP_Pv2 Homo sapiens	3.91	4.88
	445507	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	3.91	3.91
	425411	AF000708	Hs.165954	hypothetical protein FLJ20701	3.90	4.50
40	446733	AA563360	Hs.26040	ESTs, Weakly similar to fatty acid omega	3.90	3.89
	424588	U54817	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	3.89	5.11
	452894	AF598065	Hs.61558	ESTs	3.88	3.73
	423070	AA475861	Hs.292454	ESTs	3.87	4.47
	439605	AF086453	Hs.54511	ESTs	3.86	4.01
45	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	3.85	3.01
	431247	ALJ21578	Hs.278469	nutrin 4	3.85	3.35
	425350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.85	5.15
	441319	AF544869	Hs.133081	ESTs, Weakly similar to T08700 hypothet	3.84	5.03
	428277	AF250789	Hs.32478	ESTs	3.84	3.26
50	444252	R21135	Hs.54985	ESTs	3.83	5.58
	416265	AA177088	Hs.190065	ESTs	3.82	3.87
	416875	W19971	Hs.233459	ESTs	3.80	2.92
	440509	BE410132	Hs.134302	ESTs, Weakly similar to 117279 hypophes	3.80	4.36
	425053	AF147078	Hs.150853	p63-responsive gene 5	3.80	7.53
55	427081	AA74533	Hs.170528	ESTs, Moderately similar to ULNCC_HUMAN 1	3.77	4.81
	458222	AW135652		hypothetical protein DKFZp434K1421	3.77	3.56
	451507	AF208121	Hs.147313	ESTs, Weakly similar to 130222 hypophes	3.77	3.20
	436283	AF480319	Hs.120058	ESTs	3.76	3.76
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	3.76	2.65
60	445986	Y07653	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	3.75	7.59
	434206	AW136973		ESTs, Weakly similar to S63890 mitogen I	3.72	3.95
	424824	AF127440	Hs.143873	ESTs	3.72	3.52
	457441	AW085961	Hs.130053	inquinolase-class homeobox protein IRX2	3.71	3.05
	452241	AL050204	Hs.28540	Homo sapiens mRNA, cDNA DKFZp596F1223 (I	3.70	4.84
65	451845	AA021631	Hs.16515	ESTs	3.69	3.69
	413922	AF535695	Hs.221024	ESTs	3.68	4.22
	422746	NM_004464	Hs.119651	glycan 3	3.68	4.29
	433934	AF4973261	Hs.216292	ESTs	3.68	4.39
	452547	AA335295	Hs.74120	apoptosis specific 2	3.66	12.23
70	400295	W72838		A-805681 IL-6T095-190199-019 BT095 Homo	3.66	9.25
	419098	AA234041	Hs.87271	ESTs	3.66	4.94
	417054	AF017060		aldehyde oxidase 1	3.65	4.51
	423974	AL118754		glcDKFZp76IP1910_r1 761 (synonym: hanny2)	3.65	4.32
	431362	AB847223	Hs.293606	ESTs	3.65	3.73
75	420506	AW977779	Hs.194613	ESTs	3.65	3.25
	448065	AA591777	Hs.172759	ESTs, Moderately similar to ALU7_HUMAN A	3.64	4.62
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65557 alpha-1C-	3.64	4.54
	451951	AF082870	Hs.210554	ESTs	3.64	3.69
	436679	AF127483	Hs.120451	ESTs, Weakly similar to unnamed protein	3.64	3.39
80	412676	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con	3.62	3.62
	412668	AA456195		hypothetical protein FLJ14621	3.62	4.22
	413859	AF083692	Hs.75608	tight junction protein 2 (zona occludens	3.62	3.06
	444726	NM_005147		interleukin regulatory factor 5	3.59	10.65
	428722	U76456	Hs.190787	issue inhibitor of metalloproteinase 4	3.59	3.31
	429973	AF423317	Hs.164680	ESTs	3.59	3.71
	452413	AW082633	Hs.215030	ESTs	3.58	4.66
	416157	NM_003243	Hs.342874	transferrin growth factor, beta recepto	3.58	4.44

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	430397	A924533	Hs.105607	bicarbonate transporter related protein	3.57	3.74
	411939	A935585	Hs.146246	ESTs	3.57	12.42
	450353	A124461	Hs.103296	ESTs. Weakly similar to S6657 alpha-1C-	3.57	4.11
	432406	A130571	Hs.343656	KIA0069 protein	3.57	2.94
	432669	AW971945	Hs.253236	ESTs	3.56	3.14
	432381	AW135957	Hs.175382	ESTs	3.56	3.48
	410173	AA706017	Hs.119944	ESTs	3.56	3.37
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	3.56	9.93
	413205	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fls, clone L	3.55	4.24
	434360	AW015415	Hs.127780	ESTs	3.55	4.77
	432973	AF036461	Hs.156574	arachidonate 12-lipoxygenase, 12R type	3.53	5.65
	426881	AB018297	Hs.159183	KIA04754 protein	3.52	4.79
	428382	AF007132	Hs.184019	Homo sapiens clone 23551 mRNA sequence	3.51	4.46
	451184	T87943	Hs.157608	transcription factor 7-like 2 (T-coil-2)	3.51	3.63
	449496	BE379077	Hs.130649	ESTs. Weakly similar to I36022 hypophelli	3.51	3.30
	426831	UA6689	Hs.159608	aldehyde dehydrogenase 3 family, member	3.48	8.66
	428212	BE274552	Hs.183109	monamine oxidase A	3.48	9.54
	425432	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog	3.48	6.05
	401760			Target Exon	3.48	7.86
	427899	AA829286	Hs.332053	serum amyloid A1	3.47	3.67
	451767	A1625014	Hs.187328	ESTs	3.46	3.65
	452849	AF004424	Hs.30792	hock2 protein	3.45	5.66
	427409	AA383206	Hs.2156	PdR-related orphan receptor A	3.45	5.02
	447165	AL042400	Hs.75568	Homo sapiens, Similar to FKBP cDNA 1700	3.45	3.61
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second type	3.45	7.71
	420876	AA919425	Hs.177744	ESTs	3.44	8.48
	421114	AF975251	Hs.290156	ESTs. Weakly similar to 178855 serine	3.44	4.47
	426233	AA372796	Hs.265339	ESTs. Weakly similar to AF161356 1 HSPC0	3.44	3.96
	428221	U95781	Hs.183075	ATPase, Ca transporting, cardiac muscle, Target Exon	3.42	4.32
	403593			hypothetical protein FLJ29207	3.42	6.35
	423467	AK000214	Hs.129014	CG-58 protein	3.42	3.34
	447731	AA373527	Hs.19335	ESTs	3.41	2.44
	456327	H68741	Hs.38774	ESTs	3.40	3.46
	413880	AA660842	Hs.110915	interleukin 22 receptor	3.37	3.61
	429501	AF700588	Hs.293308	ESTs. Weakly similar to A34612 zinc fing	3.37	3.44
	437515	AW944355	Hs.35229	hypothetical protein MGC11242	3.36	4.87
	420231	R06866	Hs.19813	ESTs	3.36	8.60
	424010	AL080188	Hs.137556	Homo sapiens mRNA cDNA DKFZ434A132 (fl	3.36	6.20
	426789	FD5096	Hs.23837	Homo sapiens cDNA FLJ11812 fls, clone HE	3.34	3.40
	424274	AA265539	Hs.116252	ESTs. Moderately similar to ALU1_h1UMAN A	3.34	3.35
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	3.34	4.05
	418318	UA7732	Hs.84072	transmembrane 4 superfamily member 3	3.33	4.36
	413163	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t	3.32	9.47
	429456	AA769986	Hs.185022	ESTs	3.32	3.88
	415349	X66089	Hs.75227	myomesin (M-protein) 2 (165kD)	3.31	4.01
	403905	AA337272	Hs.293656	ESTs. Moderately similar to S72481 proba	3.31	3.31
	443072	A1937532		gb-w78002.x1 NC1_CGAP_Bm25 Homo sapien	3.31	4.40
	437596	AA761490		ESTs. Moderately similar to S65657 alpha	3.30	5.31
	444094	AF05764	Hs.202394	ESTs	3.29	3.47
	437150	RS1407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A	3.29	3.76
	407334	AA494411	Hs.266031	ESTs	3.28	4.30
	423017	AW178781	Hs.227948	serine (or cysteine) proteinase inhibitor	3.28	3.78
	447875	R22229	Hs.13295	ESTs	3.28	3.44
	418969	WC1311	Hs.28907	hypothetical protein FLJ20258	3.27	3.71
	411982	AA099500		gb-zk85012.1 Soares_pregnant_virus_NH4	3.27	4.28
	424395	AA165082	Hs.146388	microtubule-associated protein 7	3.27	3.82
	420448			CHSP000002389707-CX30 (Fragment)	3.27	5.60
	420418	R98852	Hs.36029	heart and neural crest derivatives expre	3.26	6.19
	429231	AA446644	Hs.692	GAT33-2 antigen; epithelial glycoprotein	3.26	4.24
	434562	T10269	Hs.4285	Homo sapiens cDNA FLJ22505 fls, clone H	3.25	5.17
	445234	AW137636	Hs.149059	ESTs	3.25	5.98
	426150	NM_003658	Hs.187218	Ear-like homeobox 2	3.25	5.21
	400176			Enx Control	3.25	3.60
	421462	AF016495	Hs.104624	osteopontin 9	3.25	3.93
	420677	AW086215	Hs.246096	ESTs	3.25	3.53
	424125	A31669	Hs.1126	inhibin, beta B (activin AB beta polypep	3.24	3.88
	443872	AA320352	Hs.5667	bulbocystamine (gamma), 2-oxoglutarate di	3.24	5.64
	420682	AA380552	Hs.88602	ESTs	3.24	4.13
	423725	AA403108	Hs.132127	hypothetical protein LOC57822	3.23	4.90
	431157	A0823969	Hs.132678	ESTs	3.23	3.97
	404069	A1489698		gb-ly40e07.s1 NC1_CGAP_P112 Homo sapiens	3.23	3.39
	449961	AW265634	Hs.133100	ESTs	3.21	5.36
	407948	AW085161	Hs.56279	ICEBERG caspase-1 inhibitor	3.21	4.61
	400835			chromosome 2 open reading frame 2	3.21	3.62
	413229	A1056885	Hs.133539	ESTs	3.21	3.43
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.21	3.72
	450860	AA021007		integrin, beta 8	3.20	5.89
	444816	Z48633	Hs.283742	H1scapeta mRNA for retrotransposon	3.19	6.84
	453855	AA029576	Hs.32658	ESTs. Weakly similar to ALU1_h1UMAN !!!	3.19	3.59
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.19	3.51
	420074	AA253425	Hs.190074	ESTs	3.18	5.50
	418481	M81945		CD34 antigen	3.18	3.65
	408522	A1541214	Hs.46320	Small proline-rich protein SPRK (human,	3.18	7.43

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5	435337	A078307	Hs.134317	ESTs, Weakly similar to PCA259 lentitin	3.17	3.51
	445502	AW379160	Hs.12813	DKFZP434J214 protein	3.17	3.62
	412477	AA150864	Hs.296259	microsome glutathione S-transferase 1	3.17	5.39
	421757	Z28891	Hs.249163	paraoxonase 3	3.16	3.60
	413836	A072727	Hs.21766	lipoic acid hydroxylase	3.16	5.56
10	420309	AW043637	Hs.22891	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.15	1.99
	444895	A0643383	Hs.21479	solute carrier family 7 (cationic amino	3.15	4.45
	414869	AA157291	Hs.21479	ubiquitin 1	3.13	4.40
	412947	AA122277	Hs.103505	glucosylceramidase 1 Scores_pregnanat_xenot_NBH	3.13	3.30
	434265	A0516207	Hs.9167	SFD domain binding glutamic acid-rich pr	3.12	4.62
15	421335	X99977	Hs.103505	ARS component B	3.11	11.54
	401905			ENSP00000252327: Sialic regulatory elem	3.10	2.85
	443514	BE464268	Hs.141337	ESTs	3.09	3.66
	418817	AA913229	Hs.19339	ESTs	3.08	3.08
	438727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	3.08	4.18
20	435858	AF254260	Hs.283009	tufelin 1	3.08	3.96
	430285	AF171602	Hs.106440	ESTs	3.07	3.30
	440106	A0004010	Hs.171941	ESTs	3.07	5.19
	432908	A0951996		ESTs	3.07	3.85
	450086	AW016343	Hs.233301	ESTs	3.07	3.38
25	451529	AF1917001	Hs.208641	ESTs	3.07	3.29
	418943	NM_005239	Hs.35145	vets swine erythroblastosis virus E26 o	3.06	4.12
	426848	H72531	Hs.36190	ESTs	3.05	4.34
	429506	D49835	Hs.171942	ras responsive element binding protein 1	3.05	3.97
	425955	T96506	Hs.248549	ESTs, Moderately similar to S65557 alpha	3.05	3.20
30	413822	AB95950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.05	3.89
	434230	AA551569		hypothetical protein PRO2622	3.04	3.63
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	3.04	8.09
	416566	A0821562	Hs.189682	ESTs	3.03	3.43
	448618	A0784459	Hs.15978	KIAA 1272 protein	3.01	3.25
35	414665	AA160873		serum amyloid A1	3.01	9.22
	446682	AW205632	Hs.211198	ESTs	3.00	3.30
	443801	AW206942	Hs.253594	intron of: trichorhinophalangeal syndro	2.99	3.74
	412446	AF768015		ESTs	2.99	4.47
	445271	AW338067	Hs.7989	Homo sapiens cDNA FLJ11946 fs, clone HE	2.99	4.35
40	435702	A003647	Hs.121001	Homo sapiens, clone IMAGE:3460293, mRNA	2.98	3.49
	403190			Target Exon	2.98	3.92
	434442	AA737415		ESTs	2.98	3.61
	435933	BE073597	Hs.124863	ESTs	2.98	3.86
	410453	AA749036		gb:BC2-BT0318-21199-011410 BT0318 Homo	2.98	3.49
45	414766	AW263452	Hs.16228	ESTs	2.97	3.63
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell	2.97	3.99
	451341	BE779383	Hs.26557	phallophilin 3	2.97	6.90
	432195	AA594712	Hs.116878	ESTs	2.97	3.30
	401747			Homo sapiens keratin 17 (KRT17)	2.97	4.10
50	431316	AA502663	Hs.145037	ESTs	2.96	3.05
	445437	A0241465	Hs.148725	ESTs	2.95	7.12
	421650	AW183667	Hs.106657	calbindin 2 (29KD, calretinin)	2.95	5.66
	456371	S76825	Hs.89965	insulin receptor	2.94	4.59
	449543	AF070832	Hs.23729	Homo sapiens clone 24405 mRNA, sequence	2.94	4.12
55	436664	AW197887	Hs.253353	ESTs	2.93	3.57
	405962	M13485		gb:Human metallothionein I-B gene, exon	2.93	2.66
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.92	7.48
	429789	AW207175	Hs.106771	ESTs	2.92	3.26
	414629	AA345824	Hs.76588	carboxylesterase 1 (monocytic/macrophage	2.92	3.48
60	444204	AF129184	Hs.143040	ESTs	2.92	3.92
	421407	T83281	Hs.182278	ESTs, Weakly similar to CGHUSC collagen	2.91	6.55
	453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.90	3.92
	429538	BE182552	Hs.139322	small proline-rich protein 2A	2.88	4.75
	452554	AW452434	Hs.58006	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.88	6.74
65	417184	N52510	Hs.266597	Homo sapiens cDNA: FLJ21499 fs, clone C	2.87	3.97
	412093	BE242681	Hs.14847	ESTs	2.86	3.48
	424135	AW594455	Hs.140978	Homo sapiens mRNA, cDNA DKFZp762h106 (fr	2.86	3.32
	437167	AL050184	Hs.21610	DKFZP434B033 protein	2.86	3.87
	454065	BE394588		gb:G131108F1 NB_MGC_44 Homo sapiens c	2.86	3.43
70	420230	AL034344	Hs.284186	forkhead box C1	2.85	3.67
	403108			ENSP00000241415: Hypothetical 67.7 kDa p	2.85	2.62
	434433	AW629759		gb:ht70e05.y1 NC_CGAP_GU1 Homo sapiens	2.84	3.33
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone C17	2.83	2.66
	429429	AW629725	Hs.334337	Hypothetical protein MG24348	2.83	3.59
75	451721	NM_005646	Hs.26915	spectrin, beta, non-erythrocytic 2	2.83	3.36
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	2.83	4.50
	429259	AA420450	Hs.292911	Phallophilin	2.81	4.81
	423623	AW259828	Hs.153650	ESTs	2.80	1.98
	433837	AW024214	Hs.102307	ESTs, Weakly	2.80	3.36
80	452089	T97294	Hs.271492	ESTs, Weakly similar to PCA211 hepatoc	2.80	3.62
	441187	AA195237	Hs.7734	Hypothetical protein FLJ22174	2.80	3.52
	421965	A0301100	Hs.346482	gb:EST14128 Testis tumor Homo sapiens cD	2.79	3.49
	432098	AF252297	Hs.91546	cytochrome P450 related metabolizing pr	2.79	2.31
	429128	AA463929	Hs.119316	ESTs	2.78	4.17
	438913	A0380429	Hs.172445	ESTs	2.77	3.65
	445029	AF196481		mdm2 2	2.76	3.79
	419923	AW081455	Hs.120219	ESTs	2.76	3.00

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5	416508	R30789	Hs.55406	ESTs. Moderately similar to ALUB_HUMAN A	2.76	3.55
	412507	L36645	Hs.73564	EphA4	2.76	3.90
	446339	AL046962	Hs.14845	forkhead box O3A	2.75	3.50
	433710	AI041867	Hs.108520	ESTs	2.75	3.33
	432375	BE53069	Hs.2967	S100 calcium-binding protein P	2.74	3.77
10	409213	U61412	Hs.51133	PTK6 protein tyrosine kinase P	2.74	3.76
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.74	8.19
	408839	AW027084		glox6p1h05x1 NCL_CGAP_Ov35 Homo sapiens	2.73	3.93
	433911	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.73	11.46
	444026	AA205759	Hs.10119	hypothetical protein FLJ14357	2.73	6.17
15	433713	AW976511	Hs.112592	ESTs	2.72	3.42
	454317	NM_002277	Hs.41696	keratin, hair, acidic, 1	2.72	4.76
	429493	BE208584	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.72	3.74
	439547	AA420710	Hs.270098	ESTs. Weakly similar to 138022 hypotheri	2.72	3.44
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	2.72	4.95
20	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.72	4.29
	435016	AD84219	Hs.130749	ESTs. Weakly similar to 138022 hypotheri	2.71	4.45
	445667	AB023227	Hs.23860	KIAA1010 protein	2.71	3.72
	407112	AA070801	Hs.51615	ESTs. Weakly similar to ALU7_HUMAN ALU S	2.70	3.82
	433848	AF095719	Hs.53764	carboxypeptidase A4	2.70	2.76
25	430152	AB001325	Hs.234642	acropapin 3	2.69	4.26
	455063	NM_006744	Hs.76461	retinol-binding protein 4, interstitial	2.69	6.72
	424471	AA341329	Hs.311524	ESTs	2.68	4.57
	453201	AI432195	Hs.135998	ESTs	2.68	3.69
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	2.68	4.25
30	404986			Tariff EBJ	2.67	4.28
	404543	AI885516	Hs.95612	ESTs	2.65	6.51
	430937	XS3463	Hs.2704	glutathione peroxidase 2 (gastric/intest	2.65	3.78
	452887	AI702223	Hs.107253	hypothetical protein DKF_Zp761F241	2.64	6.38
	444169	AW649170	Hs.58755	ESTs	2.64	3.40
35	428900	AI819395	Hs.184641	fatty acid desaturase 2	2.64	4.47
	408365	BE072425	Hs.44479	hypothetical protein FLJ20199	2.64	4.01
	430293	H28383		glyf52d03.r1 Soares breast 3NHdEst Homo	2.63	4.08
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	2.62	2.51
	447335	BE617095	Hs.286192	hypothetical protein FLJ20940	2.61	3.62
40	429343	AA000785	Hs.193480	Homo sapiens. Similar to epain 3, clone	2.61	3.68
	431166	AW971186	Hs.293839	ESTs	2.61	3.33
	406659	AF134160	Hs.7327	claudin 1	2.61	3.53
	413542	BE259738	Hs.73424	inhibitor of DNA binding 1, dominant neg	2.61	4.48
	413856	AB213511	Hs.131133	ESTs. Weakly similar to ALU7_HUMAN ALU S	2.60	3.51
45	407299	AA480206	Hs.289770	ESTs. Weakly similar to 138022 hypotheri	2.59	3.82
	449539	W80363	Hs.58446	ESTs	2.58	4.05
	413884	AF668892	Hs.235758	hypothetical protein FLJ12389 similar to	2.58	4.19
	445620	A245225	Hs.17441	ESTs	2.57	3.44
	433688	AF628467	Hs.112572	Homo sapiens cDNA FLJ14130 fls, clone MA	2.56	3.57
50	424834	AA001432	Hs.153408	Homo sapiens cDNA FLJ10570 fls, clone NT	2.56	3.47
	407083	Z48511		H.sapiens XG mRNA (clone PEP11)	2.55	3.61
	406790	AA233303		ribosomal protein L27a	2.54	4.36
	450472	AI190071	Hs.55278	ESTs	2.54	4.30
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.54	3.82
55	454034	NM_000891	Hs.575	aldohyde dehydrogenase 3 family, member	2.54	3.44
	430821	AA487264	Hs.154974	Homo sapiens mRNA: cDNA DKF_Zp667N064 (tr	2.54	4.55
	402575			Rho GTPase activating protein 1	2.53	5.47
	429554	NM_012275	Hs.207224	interleukin 1, delta	2.53	2.40
	431631	AA548906	Hs.122244	ESTs	2.52	3.79
60	408806	AW647814	Hs.75608	Homo sapiens cDNA: FLJ21532 fls, clone C	2.52	4.51
	420235	AA256736	Hs.31178	ESTs	2.51	4.21
	436314	AI983409		ESTs	2.51	3.11
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog	2.50	5.62
	429547	AW009166	Hs.99376	FGFESLH predicted novel secreted protein	2.49	2.60
65	410532	TS3088	Hs.155376	hemoglobin, beta	2.48	4.73
	413475	AW021488	Hs.26981	ESTs	2.48	3.90
	429325	AW088739	Hs.243770	ESTs	2.48	3.71
	424604	AW865388	Hs.151076	KIAA1243 protein	2.48	4.16
	414320	U13615	Hs.75933	ankyrin 3, node of Ranvier (ankyrin G)	2.48	3.80
70	423929	AB9136	Hs.139626	chymase 1, mast cell	2.48	4.47
	410275	UB5658	Hs.61796	transcription factor AP-2 gamma (activat	2.47	2.05
	444935	AA262449	Hs.223569	ESTs	2.47	5.96
	445389	NM_016631	Hs.12292	period (Drosophila) homolog 3	2.47	3.41
	437887	AA710561	Hs.145170	hypothetical protein FLJ23969	2.47	6.80
75	446292	AF081497	Hs.275682	Rh type C glycoprotein	2.46	7.37
	409178	BE393940	Hs.50915	laktikasin 5	2.46	5.59
	452895	AI624646	Hs.119567	ESTs. Weakly similar to A47582 B-cell gr	2.46	6.03
	447179	AW015633	Hs.157299	ESTs	2.46	3.23
	414459	Y11255	Hs.75171	CCNA1/tenascin binding protein (CEBP),	2.46	3.56
80	428188	MS8447	Hs.22	transglutaminase 1 (K) polypeptide epide	2.45	3.94
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	2.44	2.17
	435039	H57130	Hs.120525	ESTs	2.44	2.94
	412810	M21514	Hs.74615	platelet-derived growth factor receptor,	2.43	4.61
	416749	AW068550.comp	Hs.79732	fibulin 1	2.43	4.46
	444672	Z59636	Hs.11665	tenascin, alpha 5	2.42	6.39
	433143	BE352155	Hs.294035	ESTs. Weakly similar to ALUS_HUMAN ALU S	2.42	3.45
	405997	U07807		metallothionein IV	2.42	3.52

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423184	NM_004428	Hs.1624	ophle-A1	2.41	4.34
421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine)	2.41	5.08
456826	A871742	Hs.302428	wingless-type MMTV integration site tam	2.41	3.92
424897	A245719	Hs.194385	hypothetical protein FLJ20734	2.41	5.18
400232			NM_001695? Homo sapiens casein kinase 2	2.41	4.82
421481	AW391972	Hs.104596	KIAA1324 protein	2.40	3.03
442083	R50192	Hs.165062	ESTs	2.39	4.21
422787	F16356	Hs.114346	cyclochrome c oxidase subunit VIIa polype	2.39	8.60
416004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.39	2.57
457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapi	2.39	3.85
418355	LA2603	Hs.1165	ATPase, H7 transporting, noncyclic, alp	2.38	3.84
431179	ALJ38644	Hs.115432	aldehyde dehydrogenase 2 family (mitoch	2.37	7.89
425653	NM_013261	Hs.198468	peroxisome proliferative activated rec	2.37	3.77
402338			Target Exon	2.37	3.46
443725	AW245580	Hs.9701	growth arrest and DNA-damage-inducible,	2.37	4.57
436723	AW975895	Hs.307486	ESTs	2.37	6.39
422659	AA215363	Hs.262958	hypothetical protein DKFZp384B044	2.37	3.92
409212	AI082423	Hs.141892	ESTs	2.36	3.70
451323	AI003313	Hs.34579	ESTs, Moderately similar to ALU6_HUMAN A	2.36	3.29
400307	AF005081		Homo sapiens skin-specific protein (x33)	2.36	9.96
421933	R27487	Hs.110671	growth arrest and DNA-damage-inducible,	2.35	5.16
451092	AG207265	Hs.13765	Homo sapiens mRNA for FLJ00074 protein,	2.34	5.24
446948	BE409053	Hs.29629	peroxisomal long-chain acyl-CoA thioeste	2.34	3.77
424405	AB031480	Hs.146824	SPR1 protein	2.34	4.43
426650	AF017307	Hs.186286	ET4-like factor 3 (ets domain transcript	2.34	5.64
425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.33	3.51
422106	DB4239	Hs.111732	Fc fragment of IgG binding protein	2.33	6.85
423603	M92843	Hs.343586	zinc finger protein homologous to Zfp-35	2.33	5.57
453999	BE328153	Hs.240087	ESTs	2.32	3.40
413358	T78763	Hs.90063	neurocanin delta	2.32	6.62
430468	NM_004673	Hs.241519	angiotensin-II-1	2.30	3.50
456876	AL044870	Hs.208780	ESTs, Weakly similar to T29647 hypotheti	2.32	3.27
454947	AW846590		gb-OUV-CT0180-011099-025-007 CT0180 Homo	2.32	4.43
429211	AF026933	Hs.196249	gap junction protein, beta 5 (connexin 3	2.31	7.22
438282	BE238268	Hs.195432	aldehyde dehydrogenase 2 family (mitoch	2.31	3.34
420202	AL036557	Hs.95910	putative lymphocyte GAG1 switch gene	2.31	8.47
419245	AT32742	Hs.87440	ESTs	2.31	3.99
444820	AW450567	Hs.236240	ESTs	2.30	3.30
417314	NE8168	Hs.55044	gb-zal101.01 Scarses fetal liver spleen	2.30	3.12
409586	AL050214	Hs.55044	DKFZP569i2123 protein	2.30	3.52
433662	W07162	Hs.150826	RAR25 RAB25, member RAS oncogene family	2.29	6.11
481176	AA045487	Hs.60677	ESTs	2.29	6.59
410531	AW972963		gb-OUV-CT0224-261099-035-g02 CT0224 Homo	2.29	3.29
425982	R06327	Hs.189726	ESTs	2.29	3.37
435684	NM_001290	Hs.4980	LIM domain binding 2	2.29	4.54
453003	AA808466	Hs.103395	hypothetical protein FLJ14146	2.28	3.70
434411	AA632549	Hs.201372	ESTs	2.28	4.40
407304	AF005081		gb-Homo sapiens skin-specific protein (x5	2.28	10.57
411579	AC005258	Hs.70830	U6 snRNA-associated Sm-like protein Lsm7	2.28	4.06
401205			Target Exon	2.27	2.71
443102	AT247472	Hs.132965	ESTs	2.27	5.66
422109	ST3265	Hs.1473	serpin-releasing peptide	2.26	3.54
434987	AW975114		ESTs	2.26	3.72
415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	2.26	3.42
422615	AA327017	Hs.176584	ESTs	2.25	6.21
424903	AF191369	Hs.187763	Homo sapiens HSPC106 mRNA, partial cds	2.25	3.62
443049	AO289613	Hs.132343	ESTs	2.25	3.13
444637	T19101	Hs.11494	fibulin 5	2.24	6.43
410026	AB912061	Hs.55016	hypothetical protein FLJ21935	2.23	3.31
418879	BE471580	Hs.86869	growth factor receptor bound protein 7	2.23	4.17
429587	AA263969	Hs.334706	Homo sapiens cDNA FLJ11801 t8, clone HE	2.23	3.79
431986	AA536130	Hs.149018	Novel human gene mapping to chromosome 20	2.22	3.54
409571	AA504249	Hs.187585	ESTs	2.22	3.87
446051	BE048061	Hs.37354	ophle-A3	2.22	4.57
422418	AK001383	Hs.116385	hypothetical protein FLJ10521	2.21	4.25
453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.21	4.07
435748	AA699796	Hs.117335	ESTs	2.20	3.36
420105	AW015571	Hs.32244	ESTs, Weakly similar to FMOO3_HUMAN FIBRO	2.19	6.55
444922	AS91760	Hs.144671	Homo sapiens cDNA FLJ11357 t5, clone PL	2.19	3.51
433052	AW971983	Hs.293003	ESTs, Weakly similar to PC4259 lamin	2.19	3.32
430310	U50115	Hs.239069	four and a half LIM domains 1	2.19	3.83
447205	BE617015	Hs.11005	ESTs, Moderately similar to T17373 plasmin	2.19	15.65
446957	RA0278	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.18	3.54
452649	F33688	Hs.284735	transferrin	2.18	3.36
417051	AB759444	Hs.188691	Homo sapiens cDNA FLJ12033 t5, clone HE	2.18	3.77
432647	AB078481	Hs.278581	fibroblast growth factor receptor 2 (bac	2.18	5.64
401192			Target Exon	2.17	3.33
421752	AK001521	Hs.107882	hypothetical protein FLJ10659	2.16	3.44
456645	AJ243662	Hs.110196	NDC-1 protein	2.16	2.39
421263	AB020638	Hs.103000	KIAA0831 protein	2.16	3.37
446555	VQ2260	Hs.21299	ESTs, Weakly similar to AF151840 1 CG-8	2.16	5.17
453524	AL042983	Hs.125063	Homo sapiens cDNA FLJ13825 t8, clone TH	2.15	3.87
429350	AB754634	Hs.131987	ESTs	2.15	3.50

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448144	AW169230		
429002	AW248439	Hs 2340	
429297	X82494	Hs 198662	
452093	AA414453	Hs 27850	
428848	NM_000230	Hs 194236	
407584	W25945	Hs 8173	
453155	AF052126	Hs 552	
453283	AA694366	Hs 296914	
456906	AF 117546	Hs 156537	
414815	AW292140	Hs 130286	
417155	T75125	Hs 259148	
416673	T77052	Hs 14039	
452208	AA024932	Hs 31095	
413966	AA132936	Hs 173704	
430967	H16791	Hs 100695	
429015	BE 168484	Hs 194737	
439518	WT6326		
426468	AA397306	Hs 117558	
407555	Z45511		
418226	AA424202	Hs 83834	
423441	R56469	Hs 278338	
436961	AW375804	Hs 156704	
432633	AI796390	Hs 210667	
426102	AF200496	Hs 166371	
45467	AD239532	Hs 15617	
437124	AA594459		
407757	BE048414	Hs 165215	
407815	AW373860	Hs 183860	
443906	AA348031	Hs 7913	
423817	AL080207	Hs 134585	
406400			
437704	AA766142	Hs 131810	
412533	AA879853	Hs 69606	
425310	NM_000029	Hs 156256	
411821	BE295336	Hs 72249	
442599	AF078037	Hs 324051	
432212	AW137742		
453469	AB014533	Hs 33010	
443652	AB00692	Hs 134229	
452955	AW390282	Hs 31130	
424464	R68537	Hs 17962	
408702	AW959693	Hs 27069	
439906	AF168021	Hs 155507	
412825	AW167439	Hs 190651	
406784	AI144297	Hs 169401	
427309	NM_005714	Hs 175218	
451935	BE241876	Hs 32362	
404246			
443679	AK001810	Hs 9670	
410669	AW805749		
446193	AI279390	Hs 144658	
440226	AJ403107	Hs 146590	
434346	AA630445		
456098	AW747800	Hs 55016	
452467	AW608015		
442866	AF743317	Hs 263622	
434699	AA543687	Hs 149425	
417553	L09190		
449142	RI5913	Hs 194987	
407597	AA043626	Hs 339352	
452299	AB020463	Hs 347408	
423031	AJ278995		
433495	AW373784	Hs 71	
430420	AW140027	Hs 26373	
420139	NM_005357	Hs 35351	
418462	BE001595	Hs 85266	
447261	NM_006091	Hs 17917	
437220	AI 117542	Hs 334305	
407601	AC020320	Hs 37129	
443595	AF 169312	Hs 9613	
409007	AI122107	Hs 49599	
408717	AF045458	Hs 47061	
420055	NM_001487	Hs 94572	
430382	NM_000627	Hs 241257	
425078	NM_002599	Hs 154437	
423527	AI206965	Hs 105881	
447151	AI022813	Hs 92679	
422101	AW404176	Hs 111611	
456653	AB075919	Hs 104620	
443444	AW952619	Hs 17235	
420924	R01026	Hs 24321	
426048	AF169853	Hs 134478	
414092	Z14244	Hs 75752	

ESTs, Moderately similar to PCA259 ferri junction plakoglobin	214	3.28
flavin 2	214	5.05
Homo sapiens mRNA: cDNA DKF Zp596M0723 (I	214	4.32
lepin (murine obesity homolog)	214	3.99
hypothetical protein FLJ10803	214	3.38
sterol 5-alpha-reductase, alpha polypep	214	2.51
ESTs	213	3.28
Cas-8a-M (murine) ectopic retroviral tr	213	3.76
ESTs	213	4.16
hypothetical protein FLJ21801	213	3.57
ESTs	213	3.43
hypothetical protein MGC4093	212	6.67
ESTs, Moderately similar to A53959 brown	212	4.76
ESTs	212	2.64
KIAA0453 protein	212	3.30
glb260004.1 Soares_tetral_heart_Nb1H19W	211	2.49
ESTs	210	3.55
gb.H.sapiens XG mRNA (clone PEP11)	210	3.65
cytochrome b-5	210	5.14
abstent in melanoma 1 like	210	3.64
ESTs	210	3.21
ESTs	210	2.58
interleukin 1, zeta	209	3.77
ESTs, Weakly similar to ALU4_HUMAN ALU S	209	3.85
KIAA0669 protein	209	3.35
hypothetical protein MGC6395	208	4.41
hypothetical protein FLJ20277	208	5.01
ESTs	208	3.40
DKF Zp34G232 protein	208	3.52
kallikrein 8 (neuropilin-2) (KLK8)	208	4.19
ESTs, Moderately similar to ALU1_HUMAN A	207	3.30
ESTs	207	3.39
neuropeptide Y receptor Y1	206	3.55
three-POZ containing protein similar to	206	5.56
RetA-associated inhibitor	205	7.23
ESTs	204	3.52
KIAA0633 protein	204	4.01
ESTs, Weakly similar to 154001 hyperten	204	3.35
transmembrane 7 superfamily member 2	203	3.64
ESTs	203	4.36
hypothetical protein FLJ22939 similar to	203	3.31
ESTs	203	3.63
Homo sapiens cDNA FLJ13625 fs, clone PL	202	5.56
apolipoprotein E	202	3.40
potassium channel, subfamily K, member 7	202	4.58
hypothetical protein DKF Zp434K1210	202	3.57
Target Exon	201	7.30
hypothetical protein FLJ10548	201	5.61
superoxide dismutase 2, mitochondrial	201	3.05
ESTs, Weakly similar to 117257 hypothe	201	2.32
protein related with psoriasis	200	5.10
ESTs	200	3.51
hypothetical protein FLJ21935	200	4.96
ESTs	200	4.66
ESTs, Weakly similar to ALU5_HUMAN ALU S	198	3.72
Homo sapiens cDNA FLJ11590 fs, clone HE	198	3.11
trichoyalin	198	2.09
ESTs	198	3.50
Homo sapiens brother of CDO (BOC) mRNA,	198	6.25
hypothetical protein MGC13102	197	3.77
ESTs	197	3.62
alpha-2-glycoprotein 1, zinc	196	4.57
Homo sapiens cDNA: FLJ23449 fs, clone H	196	6.09
igf2nc, homous-sensitive	195	5.77
integrin, beta 4	195	6.09
extracellular link domain-containing 1	195	3.33
GS1989all	194	3.45
sodium channel, nonvoltage-gated 1, beta	194	5.46
PP4F19amruij angiotensin related protein	194	4.67
Homo sapiens mRNA: cDNA DKF Zp434G0827 (I	194	3.59
unc-51 (C. elegans)-like kinase 1	194	4.29
GDNF (general control of amino-acid cycl	194	3.38
lens crystallin growth factor beta b	193	3.33
phosphodiesterase 2A, cGMP-stimulated	193	4.06
hypothetical protein FLJ13824	193	4.70
Homo sapiens clone CDABP0014 mRNA sequen	191	3.77
ribosomal protein L27	191	3.18
Homo sapiens cDNA FLJ13694 fs, clone PL	191	3.41
Homo sapiens clone TCCCA00176 mRNA sequ	191	3.52
ESTs	191	3.22
ESTs	190	3.56
cytochrome c oxidase subunit VIII	190	4.15

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5	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.90	5.88
	428368	BE440042	Hs.83326	melix metalloproteinase 3 (stromelysin	1.90	2.28
	418418	RI1527	Hs.237517	ESTs	1.90	3.56
	440372	AA001295	Hs.133521	ESTs	1.89	3.90
	438752	AW238673	Hs.146038	ESTs	1.89	5.24
10	428193	NM_004235		Knoppel-like factor 4 (gut)	1.89	5.21
	432351	AB040955	Hs.322735	KIAA1522 protein	1.89	5.00
	433560	Z25942	Hs.243660	N-myc downstream-regulated gene 2	1.89	7.09
	427795	BE268268	Hs.188842	ribosomal protein L13	1.89	4.16
	410209	AI563651	Hs.65043	hypothetical protein PRO1635	1.80	3.35
15	449243	AW295031	Hs.198571	ESTs	1.89	4.26
	420225	AW243045	Hs.262076	Homo sapiens mRNA for KIAA1650 protein,	1.88	6.20
	443932	AW888222	Hs.5979	tenin	1.88	2.28
	427929	BE13835	Hs.181159	Homo sapiens mRNA, cDNA DKFpZp34CF017 (f	1.87	4.25
	400078			Est. Control	1.87	6.73
20	427539	AD29377	Hs.173724	creatine kinase, brain	1.87	5.51
	447374	AF253462	Hs.15375	KIAA1319 protein	1.87	3.42
	430346	AK000331	Hs.291541	KIAA0462 protein	1.87	4.15
	428223	AA424313	Hs.98402	ESTs	1.87	3.70
	408792	L29433	Hs.47913	coagulation factor X	1.87	4.08
25	433955	AA634682	Hs.307550	ESTs	1.87	4.16
	451583	AB53737	Hs.24133	ESTs	1.87	3.81
	426377	AK001921	Hs.159575	hypothetical protein MGC2550	1.86	5.55
	431647	AL138578	Hs.295738	hypothetical protein dJ79917.1	1.86	3.74
	422055	NM_014320	Hs.111029	putative heme-binding protein	1.86	4.68
30	422750	AL050276	Hs.42602	zinc finger protein 285	1.86	4.04
	422491	AA338548	Hs.117546	neuronal	1.86	4.37
	438942	AW975393	Hs.6451	PRO0659 protein	1.86	5.06
	400198			Est. Control	1.85	5.22
	427135	AL117415	Hs.173716	a disintegrin and metalloproteinase doma	1.85	3.41
35	427605	NM_000957	Hs.337445	ribosomal protein L37	1.85	4.73
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fs, clone HE	1.84	5.94
	441912	AA371484	Hs.159538	ESTs	1.84	3.73
	421632	AA325426	Hs.334689	ESTs, Weakly similar to ALU1, HUMAN ALU S	1.83	3.62
	440902	AF43461	Hs.222627	ESTs	1.83	2.39
40	431882	NM_001426	Hs.271977	engrailed homolog 1	1.83	3.30
	420772	AW752656	Hs.222707	KIAA1718 protein	1.83	3.73
	429197	H24471	Hs.26530	ESTs, Weakly similar to T20272 hypothet	1.82	3.41
	420736	NM_001038	Hs.25462	enograilin	1.82	3.38
	425922	AF037062	Hs.172914	retinol dehydrogenase 5 (11-cis and 9-cis	1.82	3.82
45	415403	AW993701		NS1-associated protein 1	1.82	3.80
	401131			NM_001651*1 Homo sapiens aquaporin 5 (AQP	1.82	5.53
	421324	BE257515	Hs.103503	deoxythymidylase I-like 2	1.81	5.53
	400079			Est. Control	1.81	6.79
	430513	AJ012008	Hs.241596	GEC protein	1.81	7.49
50	426508	W23184	Hs.170171	glutamate-ammonia lyase (glutamine synt	1.81	3.55
	425883	AL137708	Hs.151031	Homo sapiens mRNA, cDNA DKFpZp344K0322 (f	1.80	5.43
	422151	AF065215	Hs.190161	phospholipase A2, group IIB (cytosolic)	1.79	5.90
	432417	AL040360	Hs.162203	ESTs, Weakly similar to alternatively sp	1.79	3.63
	406467			Target Exon	1.79	4.16
55	444135	AK000374	Hs.10346	hypothetical protein FLJ20154	1.79	3.32
	426402	BE307327	Hs.03075	polymerase (RNA) II (DNA directed) poly	1.78	3.51
	412924	AA417813	Hs.444208	hypothetical protein FLJ22153	1.78	3.72
	426880	X01630	Hs.160786	argininosuccinate synthetase	1.78	3.29
	400300	X03363	Hs.25208	HER2 receptor tyrosine kinase (c-erb-b2,	1.78	3.44
60	451304	M92642		collagen, type XVI, alpha 1	1.78	3.57
	400082			Est. Control	1.78	3.82
	446603	NM_014635	Hs.15519	oxysterol-binding protein-related protei	1.77	3.48
	425415	M13903	Hs.157091	involucrin	1.77	4.64
	400083			Est. Control	1.77	6.31
65	427520	NM_003705	Hs.179866	schlier carrier family 25 (mitochondrial	1.76	3.47
	445971	AI652143	Hs.288382	hypothetical protein FLJ13111	1.76	4.21
	429807	AK002138	Hs.305227	Homo sapiens cDNA FLJ11276 fs, clone PL	1.76	2.83
	445550	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fs, clone HT	1.76	3.82
	412824	AW888075	Hs.11281	small proline-rich protein 2A	1.76	4.31
70	439927	AA854650	Hs.124597	ESTs	1.75	3.63
	410223	373775	Hs.650708	cathepsin B1 (fast-swift, skeletal m	1.75	3.79
	414500	W24067	Hs.76285	DKFpZP564B157 protein	1.75	3.55
	445182	AF244137	Hs.20397	hist. cell factor homolog	1.75	3.40
	439551	AF098480	Hs.59295	ESTs	1.75	2.85
75	430486	BE052109	Hs.241551	chloride channel, calcium activated, fam	1.75	3.54
	424389	AA339795		lymphocyte-specific protein 4	1.75	4.48
	450837	D58453	Hs.85969	hypothetical protein FLJ12270	1.74	3.40
	425920	AL040877	Hs.152208	claudin B	1.74	3.33
	435680	HS0946	Hs.284183	Homo sapiens galactin-related inhibitor	1.74	3.47
80	439639	AA370045	Hs.6507	AXIN1 up-regulated	1.73	5.22
	416950	AL049798	Hs.80552	dermoliponin	1.73	4.99
	400199			Est. Control	1.73	6.25
	409737	AB011539	Hs.56186	ESF-like domain, multiple 3	1.73	4.28
	424420	BE514743	Hs.149588	prostaglandin E synthase	1.72	3.42
	421545	AA292910	Hs.90034	hypothetical protein FLJ21915	1.72	2.12
	414323	NM_014759	Hs.334588	KIAA0273 gene product	1.71	4.82
	427226	M25079	Hs.153376	hemoglobin, beta	1.70	7.02

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5	406643	N77976	Hs.347339	hemoglobin, alpha 2	1.70	3.60
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.70	5.10
	439713	AL365412	Hs.107203	hypothetical protein from EUROMAGE 1759	1.69	2.92
	415512	Y15270	Hs.78482	paralamin	1.69	4.92
	407100	R29657	Hs.158203	gp.F1-117D-22 weak cell human fetal live	1.68	3.96
10	425903	W62517	Hs.158203	actin binding LIM protein 1	1.68	5.97
	433738	A1684802		ESTs	1.68	2.88
	406791	AJ220684	Hs.347339	hemoglobin, alpha 2	1.68	3.44
	428675	NM_004612	Hs.194594	mitogen-activated protein kinase kinase	1.68	2.44
	436661	AF220263	Hs.193920	MOIST 2 protein	1.67	3.56
15	463917	BRCA1b		Eos Control	1.67	3.34
	426923	AF112577	Hs.172887	phosphoryl-CoA hydrolase (RefSeq diseases	1.67	4.53
	426582	AV600208	Hs.2056	UDP-glycyltransferase 1 family, polype	1.67	3.36
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.67	5.22
	437201	F26279	Hs.171625	hypothetical protein MGCI4697	1.67	5.75
20	454478	AW805749		superoxide dismutase 2, mitochondrial	1.67	4.55
	405710	AJ703847	Hs.184014	ribosomal protein L31	1.66	3.80
	431593	NM_002108	Hs.276590	ESTs	1.65	2.45
	457820	AA341497	Hs.31408	RAR (RAS like GTPase)	1.66	2.44
	414899	AJ372588	Hs.8022	TUSA protein	1.66	4.06
25	414186	U33446	Hs.75799	protease, serine, 8 (procathepsin)	1.65	6.52
	418116	AA252457	Hs.85543	ESTs, Moderately similar to T02266 hypot	1.65	3.44
	403105			Target Exon	1.64	4.12
	450014	N41322	Hs.18441	ESTs	1.64	2.90
	436585	W26661	Hs.5288	Homo sapiens mRNA, cDNA DKFZp434M4245 (h	1.64	4.49
30	401429			C140007027/h41264649gBA36581.1) (AB	1.64	3.82
	420983	W56228	Hs.100764	cathepsin G	1.64	3.94
	433126	AB021262	Hs.93816	beta-catenin-interacting protein ICAT	1.63	3.29
	428150	AW950547	Hs.70312	cytochrome c oxidase subunit VIIa polype	1.63	7.05
	412295	AW608826	Hs.70312	poly(A)-binding protein, nuclear 1	1.63	4.01
35	430831	AA703230	Hs.269804	ESTs, Weakly similar to ALU1_HUMAN ALU 5	1.63	3.60
	429348	AJ242859	Hs.199731	Langenhans cell specific c-type lectin	1.62	2.84
	407082	Z47055	Hs.33905	glu.Human partial cDNA sequence, farnesyl	1.62	2.13
	452556	H78517	Hs.33905	glucosylceramidase 1	1.62	4.84
	415680	AA168963		ESTs, Moderately similar to S142946 ovarian cancer	1.62	3.33
40	446515	AL048875	Hs.199731	hypothetical protein DKFZ55681.33	1.62	3.96
	446919	TS3519	Hs.334692	hypothetical protein MGCI41411	1.62	5.65
	447330	BE279949	Hs.18141	lactacin 1	1.61	5.61
	412374	X01388	Hs.73849	apoptoprotein C-III	1.61	5.18
	402229			NM_001274*1 Homo sapiens nuclear receptor	1.61	3.57
45	414814	D14697	Hs.77393	farnesyl diphosphate synthase (farnesyl	1.61	2.08
	424069	A1850320		glucosylceramidase 1 (GABA) A recepto	1.60	3.89
	451335	AB023192	Hs.26285	imidazole receptor candidate	1.60	5.54
	420156	BE244537	Hs.167382	retinoid X receptor	1.60	4.79
	456267	A1127958	Hs.83393	cystatin E/M	1.60	2.50
50	436950	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	1.60	3.98
	417397	S67368	Hs.103598	gamma-aminobutyric acid (GABA) A recepto	1.60	3.28
	410032	J05841	Hs.89503	muscle 1, transmembrane	1.60	3.69
	440160	BE560269	Hs.7010	NP0002 protein	1.59	2.40
	417481	AA203281	Hs.6191	ESTs	1.59	3.60
55	406778	H06273	Hs.101651	Homo sapiens mRNA, cDNA DKFZp434C107 (fr	1.58	3.98
	422891			Target Exon	1.58	3.36
	425169	AW292600	Hs.128514	ESTs	1.58	4.00
	446429	A1681807	Hs.201391	ESTs	1.58	3.20
	426445	AA378739	Hs.187711	ESTs	1.57	3.63
60	425195	AL133715	Hs.155097	carbonic anhydrase II	1.57	3.44
	425281	NM_018339	Hs.118502	Link guanine nucleotide exchange factor	1.57	3.54
	440054	AW661947	Hs.5891	splicing factor, arginine/serine-rich 6	1.56	3.39
	419888	BE407713	Hs.78943	bleomycin hydrolase	1.56	2.43
	414160	AW451330	Hs.348198	hypothetical protein FLJ20262	1.55	3.38
65	420462	A1571496	Hs.30258	ESTs	1.55	3.65
	449518	BE395253	Hs.30861	ESTs	1.55	3.80
	420075	AF142482	Hs.203846	TEA domain family member 3	1.55	3.81
	406799	AA080548		glucosylceramidase 1 (GABA) A recepto	1.54	3.87
	450787	AB006190	Hs.25475	arapapin 7	1.54	4.05
70	419659	AB023006	Hs.92186	Leman cold-shock protein	1.54	3.82
	408543	N78038	Hs.44289	ESTs	1.54	3.10
	410169	AJ373141	Hs.59384	hypothetical protein MGC3047	1.54	4.73
	426068	AF029778	Hs.166154	pigeon 2	1.54	4.82
	432191	AA043193	Hs.273186	hypothetical protein, clone Telothelion/ta	1.54	5.54
75	415166	NM_003652	Hs.78068	carboxypeptidase Y	1.54	4.58
	410048	W76467	Hs.343874	proline oxidase homolog	1.54	4.66
	430502	A1123657	Hs.127264	ESTs, Weakly similar to JC3314 CDC28bdc	1.53	3.41
	432840	AW390125	Hs.240443	Homo sapiens cDNA, FLJ23238 fs, clone L	1.53	4.57
	413353	AW252542	Hs.75309	exonuclease III	1.53	3.59
80	431021	A1869864		thiosulfate sulfurtransferase (rhodanese	1.53	3.73
	431243	U46455	Hs.252189	syndecan 4 (amphiphysin, ryndocan)	1.52	6.09
	433019	AJ008113	Hs.279315	translocase of inner mitochondrial membr	1.52	4.49
	406801	AW424054	Hs.198318	hypothetical protein L5	1.51	5.56
	427461	AA531527	Hs.332400	hypothetical protein MGCI3010	1.51	3.77
	432894	AW167668	Hs.279772	brain specific protein	1.51	6.72
	415550	L13720	Hs.17801	growth arrest-specific 6	1.50	4.00
	424070	BE061914	Hs.10544	Homo sapiens cDNA FLJ14475 fs, clone MA	1.49	4.21

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445071	A1280246	Wt_145054	ESTs	1.48	3.39
440163	AB028988	Wt_7407	KIAA1065 protein	1.48	4.03
451588	AF436028	Wt_27410	proteasome regulatory factor PRF-1	1.47	3.58
427041	AW083257		hypothetical protein MG25306	1.47	3.61
426335	A054347	Wt_2017	abnormal protein 136	1.47	3.75
454508	W27953	Wt_292911	Plakophilin	1.46	0.95
456766	RB7310	Wt_7740	crystallin binding protein-like 1	1.46	3.40
440526	AS52243		ESTs	1.46	3.38
452586	AW058479	Wt_289043	spoditin	1.45	3.48
433399	N46406	Wt_84700	similar to phosphatidylcholine transfer	1.45	3.48
302328	N72519	Wt_236545	hydroxyacid oxidase 2 (long chain)	1.45	4.00
425456	T70445	Wt_157880	abnormal protein 109	1.45	4.75
450229	AF110638		period (Drosophila) homolog 1	1.45	4.43
433638	AW672507	Wt_3462	cyclochrome c oxidase subunit Vite	1.44	3.85
445156	N83637	Wt_12373	adenylate cyclase 6	1.44	3.60
446576	AE59477		dystrolysin (a dystrophin-associated) gly	1.44	3.07
440433	AA252462	Wt_7187	hypothetical protein FLJ17070	1.43	3.67
434536	NI_4486	Wt_3803	C-22 effector protein 4, binder of Rho	1.42	3.35
423513	AF035960	Wt_129719	transglutaminase 5	1.42	3.92
418681	AA287786	Wt_23445	inulin-N-acetyl glucosyl kinase subunit	1.42	3.38
421535	AA113152	Wt_105672	OMP-NovaC (beta)-N-acetylglucosaminide	1.41	4.04
407122	MT_212	Wt_77336	myosin, light polypeptide 6, alkali, sm	1.41	4.21
413944	AW001575	Wt_564	Homo sapiens mRNA for beta-tubulin T1 protein,	1.41	3.80
439879	AW084863	Wt_30002	SH3-containing protein SH3EL2, KIAA1548	1.41	3.51
417567	BE244373	Wt_1119	nuclear receptor subfamily 4, group A, m	1.40	4.07
419659	AW086061	Wt_59386	p53-induced protein	1.40	3.59
414203	AW142013	Wt_266847	cat malic dehydrogenase 1	1.40	4.38
406713	U02629	Wt_77336	myosin, light polypeptide 6, alkali, sm	1.40	4.39
439606	W79123	Wt_58561	G protein-coupled receptor 8.7	1.39	3.65
430135	NW_000036	Wt_24324	delta-8, delta-fructose-bisphosphate	1.37	3.99
422882	NO5239	Wt_94316	ESTs, Weakly similar to T131613 hypothal	1.36	3.36
406198	AA131111		gastroc15R65.1 (Stratagene clone (557204)	1.36	3.33
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437141	BE_204917	Wt_31087	hypothetical protein FLJ21478	1.34	3.47
406250	RS2918	Wt_19587	KIAA1594 protein	1.34	3.85
430012	NM_015373	Wt_227637	chromosome 22 open reading frame 2	1.32	4.32
425183	W76098	Wt_19223	HCCA2 protein	1.32	3.82
427706	AW971225	Wt_293800	ESTs, Weakly similar to ALU1_HUMAN ALU I	1.32	3.50
430603	AB028598	Wt_6147	KIAA1075 protein	1.32	3.71
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442533	AA161224	Wt_8372	ubiquitin-chromatin reductase (E. flo) G0	1.31	3.43
428475	AF172840	Wt_18442	CG-127 protein	1.31	3.43
406742	AA048091	Wt_278860	tumor protein, translationally-controlled	1.30	3.34
432295	BE019495	Wt_343665	ribosomal protein S16a	1.30	3.29
422659	AV67015		paired immunoglobulin-like receptor beta	1.29	3.53
406587			ENSP00000240027, KIAA1335 protein (fragm	1.29	3.34
406743	AA911568	Wt_278860	tumor protein, translationally-controlled	1.24	3.70
437142	A7918167	Wt_145058	ESTs, Moderately similar to A65010 X-h	1.23	4.48
424372	AH532803	Wt_21732	Homo sapiens cDNA, FLJ no.145, clone He	1.18	2.44
414716	AF119538	Wt_57044	Wt chondrocyte interacting protein 2	1.16	3.35
431931	AB036302	Wt_272212	cadherin 5, type 2 (T1-cadherin)	1.15	2.25
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405574	AW419080	Wt_250045	ESTs	1.00	3.60
417435	NW_305181	Wt_82129	carboxyl acetylcholinesterase II, muscle specific	1.00	3.44
402075			ESTs	1.00	3.37</

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			BF445077 AA055024 AA025543 AW737103 AW157444 AA580002 AW103144 AB046554 AA571115 AA923031 A0065435 A1353865 AA843267 AB02604	
			AA732370 AW002702 A1295540 AA621697 A1950635 AA904277 AB875227 BF437695 AA080593 AB784144 AA548538 AW752557 AV752603 AA025642	
			AA745474 AA149075 N30700 H82003 W75523 A1762795 AA282784 H78923 AA252875 H98107 R23754 AA005152 N99229 H74632 H80133 H24710	
25	410229	462_3	R38057 R66388 R42465 R52648 H11010 R98493	
			NW102124 U24898 X72613 BE559221 BF436030 F18898 AL567447 BQ033127 BG742757 BF823716 AA371502 AL13578 AL577766 B1490529	
			AA021622 A151679 AA745053 AA454198 R85506 AA016915	
			A1650320 AA342023	
30	424397	893246_1	AA080548	
	406799	0_0	NW103312 BQ01048 AC000862 D72992 BF7009214 BF972766 BG740474 B1771552 BG115569 BM120468 B1252033 AB169664 AA314620 BF724353	
	413021	10409_1	BG194276 BG15282 BE524679 BF435689 AA030546 AA481682 AW780207 AB00832 AL380540 BE226777 AV300707 AA81445 AW015993 A1381541	
			AA785558 AW138759 AA432063 AA948713 AB169485 AC007415 AC365589 AB031672 BF055581 A1312785 A521208 A122915 A1989759 W78015	
35	427841	12616_1	B718621 AB27564 A1795905 A1335381 BF334524 AW07444 AA706757 AA975176 AA84726 AA433837 AA533857 AB026464 A1271327 AA033419	
	440526	1078274_1	W75704 A594443 BG052614 BF343558 AW083336 AA043660 AA478232 A0603071 BE714413 AW07860 AW047016 R232364 B672551 A1568223	
	440526	1078274_1	AA03459 AA444748 BF055446 BF768595	
	446578	629517_1	W74622 BF055071 AW135349 A1184884 A1335527 AB30476 AA110691 A400726 AW183266 B13655 AW883367 A950307 BF664042	
40	440526	1078274_1	A1382243 AJ142543 AW063970 A1888497	
	446578	629517_1	B157086 T89902 D1518252 A859477 T89626 H22349	
	440518	102854_1	AA133655 A141105 AA053057	
	409800	0_0	AA055535	
45	422959	HH905_3	AJ400845 A154159 AL041618 AL028269 AA769325 AW780241 AW129462 A1271476 BF798303 AA836991 AW273346 A1436321 A1375545 AL040967	
			AA289455 A1522524 AA598667 AA423804 AL040910 N60292 A554063 AB239568 AA000576 AA748419 BE677845 AW020788 AB060236 AW0515209	
			A1976291 A1974735 AW476355 AA052385 A0171095 AA030490 AB457005 A021533 A550706 A011516 AB005569 A136159 BF730046 A140265	
			AB2466 A1974742 B4511753 A005880 BE671796 AA131957 A118703 A1878429 A1273421 AA87667 AA586459 BE241523 AF161081 NM_013440	
50			BE073169 AW70073 A1669581 A1698476 A6688081 A1698226 A1132636 BF036166 BF917106 AF762653 B064033 BE168145 AA778650	
			A1984255 W69468 AA132452 N53166 A1949278 AW168519 T26366 AA908333 F37181 B1002729	
55	TABLE 64C:		Unique number corresponding to an Eos probe set	
	Play:	Ref	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. 'Dunham, et al.' refers to the publication entitled 'The DNA	
			sequence of human chromosome 22' Dunham, et al. (1999) Nature 402:489-495.	
	Strand:		Indicates DNA strand from which exons were predicted	
60	NL_position:		Indicates nucleotide positions of predicted exons.	
65	Pkey	Ref	Strand	NL_position
	401781	7249190	Minus	83215-83435, 83531-83656, 83740-83801, 8423
	401780	7249190	Minus	26327-26517, 29220-29045, 29135-29296, 2941
	401203	9743387	Minus	17296-173056, 173868-173928
70	401785	7249190	Minus	165776-165596, 166189-166314, 166408-16656
	402294	1282012	Minus	2575-3000
	402645	5365286	Plus	150451-160617, 160788-161099
	403710	8437516	Plus	27413-28578
75	401780	9629699	Plus	83126-83250, 83280-85400, 94719-95287
	403593	6862950	Minus	62554-62712, 69449-69002
	404054	9714719	Plus	169445-170272
	402835	8564121	Plus	68346-68927
80	401905	8671966	Plus	153965-154441, 150599-150819
	403180	7523976	Minus	63603-63759
	401747	9789672	Minus	116596-118116, 119119-119244, 119609-11976
	403108	8580555	Plus	53263-53561
85	404996	6007890	Plus	37999-38145, 38652-38998, 39727-39872, 4005
	402575	9848340	Minus	109742-109883
	402338	6567891	Minus	35915-37250
	401205	9743388	Plus	167173-167433, 167936-168031
90	401152	9715002	Minus	69558-70101
	405400	9256298	Plus	1553-1712, 1718-2140, 4252-4385, 5922-6007
	404246	7406775	Plus	82477-82628, 82721-82817, 82910-83071, 8314
	411311	86595812	Minus	94802-94919, 95804-95887, 96323-96487, 9759
95	405447	9795551	Plus	18212-18298
	403105	8580016	Minus	145287-145744
	401429	8217850	Minus	86946-87579
	402951	7631034	Plus	161294-161579
100	402956	9480727	Minus	135001-136205
	403607	8189223	Minus	125703-126718
	402075	8117407	Plus	121907-122035, 122804-122921, 124019-12416
	404175	9931117	Minus	107420-107547, 109625-107596

TABLE 65A: ABOUT 838 GENES DOWNREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN

Table 65A lists about 838 genes downregulated in benign nevi relative to normal skin. Genes were selected from 59680 probesets on the Eos4Alymexis Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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	PKey:	Unique Euc probe/seq identifier number	Unigene Title	R1	R2	
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
5	R1:	90th percentile of normal skin AIs divided by the average of benign nevus AIs				
	R2:	90th percentile of normal skin AIs divided by the average of benign nevus AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator				
10	PKey	ExAccn	UnigeneID	Unigene Title	R1	R2
	420813	XS1501	Hs.59949	prolactin-induced protein	27.72	28.59
	406591	AF015224	Hs.46452	mammaglobin 1	26.40	28.34
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	21.33	21.57
	418026	BE379727	63213	fatly acid binding protein A4, adipocyte	18.66	18.96
	425441	AJ224112	Hs.204065	lipoprotein 8 (retinol-binding family member)	16.51	16.05
15	420807	AA100573	Hs.182421	troponin C2, fast	14.70	14.60
	407245	X90568	Hs.172004	titin	13.08	13.84
	428624	W23624	Hs.173059	ESTs	12.89	13.36
	425530	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	12.76	13.98
	444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	12.26	9.85
20	453309	AI791809	Hs.32949	defensin, beta 1	12.02	10.62
	4223024	AA593731	Hs.328823	ESTs, Moderately similar to ALUS_HUMAN A	11.90	10.86
	445227	A281459	Hs.270114	ESTs	11.79	12.22
	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	11.19	10.82
	432877	AW974111	Hs.292477	ESTs	11.18	11.30
25	426752	X58490	Hs.172004	titin	10.97	12.63
	422899	AA528286	Hs.323053	sarcom amyloid A1	10.85	13.85
	407230	AA157857	Hs.182265	keratin 19	10.79	11.40
	451029	AA852907	Hs.25829	ras-related protein	10.78	10.35
	421266	NM_002666	Hs.103253	potilin	10.73	11.25
30	431211	M65849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.66	7.24
	422633	X55832	Hs.118804	evodius 3, (beta, muscle)	10.57	9.82
	405121			mitogen-activated protein kinase 8 inter	10.41	10.54
	450912	AW932951	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	10.26	23.20
35	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	10.25	9.45
	410850	AW32867	Hs.302238	Homo sapiens cDNA FLJ21425 fs, clone C	10.15	8.88
	416931	D45371	Hs.80465	adipose most abundant gene transcript 1	10.13	11.58
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	10.09	5.51
	401203			Target Exon	9.55	10.74
40	425545	N05629	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	9.94	11.47
	425540	L11444	Hs.1907	galactin	9.60	9.56
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIII	9.45	6.44
	420919	M57892	Hs.100322	carbonic anhydrase VI	9.41	10.49
	443162	T49951	Hs.9079	DKFZP434G032 protein	9.36	10.58
45	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibito	8.51	10.27
	425232	BE566343	Hs.28988	glutaredoxin (thioltransferase)	8.90	7.26
	430071	AA355986	Hs.232068	transcription factor 8 (represses interi	8.86	8.94
	417240	N57566	Hs.48028	EST	8.81	18.90
	415477	NM_002228	Hs.78465	v-jen avian sarcoma virus 17 oncogene ho	8.72	6.85
50	430130	AL137311	Hs.234074	Homo sapiens mRNA, cDNA DKFZp761G02121 (8.39	10.25
	408491	AX088063	Hs.7882	ESTs	8.00	8.20
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	7.99	8.14
	408738	BE222975	Hs.56205	insulin induced gene 1	7.95	7.75
	422221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.89	9.86
	451831	NM_001674	Hs.460	activating transcription factor 3	7.79	7.51
	410867	X63556	Hs.750	fibritin 1 (Marfan syndrome)	7.76	7.55
	444984	H15474	Hs.132898	fatly acid desaturase 1	7.75	5.64
	413076	U10564	Hs.75188	weel (S. pombe) homolog	7.58	5.65
	410532	T53088	Hs.155376	hemoglobin, beta	7.64	4.73
	442757	AI739628	Hs.28345	ESTs	7.62	7.66
60	412047	AA594589	Hs.49696	ESTs	7.61	7.48
	410052	AA525225	Hs.334630	Homo sapiens cDNA FLJ14462 fs, clone MA	7.52	7.28
	438394	AA146260	Hs.56105	ESTs	7.52	7.27
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	7.51	6.27
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	7.45	4.10
65	445625	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	7.49	8.08
	427334	AA494411	Hs.296031	ESTs	7.48	6.78
	414449	AA557660	Hs.76152	deceon	7.39	8.30
	432305	M62402	Hs.274313	insulin-like growth factor binding prote	7.38	8.79
70	407328	AA508857		ESTs, Weakly similar to ALU1_HUMAN ALU S	7.35	7.20
	431842	NM_005764	Hs.271473	spHsf1 protein up-regulated in carc	7.00	6.93
	425488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	7.03	7.03
	445502	AW379160	Hs.12813	DKFZP434J214 protein	7.01	6.63
	419285	D31587	Hs.89868	KIAA0062 protein	7.01	5.82
	405024	AW885629	Hs.173630	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.99	4.58
75	427863	MT5141	Hs.13254	ESTs	6.99	4.96
	447918	AI129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	6.98	6.49
	410530	M25809	Hs.64173	ATPase, H transporting, lysosomal (vacuo	6.96	7.04
	442381	8E387335		ESTs, Weakly similar to S64054 hypophal	6.95	8.08
	411993	AW963705	Hs.301183	molecule possessing ankyrin repeats indu	6.94	7.12
80	443060	D73874	Hs.8944	procollagen C-endoproteinase enhancer 2	6.94	6.79
	427890	AA435761		ESTs	6.94	6.68
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.93	4.66
	442083	R59192	Hs.165062	ESTs	6.92	6.92

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441633	AW958544	Hs.112242
407722	BE252241	Hs.38041
444251	N48373	Hs.10247
414541	H55601	Hs.77490
430314	AA36601	Hs.235138
427704	AW971053	Hs.292882
431713	AK000388	Hs.267957
451253	H40259	Hs.26126
455187	A1161383	Hs.34549
400304	AF05082	Hs.113261
434625	W01370	Hs.46824
408093	BE26848	Hs.42346
425380	U31519	Hs.18372
411388	X72525	Hs.69752
413731	BE243845	Hs.75511
455963	AA507305	Hs.36475
412247	AF022375	Hs.73793
407102	AA007626	
421407	T82331	Hs.182278
406667	AA157857	Hs.182265
425504	X59133	Hs.204238
446945	A1193115	Hs.16611
413172	M36180	Hs.38386
407395	AF05082	
450626	AW195989	Hs.1508
450713	AL133611	Hs.25362
437596	AA761490	
430191	AI149680	Hs.188899
433913	AW657511	Hs.112592
420107	AL43596	Hs.788
472069	AJ10063	Hs.343603
437176	AW176909	Hs.42346
433412	AV653729	Hs.8185
437355	BE617636	Hs.286192
413963	AL187337	Hs.75184
440116	AI798851	
454229	AW557744	Hs.279469
441188	AW262830	Hs.255609
451144	AW555103	Hs.61712
431319	AA873350	Hs.302232
424268	U54617	Hs.8384
414555	N68569	Hs.78422
416321	C63417	Hs.84087
443072	A183532	
423712	W46802	Hs.81988
426279	RS3718	
424824	AL217440	Hs.143873
413719	BE438580	Hs.75498
428358	AA903222	Hs.101915
430821	AA487264	Hs.154974
424670	W61215	Hs.116651
424673	AA345051	Hs.294022
418205	L21715	Hs.63760
404440	X83057	Hs.83870
444239	RS7988	Hs.10706
415517	AF032107	Hs.90797
432626	AA471026	Hs.278544
407584	W25945	Hs.8173
449335	AW150717	Hs.343728
445607	AA485107	Hs.30156
424571	BE31976	
412630	AA738437	Hs.26226
408819	AW163483	Hs.48320
430027	AF191018	Hs.279923
456704	M21655	Hs.529
408515	AI289507	Hs.269883
443827	A1087967	Hs.134667
429693	BE254962	Hs.211612
437373	AB007972	Hs.130760
428666	AI080190	Hs.183242
421834	BE543205	Hs.288771
427081	AI474533	Hs.170528
419731	S47242	Hs.52909
420787	AA584248	
420692	AI380552	Hs.88602
410541	AA065003	Hs.64179
413160	NM_000427	Hs.251680
418127	BE243682	Hs.83532
433332	RS1790	Hs.238483
427850	AA416756	Hs.161051
429679	NM_006290	Hs.211600
422882	AA016188	Hs.111244
419461	AA528261	Hs.288899

normal mucosa of esophagus specific 1	6.87
pyridoxal (pyridoxine, vitamin B6) kinase	6.87
activated leucocyte cell adhesion molecule	6.84
glutathione S-transferase theta 1	6.84
pre-B cell colony-enhancing factor	7.14
ESTs	6.72
EHM2 gene	6.72
claudin 10	7.21
ESTs. Highly similar to S94541.1 clone 4	6.68
Homo sapiens skin-specific protein (sp33)	6.64
ESTs	6.61
calcineurin-binding protein calyculin-1	6.60
phosphatidylinositol carboxylkinase 1 (psi)	6.55
desmocollin 1	6.55
connective tissue growth factor	6.52
ESTs	6.50
vascular endothelial growth factor	6.49
glycerol 3-phosphate dehydrogenase 1 (iso	6.47
ESTs. Weakly similar to CGHUSC collagen	6.47
keratin 19	6.44
lipocalin 2 (ononogene 24p3) (NGAL)	6.43
tumor protein D52-like 1	6.43
hydruoy-delta-5-steroid dehydrogenase, 3	6.39
gh-Homo sapiens skin-specific protein (x	6.39
insulin-degrading enzyme	6.37
Homo sapiens mRNA: cDNA DKFZp434O1317 (1	6.37
ESTs. Moderately similar to S65657 alpha	6.36
ESTs	6.34
ESTs	6.34
perlecan (Drosophila) homolog 1	6.33
lin-csp (telephone)	6.33
calcineurin-binding protein calyculin-1	6.30
CGI-44 protein, sulfide dehydrogenase II	6.29
hypothetical protein FLJ20940	6.28
chitinase 5-like 1 (partridge glycoprotein	5.58
hemoglobin, gamma G	6.18
lactin-like protein rich protein	6.17
ESTs	6.12
pyruvate dehydrogenase kinase, isoenzyme	6.12
ESTs	6.11
Homo sapiens pyruvate dehydrogenase kinase	6.10
phospholipase A2, group IIA (platelets,	6.08
KIAA0143 protein	6.08
gh-wp7602.1 NCL CGAP, Em25 Homo sapien	6.07
disabled (Drosophila) homolog 2 (mitogen	6.04
hypothetical protein FLJ10659	6.03
ESTs	6.02
small inducible cytokine subfamily A (Cy	6.01
Stargardt disease 3 (autosomal dominant)	5.54
Homo sapiens mRNA: cDNA DKFZp667N064 (tr	5.92
epithelial V-like antigen 1	5.92
ESTs. Weakly similar to I38022 hypoteth	5.81
Integron 1, leukotact, fast	5.91
nebulin	5.89
epithelial protein lost in neoplasm beta	5.89
Homo sapiens clone Z3620 mRNA sequence	5.86
acetyl-Coenzyme A acetyltransferase 2 (a	5.86
hypothetical protein FLJ10803	5.81
STAT induced STAT inhibitor 3	5.79
ESTs. Weakly similar to unnamed protein	5.78
polymerase (RNA) II (DNA directed) poly	5.78
Homo sapiens cDNA: FLJ21295 fls, clone C	5.76
double ring-finger protein, Dofrin	5.71
putative nucleotide binding protein, est	5.70
myosin, heavy polypeptide 7, cardiac mus	5.68
hypothetical protein FLJ23395	5.67
ESTs	5.67
SEC24 (S. cerevisiae) related gene fam11	5.67
myosin phosphatase, target subunit 2	5.66
Homo sapiens mRNA: cDNA DKFZp434A202 (tr	5.16
DKFZp586A0522 protein	4.59
ESTs. Moderately similar to ALLUC_HUMAN 1	5.65
SON DNA binding protein	5.64
ESTs. Weakly similar to I38022 hypoteth	5.64
ESTs	5.63
synenin-2 protein	5.62
luteolin	5.61
membrane cofactor protein (CD46, trophob	5.61
Human clone Z3513 mRNA sequence	5.60
ESTs. Moderately similar to ALLUC_HUMAN A	5.51
tumor necrosis factor, alpha-induced pro	5.49
hypothetical protein	5.49
nuclear receptor subfamily 2, group F, m	5.49

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430714	AA494757	Hs.287601	Homo sapiens cDNA FLJ13830 fs, clone 1H	5.48	5.38
407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1)	5.46	5.11
400494	HA5100	Hs.49753	ENSP00000238970: CIG30 (Fragment)	5.45	3.63
415052	BE178993	Hs.23440	uvul autoantigen with coiled coil domain	5.43	4.25
435538	AB011540	Hs.4930	KIAA1155 protein	5.41	3.82
417035	AA192455	Hs.22968	low density lipoprotein receptor-related	5.41	2.62
434535	AA511729	Hs.167619	Homo sapiens clone IMAGE-451939, mRNA se	5.40	5.40
430055	K25929	Hs.342949	ESTs, Moderately similar to ALUC_HUMAN 1	5.40	5.20
413778	AA090235	Hs.75535	ADP-ribosylation factor-like 5	5.39	4.69
436090	AU640535	Hs.332879	myosin, light polypeptide 2, regulatory,	5.37	14.96
408050	AB68003	Hs.296031	EST	5.37	5.33
426510	AW861225	Hs.251928	ESTs	5.35	5.49
426705	X03740	Hs.231581	GNAP homolog, SMAR1 homolog	5.35	5.83
456332	AA228357	Hs.110630	myosin, heavy polypeptide 1, skeletal mu	5.34	7.50
421999	U50535	Hs.110630	gb.nc.79d05.1 NCI_CGAP_P12 Homo sapiens	5.34	4.88
419479	AA229976	Hs.7869	Human BRCA1 protein, mRNA sequence CG005	5.34	4.75
417059	AL037572	Hs.81071	mannosidase, alpha, class 1A, member 2	5.34	3.99
424008	R02740	Hs.137555	extracellular matrix protein 1	5.34	4.71
415694	AW194301	Hs.339283	putative chemokine receptor, GTP-binding	5.34	4.75
452747	BE153855	Hs.61450	Human DNA sequence from clone RP1-167J11	5.34	8.69
445271	AW330657	Hs.7869	Ig superfamily receptor LMR	5.31	5.81
437335	AL038624	Hs.208752	ESTs, Weakly similar to ALUR_HUMAN ALU S	5.30	4.35
419925	AA159550	Hs.53765	ESTs	5.29	4.92
453599	D17793	Hs.78183	lipoma HMGIC fusion partner	5.28	5.33
449958	BE328153	Hs.240287	aldo-keto reductase family 1, member C3	5.28	3.40
452496	AA114926	Hs.169531	signal recognition particle 54D	5.28	2.84
424058	AL121516	Hs.138617	ESTs	5.28	5.48
443265	AB16207	Hs.9167	thyroid hormone receptor interactor 12	5.27	3.72
427013	U59537	Hs.83890	SH3 domain binding galactam acid-rich pr	5.26	4.52
414602	AW633088	Hs.76550	gb:human nebulin mRNA, partial cds	5.26	6.21
410284	U59039	Hs.61828	Homo sapiens mRNA; cDNA DKFZ564b1264 (f	5.26	4.21
445107	AD208121	Hs.147313	amyloid beta precursor protein-binding p	5.26	4.43
445267	AA451013	Hs.151124	ESTs, Weakly similar to 130022 hypotheri	5.25	5.61
422278	AF072873	Hs.114218	ESTs	5.24	4.44
448585	AB020676	Hs.21543	fizzled (Drosophila) homolog 5	5.23	3.14
421993	R22487	Hs.110571	KIAA0895 protein	5.23	6.21
414407	AA147026	Hs.76704	growth arrest and DNA-damage-inducible,	5.22	6.64
423720	AL044191	Hs.23398	ESTs	5.22	5.25
415997	NM_003590	Hs.78945	hypothetical protein DKFZ534F0318	5.22	5.85
415311	AB014511	Hs.70604	cullin 3	5.21	3.66
441619	NM_014056	Hs.7917	ATPase, Class II, type 9A	5.21	3.95
435522	NM_001262	Hs.4854	DKF ZP564K247 protein	5.20	4.38
415167	AA160784	Hs.25410	cyclic-dependent kinase inhibitor 2C (p1	5.19	4.52
431416	AA532718	Hs.178904	ESTs	5.19	3.13
439995	AL137480	Hs.5834	ESTs	5.18	5.36
416784	AA334592	Hs.79814	KIAA1014 protein	5.17	3.14
446082	A274133	Hs.158452	lumican	5.17	6.18
400196			ESTs	5.16	5.14
414525	C14904	Hs.45184	Eos Control	5.16	5.05
414242	AA743230	Hs.28433	Homo sapiens cDNA FLJ12284 fs, clone MA	5.16	4.31
430899	AW969847	Hs.292718	dolichyl-phosphate (UDP-N-acetylglucosam	5.15	4.89
440383	AA884208	Hs.30484	ESTs, Weakly similar to RET2_HUMAN RETIN	5.14	5.22
431628	AF146277		ESTs	5.13	5.09
407047	W63955		CD2-associated protein	5.13	5.03
433988	AA529467	Hs.112572	gb:41a3pions SOD-2 gene for manganese su	5.13	4.31
437704	AA756142	Hs.131810	Homo sapiens cDNA FLJ14130 fs, clone MA	5.12	3.57
426101	AL049987		ESTs, Moderately similar to ALU1_HUMAN A	5.12	3.30
428287	AA236291	Hs.183583	Homo sapiens mRNA; cDNA DKFZ564F112 (f	5.11	6.08
416382	BE6885	Hs.75275	serine (or cysteine) proteinase inhibito	5.10	4.31
437150	BE1407	Hs.77910	KIAA0232 gene product	5.10	3.79
454947	AW845590		3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.10	6.58
434647	W74158	Hs.103189	gb:CDV-CT0180-011099-025-d07 CT0180 Homo	5.09	4.82
418630	AA091027	Hs.326625	lipopolysaccharide specific response-68	5.09	4.59
449338	AF134444	Hs.394	Homo sapiens clone Z9388 mRNA sequence	5.09	3.46
438962	BE046554		adrenomedullin	5.09	6.26
431693	AA59519		gb:hm4f11x1 NCI_CGAP_R0F2 Homo sapiens	5.08	5.60
420583	H17859	Hs.65450	serine (or cysteine) proteinase inhibito	5.07	2.83
431048	BE0263	Hs.269199	retinol 4	5.06	6.71
432125	AW072657	Hs.483006	cell death-inducing DFFA-like effector a5	5.06	6.06
447945	AB22388	Hs.9670	Homo sapiens cDNA FLJ11230 fs, clone MA	5.05	3.72
442547	AA306997	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.05	2.86
414176	BE140638	Hs.75794	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.05	2.86
445253	BE7546	Hs.43566	EDG-2 (endothelial differentiation, lys	5.03	4.43
448490	AA523897	Hs.271692	ESTs, Weakly similar to 130022 hypotheri	5.03	6.67
450515	AW304226		biphenyl hydrolase-like (serine hydrolas	5.03	4.36
440624	AF017987	Hs.7306	secreted frizzled-related protein 1	5.01	5.46
417165	R030137	Hs.382338	Homo sapiens cDNA FLJ21425 fs, clone C	5.01	5.01
417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	5.01	5.32
413475	AAW21488	Hs.25981	ESTs	5.01	3.90
414792	BE314949	Hs.87128	hypothetical protein FLJ23309	5.00	4.34
424074	A902456	Hs.210761	ESTs, Weakly similar to 130022 hypotheri	5.00	3.19

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	458571	AL115206	Hs.101874	ESTs, Weakly similar to ALU1_HUMAN ALU S
	433256	AW604447	Hs.239408	ESTs, Weakly similar to S26685 hypothetical
	440596	H13032	Hs.103378	hypothetical protein MGC11034
5	427519	AA173542	Homo sapiens mRNA: cDNA DKF2p564H1916 (f	
	424651	AW53206	Hs.32425	ESTs
	436701	AW595032	Hs.178855	ESTs, Moderately similar to 178855 serin
	413561	AB021173	Hs.75478	ATPase, Class VI, type 11B
	446825	AW507086	Hs.178470	hypothetical protein FLJ22652
	430623	A460319	Hs.120068	ESTs
	451710	AW867467	Hs.278712	eukaryotic translation initiation factor
	436085	BA23133	Hs.5961	Homo sapiens cDNA: FLJ21954 fls, clone H
	434657	AL133033	Hs.4084	KIAA1025 protein
	402254			Target Exon
15	424658	AF077374	Hs.135322	small proline-rich protein 3
	406648	AA563730	Hs.277477	major histocompatibility complex, class
	428423	ALJ076517	Hs.184276	solute carrier family 9 (sodium/hydrogen
	441586	AA604110	Hs.151725	ESTs
	400109			Est Control
20	419740	AB037835	Hs.52991	KIAA1414 protein
	421481	AW391572	Hs.104656	KIAA1324 protein
	440266	AA068909	Hs.19525	hypothetical protein FLJ22794
	421675	AW662518	Hs.233150	hypothetical protein MGC2559
	408102	AW595653	Hs.27059	hypothetical protein FLJ22929 similar to
	418021	MI5881	Hs.1137	uronosidin (uronosid, Tamn-Horsfall gly
25	422068	AIJ07519	Hs.104520	Homo sapiens cDNA FLJ13694 fls, clone PL
	421668	AL137438	Hs.110454	SEC15 (S. cerevisiae)-like
	414786	AL296328	Hs.97411	hypothetical protein MGC12335
	410132	NM_003490	Hs.300948	Microfilin-associated glycoprotein-2
30	448943	R85337	Hs.24030	solute carrier family 31 (copper transpo
	424339	AB050687		AB050687 JL-81095-181099-015 BT095 Homo
	422924	AW592039	Hs.97199	complement component C1q receptor
	454000	AA040520	Hs.5672	hypothetical protein AF140225
	404730			Target Exon
35	449943	AF104268	Hs.24212	lathrophin
	414210	AL305298	Hs.279568	Homo sapiens cDNA: FLJ21165 fls, clone L
	435952	AI033255	Hs.118317	Homo sapiens cDNA FLJ12085 fls, clone HE
	421311	N71848	Hs.283659	hypothetical protein PR02032
	446785	AI225225	Hs.288300	hypothetical protein FLJ22331
	437611	AA697108		glutathione S-transferase, cytosolic, S1 Homo s
	419812	AL498267	Hs.110613	KIAA0421 protein
	414496	W73853		ESTs
	450306	AL080080	Hs.24766	thioredoxin domain-containing
	444895	AB743983	Hs.22891	solute carrier family 7 (cationic amino
45	422559	AW452948	Hs.257831	ESTs
	442554	AW467376	Hs.125640	ESTs
	421429	NM_014922	Hs.104305	death effector filament-forming Ced-4-i
	422313	AF045941	Hs.115166	scellin
	435746	AA695956	Hs.117335	ESTs
	433053	AA694386	Hs.250914	ESTs
50	441925	R83113		protein kinase C substrate 80K-H
	440030	AA532653		EST
	446515	AL448875		hypothetical protein DKF2p569133
	406707	ST3940	Hs.931	myosin, heavy polypeptide 2, skeletal mu
55	432341	AL137662	Hs.274401	Homo sapiens mRNA: cDNA DKF2p434P086 (f
	410453	AW749036		gt.RC2-BT0318-211-195-011-1410 BT0318 Homo
	450196	AW956688	Hs.24608	DKF2P564D177 protein
	444147	AB022306	Hs.10051	HGA-0008 protein
	427809	N68380	Hs.180878	lipoprotein lipase
	428157	AL738719	Hs.158427	hexokinase 2
60	413259	AA857487	Hs.75275	ubiquitination factor E4A (homologous to
	440245	AA001513	Hs.7100	hypothetical protein
	442279	NM_004613	Hs.82626	transglutaminase 2 (C polypeptide, prote
	408686	BE066047	Hs.86412	chromosome 5 open reading frame 5
65	403061	AI033955	Hs.239526	cleaved-C4-methyl oxidase-like
	414489	AB026977	Hs.73105	ESTs
	417731	AA372527	Hs.19385	CSG-6 protein
	443155	BE148235	Hs.153063	Homo sapiens cDNA FLJ14201 fls, clone NT
	448503	BE243146	Hs.21332	B1B (PC2) domain containing 1
	423546	BE167178	Hs.180638	hypothetical protein FLJ13081
	445820	AL243225	Hs.17441	ESTs
70	454065	BE304588		gh.5013111808F1 NIH_MGC_44 Homo sapiens c
	418802	AB028589	Hs.88500	mitogen-activated protein kinase 8 inter
	431816	T87431	Hs.190738	ESTs
	429138	AB026857	Hs.157298	NS1-binding protein
75	425643	AA857131	Hs.171595	HN1A1 specific factor 1
	448943	AI608810	Hs.153288	ESTs
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h
	403593			Target Exon
	408104	AW572927	Hs.293658	ESTs
80	429624	AA458648	Hs.59476	ESTs, Weakly similar to 1313194B alpha1
	429538	BE182552	Hs.139322	small proline-rich protein 2A
	414505	RA5389	Hs.23558	ESTs, Weakly similar to A45042 lysosomal
	438533	AI440256	Hs.170673	ESTs, Weakly similar to 124632 hypotheli

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426143	BE379836		proteasome (prosome, macropain) subunit,	4.15	5.12
414527	BE241739	Hs.76359	catalase	4.14	5.13
422287	F15365	Hs.114346	cytochrome c oxidase subunit VIa polype	4.13	8.50
408199	AA130637	Hs.15396	Homo sapiens, clone IMAGE-394909, mRNA,	4.12	5.94
412477	AA150804		microsomal glutathione S-transferase 1	4.11	10.00
411558	AA102670	Hs.70725	gemina aminobutylic acid (GABA) A receptor	4.09	5.39
444252	R21135	Hs.54985	ESTs	4.07	6.01
404295	WY7236		AJ905687JL-BT095-190199-019 BT095 Homo	4.06	13.32
438746	AB85515	Hs.184727	Human melanoma-associated antigen p67 (m	4.07	7.57
423856	AA597576	Hs.225951	topoisomerase-related function protein 4	4.06	5.24
422168	AA568894	Hs.117408	S100 calcium-binding protein A7 (psorias	4.01	4.61
439310			C4000160g112735793epXP_011928.1[pr	4.00	4.06
405643	N17976	Hs.347939	hemoglobin, alpha 2	3.97	7.22
435372	AW072301	Hs.31298	ESTs	3.96	5.41
428340	AF261088	Hs.154721	aconitase 1, soluble	3.94	5.33
424604	AW865388	Hs.151076	KIAA1243 protein	3.91	7.59
428653	AA530892	Hs.171595	dual specificity phosphatase 1	3.91	14.81
410204	AJ243425	Hs.328035	early growth response 1	3.87	9.98
448520	AE0C2367	Hs.21335	doublecortin and CaM kinase-like 1	3.87	5.09
443021	AA368546	Hs.8504	Ig superfamily protein	3.86	7.55
430418	R88862	Hs.36029	heart and neural crest derivatives expe	3.81	6.19
447995	AW553622	Hs.223025	RAB31, member RAS oncogene family	3.76	5.10
419407	AW140377	Hs.41502	hypothetical protein FLJ12215	3.76	5.12
443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducib	3.75	5.46
425281	AK000967	Hs.159111	oxidation resistance 1	3.74	5.14
423973	AFJ08461	Hs.136574	arachidonate 12-lipoxygenase, 12R type	3.74	6.30
444294	AW137635	Hs.146589	ESTs	3.72	5.59
457411	AW085961	Hs.130903	ironoic-class homeobox protein IRX2	3.71	4.85
455063	NM_006744	Hs.76481	retinol-binding protein 4, interstitial	3.71	6.72
413880	AF662842	Hs.110915	interleukin 22 receptor	3.70	4.01
422840	MT9384	Hs.118845	hepatin C, slow	3.71	6.99
455241	AL050204	Hs.28540	Homo sapiens mRNA: cDNA DKFp586F1223 (I	3.71	4.21
453560	AA348626	Hs.5890	hypothetical protein FLJ23036	3.69	5.13
410197	NM_005518	Hs.59869	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.69	7.69
413922	AS55896	Hs.102434	ESTs	3.68	4.80
428698	AA852773	Hs.334638	KIAA1866 protein	3.64	5.22
451951	AW082870	Hs.210994	ESTs	3.64	3.69
452308	AI167560	Hs.61297	ESTs	3.64	4.35
441128	AA570296		ESTs, Weakly similar to T32373 hypothet	3.63	2.91
421978	AJ245692	Hs.110196	NICE-1 protein	3.63	5.65
418533	NM_004533	Hs.85937	myosin-binding protein C, test-type	3.61	6.22
452413	AW082833	Hs.219030	ESTs	3.58	3.03
453003	AA308486	Hs.103395	hypothetical protein FLJ14146	3.55	3.99
405522	AS51214	Hs.45320	Small proline-rich protein SPRK (human,	3.54	10.58
423503	M92843	Hs.343586	zinc finger protein homologous to Zip-36	3.53	15.11
419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.53	5.29
428332	AF007132	Hs.184019	Homo sapiens clone Z3551 mRNA sequence	3.51	4.46
447155	AL042400	Hs.75568	Homo sapiens, Similar to RIFEN cDNA 1700	3.51	3.67
419307	AI127958	Hs.83393	cystatin GM	3.51	3.74
420202	AL036557	Hs.95910	putative lymphocyte GcGT1 switch gene	3.50	14.64
432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fls, clone C	3.50	2.79
442321	AF207694	Hs.82330	a disintegrin-like and metalloprotease (3.48	7.91
450860	AA521037		integrin, beta 5	3.47	5.89
414655	AA150873		serum amyloid A1	3.46	9.22
413653	BE247585	Hs.75452	BTG family, member 2	3.46	5.63
427408	AA383206	Hs.2156	RAR-related orphan receptor A	3.45	3.08
430111	AF985289	Hs.234755	skin-specific protein	3.45	4.77
453655	AW990427	Hs.342874	transforming growth factor, beta receptor	3.42	8.09
450607	AL050373	Hs.25213	hypothetical protein	3.41	6.43
412596	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi	3.41	6.10
427681	AB015263	Hs.180338	tumor necrosis factor receptor superfamily	3.39	6.59
444600	AB63446	Hs.263306	muscle serine protease	3.38	3.94
452669	AA216363	Hs.262598	hypothetical protein DKFp434B044	3.31	10.06
422101	AW404176	Hs.111611	ribosomal protein L27	3.30	3.93
431986	AA536136	Hs.145018	Novel human gene mapping to chromosome 20	3.30	3.54
412649	NM_002205	Hs.74269	integrin, alpha 7	3.28	3.28
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	3.28	5.44
425163	D10040	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain	3.28	5.93
412061	AA830763	Hs.330211	ESTs	3.27	5.75
437592	NM_003851	Hs.57110	collagen suppressor of E1A-stimulated gen	3.27	5.83
452846	AF044924	Hs.30792	hoxd2 protein	3.26	5.66
421462	AF015495	Hs.104624	aquaporin 9	3.25	4.98
422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.24	6.56
444935	AA262849	Hs.223569	ESTs	3.24	5.95
422057	AQ20576	Hs.30348	ESTs	3.22	5.72
410017	AW952426	Hs.109438	Homo sapiens clone 24775 mRNA sequence	3.21	5.26
407948	AW085161	Hs.55279	ICEBERG caspase-1 inhibitor	3.21	4.51
452089	T97294	Hs.271452	ESTs, Weakly similar to PC4211 hepatocel	3.19	4.42
446249	AW855381	Hs.337124	ESTs	3.18	2.99
430859	D10511	Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	3.17	5.86
443623	AA345519	Hs.9541	complement component 1, q subcomponent,	3.16	12.00
452865	AB24046	Hs.119557	ESTs, Weakly similar to A47582 B cell gr	3.16	6.03
452992	L29815	Hs.507	comodestatin	3.15	5.70

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410231	AA314163	Hs.61153	proteasome (prosome, macropain) 26S subu	3.15	5.87
420309	AW043637	Hs.21766	ESTs, weakly similar to ALUS, HUMAN ALU S	3.15	4.98
406791	A220684	Hs.347939	hemoglobin, alpha 2	3.13	17.37
419648	173661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.12	4.63
421485	AA243499	Hs.104600	hypothetical protein FLJ10134	3.12	3.02
432575	BE536069	Hs.2962	S100 calcium-binding protein P	3.12	8.51
417713	D42947	Hs.82432	KIAA0069 protein	3.12	5.82
446848	BE409053	Hs.299029	peroxisomal long-chain acyl-CoA thioester	3.11	6.61
444795	AB002351	Hs.10557	KIAA0353 protein	3.11	5.44
415704	NM_001677	Hs.78529	ATPase, Na ⁺ transporting, beta 1 polypep	3.10	6.61
401905			ENSP0000025223? Several regulatory eleme	3.10	5.52
443771	AL080021	Hs.8986	complement component 1, q subcomponent,	3.10	5.10
427055	AA316080	Hs.173554	ubiquitin-like protein c-reductase core pr	3.10	3.79
413635	A227277	Hs.249163	fatty acid hydroxylase	3.08	5.56
448106	AB004070	Hs.171941	ESTs	3.07	5.19
432908	AB861896		ESTs	3.07	3.47
422158	L10343	Hs.112941	protease inhibitor 3, skin-derived (SKAL)	3.07	7.48
429506	D49835	Hs.171942	fib. responsive element binding protein 1	3.05	3.97
424998	US8515	Hs.154138	chitinase 3-like 2	3.02	6.75
419358	T78763	Hs.90063	neurocalin delta	3.00	7.68
414541	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member	2.99	5.44
426402	BE387327	Hs.80475	polymyosin (RNA) II (DNA directed) polyp	2.99	6.84
459472	A1190071	Hs.55278	ESTs	2.98	5.06
421335	Y99977	Hs.103505	ARS component B	2.97	9.31
431316	AA502663	Hs.145037	ESTs	2.96	4.00
420996	AK001927	Hs.100895	hypothetical protein FLJ10462	2.96	2.97
451178	AA064652	Hs.66677	ESTs	2.95	6.58
444204	A1129194	Hs.143540	ESTs	2.93	3.92
436723	AW975895	Hs.307486	ESTs	2.93	6.64
438664	AW197887	Hs.253533	gb.Hsman metallothionein L-8 gene, exon	2.93	3.82
408962	M13485		resin (Rood-Stenberg cell-expressed in	2.93	3.10
429922	Y94439	Hs.31538	7-dehydrocholesterol reductase	2.93	5.35
444734	NM_001360	Hs.11806	four and a half LIM domains 1	2.91	9.84
430310	U60115	Hs.230609	ESTs	2.91	7.02
420876	AAJ18426	Hs.177744	ESTs	2.91	5.41
420550	AF171307	Hs.168596	ETfA-like factor 3 (pis domain transcript	2.91	5.64
428232	BE272452	Hs.183709	monomeric oxidase A	2.90	9.94
413796	AW408094	Hs.75545	interleukin 4 receptor	2.89	5.37
413884	AI658982	Hs.288758	hypothetical protein FLJ12369 similar to	2.88	5.34
413372	A1474851	Hs.213289	low density lipoprotein receptor (fam1)	2.86	6.31
428500	AB153395	Hs.104641	fatty acid desaturase 2	2.86	3.93
444135	AK000374	Hs.10346	hypothetical protein FLJ20154	2.86	6.05
452689	F33868	Hs.284176	transferrin	2.85	6.11
435108			ENSP00000241415?hypothetical 67.7 KDa p	2.85	3.17
434333	AW620758		gb.hh.Dm5y.1 NCL CGAP_GU1 Homo sapiens	2.84	3.35
434952	T10269	Hs.4285	Homo sapiens cDNA, FLJ22505 fs, clone H	2.83	4.05
420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	2.83	3.57
408922	S70284	Hs.119597	gb.Stearyl-CoA desaturase (human, adip)	2.82	3.80
413470	AL320147	Hs.134742	hypothetical protein DMF2G47005	2.82	6.40
428807	AK0002138	Hs.305227	Homo sapiens cDNA FLJ12175 fs, clone PL	2.82	2.97
425180	U00115	Hs.155024	B-cell CLL/lymphoma 6 (zinc finger prote	2.81	5.15
415409	AW993701		NS1-associated protein 1	2.80	6.16
433848	AF098719	Hs.93764	carboxypeptidase A4	2.80	2.98
425750	AL58276	Hs.42400	zinc finger protein 288	2.79	5.99
433638	AW872507	Hs.3462	cytochrome c oxidase subunit VIc	2.78	5.25
429128	AA446889	Hs.119316	ESTs	2.78	4.17
444292	AF081497	Hs.279682	Rh type C glycoprotein	2.77	3.37
430429	AW140827	Hs.26373	Homo sapiens cDNA, FLJ23440 fs, clone H	2.76	6.09
419923	AW081455	Hs.120219	ESTs	2.76	4.31
407555	Z48511		gb.Hsapiens XG mRNA (clone PEP11)	2.76	4.12
425240	AA306495	Hs.1869	phosphoglucomutase 1	2.74	5.92
453317	BRCA1b		Esor Control	2.74	19.85
428819	N92165	Hs.93231	ESTs	2.74	5.72
408839	AW277084		gb.xp61009.x1 NCL CGAP_Ox39 Homo sapiens	2.73	3.93
418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fs, clone HE	2.72	5.94
409453	AB885516	Hs.95512	ESTs	2.72	6.11
406625	Y13647	Hs.111987	stearyl-CoA desaturase (delta-9-desatur	2.72	3.80
420074	AA253425	Hs.190074	ESTs	2.71	4.04
429547	AW009166	Hs.99316	FGENESH predicted novel secreted protein	2.71	2.84
444026	AA205759	Hs.10119	hypothetical protein FLJ14957	2.71	6.11
427112	AA070601	Hs.51616	ESTs, weakly similar to ALUP, HUMAN ALU S	2.70	5.23
429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	2.69	5.33
419088	AA234041	Hs.87271	ESTs	2.69	3.22
424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (tssc	2.69	6.64
443102	A247472	Hs.132965	ESTs	2.68	5.85
411939	AA385595	Hs.146246	ESTs	2.68	5.38
453201	AA432195	Hs.135058	ESTs	2.68	3.69
420231	R06866	Hs.19813	ESTs	2.67	4.70
404996			Target Exon	2.67	4.57
422955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.66	6.36
447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasm	2.65	15.65
417365	DS0683	Hs.82028	transforming growth factor, beta receptor	2.65	7.74
444169	AV048170	Hs.58756	ESTs	2.64	3.40

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5	431247	AL021578	Hs.278489	mainlin 4	2.64	3.35
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	2.63	5.12
	432093	H28383		gdy652c03.r1 Soares breast 2bHtBst Homo	2.63	4.08
	408669	AA432591	Hs.78146	platelet/endothelial cell adhesion molec	2.61	6.44
	446924	AF151872	Hs.7527	small fragment nuclease	2.59	6.37
10	416232	AW502678	Hs.70900	exorpin 1 (CPM1, yeast, homolog)	2.59	6.46
	425320	U29344	Hs.83190	fatty acid synthase	2.59	3.93
	402215			NM_003430Homo sapiens zinc finger prote	2.58	6.09
	449539	W80363	Hs.58446	ESTs	2.58	4.05
	418271	NM_000919	Hs.83920	peptidylglycine alpha-amidating monooxy	2.58	5.61
15	449967	RA0978	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.58	3.54
	438752	AW238873	Hs.146036	ESTs	2.58	5.24
	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	2.57	5.16
	438753	AS683207	Hs.99029	CCAA1/tenascin binding protein (CIEBP)	2.57	4.45
	413630	AL036883	Hs.75450	delta sleep inducing peptide, immunosac	2.56	6.38
20	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fs, clone NT	2.56	2.90
	427656	AF791495	Hs.180142	calmodulin-like stim protein (CLSP)	2.56	2.67
	426403	NM_000361	Hs.2030	thrombomodulin	2.55	5.19
	432906	BE265488	Hs.3123	lethal giant larvae (Drosophila) homolog	2.55	5.62
	420924	R01026	Hs.245321	ESTs	2.55	3.22
25	427527	AB090657	Hs.153261	immunoglobulin heavy constant mu	2.55	5.45
	407083	Z46511		HLsapiens XG mRNA (clone PEP11)	2.55	4.50
	445437	A224165	Hs.148725	ESTs	2.54	4.72
	425097	NM_014247		PDZ domain containing guanine nucleotide	2.54	5.28
	420105	AW015671	Hs.32244	ESTs, Weakly similar to FNOD_HUMAN FIBRO	2.53	6.55
30	429554	NM_012275	Hs.207224	interleukin 1, delta	2.53	2.84
	408896	AF104447	Hs.48778	riban protein	2.53	7.08
	409169	F00991	Hs.50889	(clone PWHLC2-24) myosin light chain 2	2.52	8.68
	420235	AA261756	Hs.31178	ESTs	2.51	4.21
	423214	AB93409		ESTs	2.51	3.11
35	440602	AT743491	Hs.293692	ESTs	2.50	2.71
	444946	AW129205	Hs.156457	hypothetical protein FLJ2408	2.48	2.86
	430235	BE268048	Hs.236404	RAB10, member RAS oncogene family	2.48	5.37
	429229	M69136	Hs.135626	chymase 1, mast cell	2.48	3.21
	427689	BE245550	Hs.171825	basic helix-loop-helix domain containing	2.48	7.88
40	421811	AA022550	Hs.108548	PABP-interacting protein 2	2.48	6.28
	414420	AA043424	Hs.76095	Immediate early response 3	2.47	8.33
	420693	NM_001972	Hs.99863	elastase 2, neurophil	2.47	2.78
	420139	NM_005057	Hs.95251	lipase, hormone-sensitive	2.46	10.12
	447179	AW015633	Hs.157299	ESTs	2.46	3.45
45	451687	AL041250	Hs.26837	Homo sapiens mRNA; cDNA DKF Zp586K1123 (f	2.46	5.47
	420322	AB014555	Hs.96731	huntingtin interacting protein-1-related	2.45	6.18
	421064	A24542	Hs.101382	tumor necrosis factor, alpha-induced pro	2.45	5.75
	421818	AW922076	Hs.50038	NM_002489Homo sapiens NADH dehydrogen	2.45	6.73
	412524	AA417813	Hs.44208	hypothetical protein FLJ2153	2.44	10.55
50	439639	AA370045	Hs.6607	AXIN1 up-regulated	2.44	5.22
	436009	H87130	Hs.120625	ESTs	2.44	2.94
	414814	D14697	Hs.77253	farnesyl diphosphate synthase (farnesyl	2.43	5.17
	434060	AA744802	Hs.197922	hypothetical protein PRQ1489	2.43	5.56
	425335	BE394327	Hs.296267	folistatin-like 1	2.43	10.52
55	406997	U07807		metallothionein IV	2.42	4.35
	421545	AF093703	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase	2.42	6.72
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G p	2.41	5.22
	412825	AW167439	Hs.190051	Homo sapiens cDNA FLJ13265 fs, clone PL	2.41	5.56
	445462	AA378776	Hs.288549	hypothetical protein MGC3077	2.41	5.24
60	448954	AB014664	Hs.22616	KIAA0694 protein	2.40	5.31
	447218	BE617762	Hs.107468	hypothetical protein DKF Zp343B195	2.40	5.24
	423810	AL132655	Hs.132955	BCL2adonovirus E1B 19kD-interacting pro	2.39	5.55
	450440	AB024334	Hs.25001	tyrosine 3-monooxygenase/hydrophoban 5-mo	2.39	7.63
	430356	NB7990	Hs.228670	Homo sapiens mRNA; cDNA DKF Zp364H0764 (f	2.38	5.99
65	418355	L42563	Hs.1165	ATPase, H ⁺ transporting, nonvacuole, alp	2.38	3.84
	416273	AW575691	Hs.79123	KIAA0084 protein	2.38	2.22
	427772	NM_001096	Hs.174140	ATP citrate lyase	2.38	5.41
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	2.35	5.13
	443679	AK001810	Hs.9670	hypothetical protein FLJ10548	2.33	5.81
70	431179	AI338644	Hs.195432	allele-specific transcript 2 family (mitocho	2.33	8.93
	418400	BE243026	Hs.301989	KIAA0246 protein	2.33	5.36
	456876	AL044870	Hs.208780	ESTs, Weakly similar to T29647 hypothe	2.32	3.27
	407082	Z47055		gb Homo panian cDNA sequence, farnesyl	2.31	4.65
	425508	W23184	Hs.170711	glutamate-ammonia ligase (glutamine synt	2.31	9.37
75	408536	AW381532	Hs.135188	ESTs	2.31	2.60
	410552	X66945	Hs.748	fibroblast growth factor receptor 1 (fms	2.30	5.94
	437201	F29279	Hs.171625	hypothetical protein MGC14697	2.30	5.75
	417214	H61618		glizal1c1Ls.1 Soares fetal liver splen	2.30	3.12
	423738	AB684802		ESTs	2.30	3.91
80	410531	AW752953		gb CVO CT0224-261099-035-g02 CT0224 Homo	2.29	3.61
	422491	AA338548	Hs.117545	neurostatin	2.29	5.66
	434411	AA632649	Hs.201372	ESTs	2.28	4.40
	451926	AW134519	Hs.96125	Homo sapiens, Similar to clone FL03816,	2.28	5.14
	401131			NM_001551Homo sapiens arguopoin 5 (AQP	2.27	5.62
	401205			Target Exon	2.27	2.98
	427109	S73265	Hs.1473	gastin-releasing peptide	2.26	3.94
	456846	AJ243662	Hs.110196	NICE-1 protein	2.26	2.52

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	443049	AI028613	Ha.132343	ESTs	2.25	3.13
	440160	BE560269	Ha.7010	NR0X002 protein	2.25	4.93
	430367	N75688	Ha.204354	ras homolog gene family, member B	2.25	5.98
5	429587	AA075975		Homo sapiens clone TCCCA00427 mRNA sequ	2.24	5.15
	421549	AA252810	Ha.50034	hypothetical protein FLJ21916	2.24	2.56
	447150	AJ030011	Ha.BE386	myeloid cell leukemia sequence 1 (BCL2r	2.23	9.03
	450014	NA11322	Ha.18441	ESTs	2.23	4.50
	426511	BE178050	Ha.171271	catenin (catenin-associated protein), b	2.22	5.64
	434309	L37677	Ha.13712	ubiquitin cytochrome c reductase, Rhesia	2.22	5.57
10	437359	BE299197	Ha.17665	cyclin-dependent kinase inhibitor 1A (p2	2.20	5.10
	446637	T19101	Ha.11454	tubulin 5	2.22	6.43
	406710	A1708347	Ha.184014	ribosomal protein L31	2.21	9.10
	424905	S78187	Ha.153752	cell division cycle 25B	2.20	6.13
	407228	M26578	Ha.155376	homolog, beta	2.20	11.34
15	455612	AL356546	Ha.14779	acetyl-CoA synthetase	2.20	7.03
	458568	AI769067	Ha.127824	ESTs, Weakly similar to T28770 hypotheti	2.20	5.68
	407370	AA682384	Ha.182084	ESTs	2.20	7.00
	438942	AW875398	Ha.6451	PR000569 protein	2.19	6.09
20	400728			NM_021724 Homo sapiens nuclear receptor	2.19	6.95
	410185	BE294068	Ha.7337	immediate early protein	2.18	11.72
	428150	AW950547	Ha.70312	cytochrome c oxidase subunit VIIa polype	2.17	7.05
	403037	AF005081		Homo sapiens skin-specific protein (p32	2.17	6.41
	424425	AB031480	Ha.146824	SPR1 protein	2.17	3.58
	414459	Y11525	Ha.761711	CCAAT/enhancer binding protein (C/EBP,	2.17	3.11
25	400082			Eos Control	2.16	8.40
	434702	AL039734	Ha.4099	nardiylin (N-arginine diabolic convertas	2.16	6.83
	439651	AF096480	Ha.56785	ESTs	2.15	3.72
	431638	AJ097229	Ha.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.15	3.34
30	420225	AW243046	Ha.282076	Homo sapiens mRNA for KIAA1550 protein,	2.14	6.20
	428848	NM_000230	Ha.194236	leptin (murine obesity homolog)	2.14	3.42
	415213	NM_002533	Ha.78224	ribonuclease, RNase A family, 1 (pancrea	2.14	5.81
	434454	AF217798	Ha.3850	USP-interacting protein NUDEL endocyt	2.14	6.75
	452467	AW500815		ESTs	2.13	4.66
35	418226	AA424202	Ha.83834	cytochrome b-5	2.13	5.41
	414815	AW925140	Ha.103206	ESTs	2.12	4.14
	430967	H16751	Ha.103895	ESTs	2.12	4.14
	426102	AF200495	Ha.166371	interleukin 1, zeta	2.12	3.77
	410223	S73775	Ha.60708	caldesmonin 1 (fast-twitch, skeletal m	2.11	5.30
40	439518	W76326		gb:09004.0.1 Soares, fetal_heart_NbH19W	2.11	4.01
	427228	AA115702	Ha.174051	small nuclear ribonucleoprotein 70KD pol	2.10	5.13
	436661	AW075694	Ha.156704	ESTs	2.10	3.33
	417139	M69043	Ha.81328	nuclear factor of kappa light polypeptid	2.10	8.13
	445831	NM_009055	Ha.13351	LinC (bacterial lamibiotic synthetase c	2.08	5.42
	431593	NM_002108	Ha.276590	ESTs	2.08	4.43
45	422887	AL090207	Ha.134585	DUF2434G232 protein	2.08	3.92
	424385	AA335785		lymphocyte-specific protein 1	2.07	5.52
	407394	AF005081		gli-Homo sapiens skin-specific protein (x	2.06	5.93
	400198			Eos Control	2.05	10.48
50	426335	AI054347	Ha.2017	ribosomal protein L38	2.04	5.57
	440652	AI080692	Ha.134229	ESTs, Weakly similar to IS4401 hypertension	2.04	3.36
	448804	AW512213	Ha.342849	ADP-ribosylation factor-like 5	2.02	3.32
	443632	AW888222	Ha.5973	tensin	2.02	9.28
	421324	BE257515	Ha.103533	deoxyribonuclease I-like 2	2.02	5.71
55	425406	AF742021	Ha.169756	complement component 1, s subcomponent	2.01	5.49
	410669	AW805749		superoxide dismutase 2, mitochondrial	2.01	3.05
	446193	AI279390	Ha.144658	ESTs, Weakly similar to T12757 hypotheti	2.01	2.77
	400078			Eos Control	2.00	11.41
	455267	AI272968	Ha.83393	cystatin EIM	1.99	5.59
60	413125	BE244589	Ha.75207	glyoxalase I	1.98	6.70
	415433	W70067	Ha.58066	ESTs	1.98	5.59
	434669	AA643687	Ha.149425	Homo sapiens cDNA FLJ11990 fis, clone HE	1.98	3.52
	417553	L09190		itchy/hydrin	1.98	3.35
	403105			Targat Exon	1.98	5.06
	414081	AW969576		matrix Gta protein	1.97	8.74
65	422639	AI929377	Ha.173724	creatine kinase, brain	1.97	5.51
	452208	AA247922	Ha.31895	hypothetical protein MGCA003	1.97	5.67
	435105	AI050715	Ha.2331	E2F transcription factor 5, p130-binding	1.97	5.75
	435265	AL134430	Ha.6906	Homo sapiens cDNA: FLJ21397 fis, clone R	1.96	5.05
	430037	BE409649	Ha.227789	mitogen-activated protein kinase-activat	1.96	5.48
70	440054	AW651947	Ha.6881	splicing factor, arginine/serine-rich 5	1.95	5.95
	417088	M54915	Ha.81170	pim-1 oncogene	1.95	1.95
	429451	BE409861	Ha.202833	heme oxygenase (hemoxygenyl) 1	1.95	5.19
	415274	AF001548	Ha.78344	myosin, heavy polypeptide 11, smooth mus	1.95	6.78
	452472	AW957300	Ha.294142	ESTs, Weakly similar to CS5063 oligodend	1.94	5.99
75	414860	BE255653	Ha.17502	methionine adenosyltransferase II, alpha	1.93	1.94
	437220	AL117542	Ha.334365	CS169994	1.94	3.42
	450461	BE409861	Ha.46736	hypothetical protein FLJ23476	1.94	5.65
	424924	AL038103	Ha.153834	pumilio (Drosophila) homolog 1	1.93	5.28
	413945	NM_000591	Ha.75427	CD14 antigen	1.93	5.38
80	428193	NM_004235		Rhophilin-like factor 4 (gru)	1.93	5.75
	415988	BE407713	Ha.78943	hexosamine hydrolase	1.92	4.65
	425783	AI026740	Ha.1548	ribosomal protein S21	1.92	9.79
	431476	BE512205	Ha.256657	histidine triad nucleotide-binding prote	1.91	7.00

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	455653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694.6s, clone FL	1.91	3.41
	401846			NM_009688"Homo sapiens ribosomal protein	1.91	5.62
	426368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	1.90	4.00
5	400199			Eos Control	1.89	15.74
	425367	AB007867	Hs.278311	plein B1	1.88	5.58
	400283			Eos Control	1.88	9.07
	433465	AV557778	Hs.3314	selenoprotein P, plasma, 1	1.88	5.16
	400079			Eos Control	1.87	8.57
10	411807	AK000290	Hs.44033	diaphosphatase 8	1.86	5.19
	409178	BE303948	Hs.50915	kallistatin 5 (neuropilin/basatin) (KLK5)	1.86	2.75
	425254	BE16678	Hs.76152	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	1.85	5.33
	443121	Z19267	Hs.9006	VAMP (vesicle-associated membrane protein	1.85	6.01
	451092	A1207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein,	1.84	2.82
	435572	U33114	Hs.245188	issue inhibitor of metalloproteinase 4	1.83	5.10
15	426812	AF105385	Hs.172613	solute carrier family 12 (potassium/chloride	1.83	6.48
	439527	AA854650	Hs.124597	ESTs	1.82	3.63
	415089	N25117	Hs.295465	ribosomal protein S26	1.82	6.69
	496400			kallistatin 5 (neuropilin/basatin) (KLK5)	1.82	2.95
	406467			Target Ecton	1.79	2.65
20	426672	AW270555	Hs.171774	hypothetical protein	1.79	5.24
	414088	AW797956	Hs.75748	proteasome (prosome, macropain) subunit,	1.78	6.02
	433271	BE621697	Hs.14317	nuclear protein family A, member 3 (Hv	1.78	5.92
	423307	AL078652	Hs.198951	jun B proto-oncogene	1.77	5.44
	433640	AK390126	Hs.240443	Homo sapiens cDNA: FLJ23530.6s, clone L	1.77	5.79
25	425503	W52517	Hs.158203	actin binding LIM protein 1	1.77	9.27
	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.77	5.44
	425875	AL007333	Hs.160483	erythrocyte membrane protein band 7.2 (b	1.77	6.97
	431021	AB089684		thioesterase sulfatransferase (rhodanese)	1.77	5.23
	432891	AF161483	Hs.279761	HSPC134 protein	1.75	5.73
30	432872	AI909894	Hs.279523	solenoprotein X, 1	1.75	5.72
	451335	AB023192	Hs.86285	imidazole receptor candidate	1.75	6.87
	422875	NM_004672	Hs.194604	mitogen-activated protein kinase kinase	1.74	3.01
	417824	AA084798	Hs.82646	DnaJ (Hsp40) homolog, subfamily B, membe	1.74	5.75
	439908	AI168031	Hs.155507	ESTs	1.74	2.63
35	427349	AA360154	Hs.177415	Finkel-Bisleri-Reilly murine sarcoma virus	1.74	6.80
	445919	TE5519	Hs.334692	hypothetical protein MGC14141	1.74	6.55
	427391	W56075		hypothetical protein FLJ10350	1.73	6.13
	425299	AW505214	Hs.155560	catenin	1.73	5.88
40	430449	AA325723	Hs.241471	ribnB	1.72	5.14
	450766	R27310	Hs.7740	cystical binding protein-like 1	1.71	3.35
	407694	U77594	Hs.37682	retinoic acid receptor responder (tazaro	1.71	6.16
	412374	X01388	Hs.73849	apolipoprotein C-III	1.70	5.18
	417483	BE549343	Hs.82208	acyl-Coenzyme A dehydrogenase, very long	1.70	7.46
	410584	AB011112	Hs.84742	NAAG540 protein	1.69	6.19
45	431882	NM_001426	Hs.271977	enraged homolog 1	1.68	2.63
	441379	AW175787	Hs.334841	selenium binding protein 1	1.67	7.42
	422115	AI878953	Hs.111811	microsomal glutathione S-transferase 3	1.67	6.93
	405742	AI488091	Hs.279860	tumor protein, translationally-controlled	1.66	6.26
	432191	AA043183	Hs.273186	hypothetical protein, clone Tethy0101a	1.65	5.93
50	425263	AF592743	Hs.94953	Homo sapiens, Similar to complement comp	1.65	7.54
	446623	AF279865	Hs.15711	kinesin family member 13B	1.65	5.36
	406912	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.65	12.30
	402002			NM_002795"Homo sapiens proteasome (pro	1.64	5.70
55	401429			C14401067-041126453chj3jBAA35581.1j	1.62	3.82
	415166	NM_003652	Hs.78068	carboxypeptidase 2	1.62	5.96
	410109	AD37341	Hs.59384	hypothetical protein MGC3047	1.61	6.60
	405713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.60	11.13
	453027	AB783441	Hs.539	ribosomal protein S29	1.60	10.87
60	416955	AW889150	Hs.80595	NM_004552"Homo sapiens NADH dehydrogena	1.60	5.90
	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.57	5.60
	402020			NM_006156"Homo sapiens neural precursor	1.57	5.32
	407048	X72632		NM_017247"Homo sapiens nuclear receptor	1.54	5.42
	430775	AI879186	Hs.200895	ribosomal protein L34	1.57	7.09
65	427380	NM_005534	Hs.177559	interferon gamma receptor 2 (interferon	1.56	5.37
	407143	C14076	Hs.332329	EST	1.56	6.54
	436127	W54824	Hs.11565	RINEX cDNA, 2010100D12 gene	1.55	6.35
	413559	BE155647		sh-PN2 HT0553.130.100-001-009 HT0553 Homo	1.55	5.96
	445624	AW140103	Hs.78880	ilvB (bacterial acetoaldehyde synthase)-1	1.55	4.09
70	435044	NM_002802	Hs.4745	proteasome (prosome, macropain) 26S subu	1.55	5.71
	410387	AF217517	Hs.63042	DNF7p564157 protein	1.54	5.14
	428071	AW794126	Hs.195453	ribosomal protein S27 (metalloproteinase)	1.54	8.70
	412915	AW087727	Hs.74623	NM_004541"Homo sapiens NADH dehydrogenas	1.54	6.57
	446429	AI681807	Hs.201391	ESTs	1.53	2.87
75	414551	AI815639	Hs.76394	enoyl Coenzyme A hydratase, short chain,	1.53	6.07
	405801	AW240054	Hs.190813	ribosomal protein L5	1.52	5.63
	437895	AB014558	Hs.58098	KOA-K265 protein	1.51	5.74
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.51	6.40
	425456	T70445	Hs.157890	ribosomal protein L9	1.51	7.08
80	409535	Z37195	Hs.55296	HLA-B associated transcript-1	1.50	5.25
	404467			Target Ecton	1.50	5.82
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	1.50	5.25
	454098	W27953	Hs.292911	Plakophilin	1.48	3.14
	429205	AI482393	Hs.198248	UDP-Gal-beta-GlcNAc-beta 1,4-galactosyltr	1.48	6.24

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428193	430_1	AF105026 U065631.NM.004235 AF022184 AU141767 AU141110 AL040569 D44830 BU111351 AF157585 AC290876 AU104784 AC393429 AI266211
		AF074323 AB206271 BF197792 AW000676.D25944 AB687367 AA621680 AV174408 BF446905 BM314505 BF514079 BM314197 AA645201
5	431021 10409_1	AW874084 BA762222 AT127241 AA262339 AS797099 AB791335 AT572470 AA573434 AB568487 BE049325 AA687950 BC392589 AI336301 AC345673
		AW745716 AA258055 U04001 HA5008 BG685216 AL155238 BA628261 BG547513 BC269365 BF566611
		NM.023122 BC0110148 AU100862 D07292 BF703014 BF973798 BF740474 BF717592 BF150595 BF520468 BF523568 AC186964 AA314620 BF74353
		BF104276 BG195292 BE524679 BF43589 AB200465 AA481682 AW780207 AB008832 AC30540 AB722277 AV030070 BA481445 AW015933 AB31541
		AA785558 AI138798 AA432063 AA548713 AB08485 AC307419 AC355859 AC01672 BF055681 AC127285 AS121208 AS278186 AB89759 M78015
		BF186121 AS927654 AD795509 AC353381 BF1334524 AUW00744 AA700797 AS975178 AB884728 AA443837 AB264654 AU217137 AA053419
		AF75704 AB58483 BG35261 AF354358 AB005336 AA643660 AA478732 AA803071 BE144413 AW017860 AW070418 D23264 BG529551 AL568823
10	427391 904L_3	AA63459 AA46748 BG25444 BF760569
		AW07099 AU150467 AI127583 BE735800 AU125772 AI373009 AT115670 AT769136 AA565848 AA451158 NS0799 AA936337 AS155427 BE577005
		AAW33820 BG151557 AA657954 AF154947 AW467279 AI128795 BF448136 AD369247 BF439175 BE207548 AB705272 B011455 AA420720 F36980
		AA424704 AA393513 AA155753 AB262675 AD044804 AB282678 BG741226 BG597491 AA180234 AB262131 AU102530 AA420765 AC373303 AB8571
15		TC03196 BF529433 AA191425 AW012996 AW005963 BC252471 AI152002 AB14909 AA477614 BE154864 AAT53564 BE085111 AW528731 AA023455
		BA470774 AW194649 AA151192 AL567164 BF6191569 AL156970 AW147137 AW276992 AL536717 BF1981783 AS177146 BF939172 BG740259
		BG755568 B054960 HE1485 AW799491 AC170437 H06413 AA585334 AU151276 AA704274 AA936883 AW131643 A1221650 AW105476 AW552994
40202	11771_2	H23835 BR039110 F273360 BF494322
		BE073890 BF045496 AA155007 AA575157 AW874610 AA816387 H29063 BM083306 AW046771 D0130308 NM.027795 D05598 BG118716 BR10891
		BF972860 BG119842 B0549053 AL530757 BE771653 BE565338 BE906573 BG109826 BE784430 BE899255 BH33973 BM010809 BE621321 B10684956
20		BE047276 BE810737 AW708990 BF971483 BE298241 BH197007 BE272092 BG120374 AW563509 BE540572 AV744947 BG943041 AW327463
		BG472870 BE330687 N028533 AA316042 N40043 AAW04246 AW820929 AA379959 AW801110 AW406977 AA379791 BG941889 BE0267254 AA360459
		AA376336 AA330056 BC5942616 D312320 AA330330 AA303371 AA371733 AA722937 AA494241 W322257 BF745937 AB03090 BG702360
		NM.001156 D23862 BF036771 BR070321 BR03145 BM66956 BG716028 BG70476 BG766814 B12031 BF712530 BG707916 B0942971 AF157472
25	402021 24179_2	AW009362 BE379126 BH185555 BF128026 N28289 BE388301 G327102 A517450 BF03400 AB84649 AB178962 AT142314 A9477058 AI150699
		BG044784 AA176826 BC383933 AV712807 W01301 BF774109 W77840 C15672 BR67016 AT152473 AA484439 C14921 N41745 C15220 F30164
		AA133181 BF768974 H00334 AA34908 AA384232 AA533297 AW407023 AA337516 F361177 AA374444 AA402758 AI141545 B0214740 AW0737914
		BF155847 BE156527
		AA505535

30	TABLE 65C:				
	Play:	Unique number corresponding to an Eos probe(s)			
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.			
	Strand:	Indicates DNA strand from which exons were predicted.			
35	NL_position:	Indicates nucleotide positions of predicted exons.			
	Play	Ref	Strand	NL_position	
	405121	8102330	Minus	35816-36004,36587-36584	
	401203	9743367	Minus	17296-173056,17368-173928	
40	404994	9714719	Plus	169845-170272	
	402294	2282012	Minus	2575-3000	
	404730	8389582	Plus	119832-120016,124110-124275	
	403593	6862650	Minus	62554-62712,69449-69602	
	403710	6437516	Plus	27413-28978	
45	401905	8671986	Plus	153955-154441,156599-156819	
	403108	6980955	Plus	93253-93667	
	404996	6007890	Plus	37999-38145,38652-39898,39727-39872,4055	
	402315	7361741	Minus	30728-32065	
	401131	8699812	Plus	94002-94087,95604-95887,96323-96487,9759	
50	401205	9743388	Plus	167373-167433,167936-168031	
	403105	8890016	Minus	145287-145744	
	401846	7712190	Minus	82775-82823,82912-83022	
	406480	9266258	Plus	1553-1712,1678-2140,4252-4385,5922-6077	
	406467	9785561	Plus	182212-182958	
55	401429	8217890	Minus	86946-87579	
	404467	8077630	Minus	24961-25853	
	406587	8199273	Minus	120577-120718	
	404175	9931117	Minus	107420-107547,109625-109795	

TABLE 66A. DISEASE INDICATIONS AND PREFERRED UTILITIES FOR SELECTED GENES

Table 66A provides disease indications and preferred utilities for about 439 selected genes. These genes were identified using Eos/iHymex Geneschip arrays.

60	Primekey:	Unique Eos probe(s) identifier number				
	ExAcn:	Exemplar Accession number				
65	UgID:	Ungene ID number				
	UgTitle:	Ungene title				
	Disease:	Diseases indicated for selected gene as described in table 1 and abbreviated as follows: AWPC (androgen independent) prostate diseases; arth (arthritic diseases), bph (benign prostatic hyperplasia), blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glo (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrotic diseases), head (head & neck diseases), leo (leukodystrophies), leuk (leukemia diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), onco (ovarian endometrial diseases), omic (ovarian mucinous diseases), panc (pancreatic diseases), pres (prostate diseases), renal (renal diseases), meta (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)				
70	Utility:	preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)				
75	Primekey	Ex Acn	UgID	Ug Title	Disease	Utility
	400289	X07820	HS.2258	matrix metalloproteinase 10 (stromelysin)	angio, blad, lung, cerv, ovar, head, esoph	mAb+diag+s.m.
	400297	AI127076	HS.306201	hypothetical protein DKFZP564D1278	breast, blad, colon, pres	mAb
	403303	AA247958	HS.79136	U1P1 protein, estrogen regulated	breast, lung, test, stom, liver, head, lung, head, leuk	mAb
	403843			NM_021027-Homo sapiens scrofin-related		s.m.
	402075			ENSP0000021059-Plasma membrane calcium	blad, lung, head, cerv, meta, esoph	mAb+diag
	402901			NM_025200-Homo sapiens hypothetical pro	blad	CTL
	402487			FGENES1 predicted novel CUB domain conta	panc, lung, colon, test, esoph	mAb+s.m.

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404682		ortholog of mouse polydomain protein	panc	diag
404675		NM_022819 Homo sapiens phospholipase A2	blad	CTL+s.m.
404977		Insulin-like growth factor 2 (somatomedin)	blad, ovar	mAb+diag
405033		C100B25Z g544327pp00047939fM05_RABIT	blad	s.m.
405547		NM_018837 Homo sapiens transporter 2, A	ovary, cerv, panc	mAb+s.m.
405640		A kallikrein 8 (neurosinovirin) (KLK8)	ovary, uter	diag
406664	M21305	FGFenes predicted novel secreted protein	angio, blad, fibro	diag
407603	AW955705	Homo sapiens, clone IMAGE4296322, mRNA	glio, blad	CTL
407792	A077175	putative secreted ligand homologous to 1	ovary, uter, cerv, panc	mAb+diag
407811	AW190602	cysteine motif superfamily 1, BMP-antagon	angio, panc, stom, uter, lung, esoph	diag
407836	T79340	B-cell CLL/lymphoma 6, member B, zinc fi	blad	CTL
407975	X89426	endothelial cell-specific molecule 1	angio, renal	diag
408243	Y00787	interleukin 8	blad, stom, headnk, cerv, lung, angio, esoph, panc	diag
408367	AK001178	Homo sapiens ophioc neurotransmitter tra	renal	mAb+s.m.
408369	R38438	SLC15A2 Solute carrier family 15 (H+lep	pros, lung, fibro, uter, glio, cerv, ovar	mAb
408380	AF123050	ubiquitin	lung, blad, headnk, panc, stom, fibro, esoph, mea	CTL
408482	NM_000676	adenosine A2b receptor	lung, esoph, headnk	mAb+s.m.
408562	AA833231	nucleoside (own guidance) receptor, Deos	uter, fibro	mAb+s.m.
408790	AW580227	neurotrophic tyrosine kinase, receptor,	lung	s.m.
408908	BE296227	serine/threonine kinase 15	blad, lung, headnk, stom	CTL+diag
409041	AB033025	hypothetical protein, XP_051860 (KIAA119	breast, pros	CTL
409079	W67707	interleukin 6 signal transducer (gp130,	ovary, breast, mea	diag
409102	AF261237	XAGE-1 protein	angio, renal, colon, stom	mAb+s.m.+CTL
409178	BE393948	kallikrein 5	renal, glio	mAb+diag
409220	BE243323	tumor necrosis factor receptor superfam	lung, headnk, panc, stom, cerv, esoph, blad	diag
409348	AA015335	ESTs	lung, blad, headnk	mAb+s.m.+CTL
409389	AG007979	Homo sapiens mRNA, chromosome 1 specifi	renal	diag
409420	Z15008	laminin, gamma 2 (picon) (100KD), kulin	diag	
409532	W74001	serine (or cysteine) proteinase inhibito	diag	
409537	AA323948	Homo sapiens mRNA; cDNA DKFZp43K0621 (f	diag	
409663	AA743750	KIAA1362 protein	renal	mAb+s.m.+CTL
409745	AA077391	hg-7814E T2 Chromosome 7 Fetal Brain cDNA	ovary, renal	diag
409757	NM_001898	cystatin SN	panc, stom, lung, blad	CTL+s.m.
409893	AW247090	microchromosome maintenance deficient (S	blad, cerv, blad, test, esoph	diag
409956	AW103334	HLN1, beta A (activin A, activin AB a	breast, panc, ovary, colon, headnk, lung, blad, esoph	diag
410001	AB041036	kallikrein 11	ovary, pros, uter, cerv, lung	s.m.
410055	AJ250339	gene for serine/threonine protein kinase	renal	CTL
410153	BE311926	hypothetical protein FLJ12691	renal, blad, renal	CTL
410274	AA381807	hypoxia-inducible protein 2	lung, renal	CTL
410309	BE343077	alpha-2-B-galactosidase III	panc	mAb+s.m.
410407	X66839	carboxyl chondrin IX	renal, lung, colon, stom, ovary, uter, blad	mAb+diag+s.m.
410418	D31382	transmembrane protease, serine 4	colon, blad, lung, ovary, panc, headnk	diag
411274	NM_002775	kallikrein 10	colon, ovary, uter, cerv, headk, panc	diag
411411	AA345041	ESTs, Weakly similar to KIAA1330 protein	renal	mAb+s.m.
411773	NM_005799	protease, serine, 21 (testisin)	ovary	diag
412078	X65699	paired box gene 8	ovary	CTL
412140	AA219691	RAB8 interacting, kinesin-like (gabinsin)	lung, blad, headnk, breast, ovary, panc, angio, test, mea	s.m.
412580	AA113282	similar to CABLES (Homo sapiens)	meia	mAb+s.m.+CTL
412592	Z48004	ocular albinism 1 (blepharophary)	meia	s.m.
412628	AJ972402	hypothetical protein MGC2648	pros	diag
412709	AL022327	KIAA0027 protein	glio	mAb+s.m.
412719	AW016810	ESTs	lung, headnk, blad, glio, cerv	s.m.
412969	D81458	KIAA0282 protein	glio	CTL+s.m.
412986	X81120	carbamidohydrolase receptor 1 (bran)	glio	mAb+s.m.
413048	M33221	mannose receptor, C type 1	glio, panc	mAb
413063	AL035737	chitinase 3-like 1 (cartilage glycoprote	glio, ovary, blad, test	diag
413273	BE363085	interleukin-stimulated protein, 15 kDa	lung, glio, renal, esoph, panc, headnk, angio, mea	diag
413324	V00571	cardiotropin releasing hormone	blad	CTL+diag
413385	M34455	indoleamine-pyrrrole 2,3 dioxygenase	blad, lung, mea, fibro, uter	s.m.
413554	AA319146	secretogranin II (chromogranin C)	panc, glio	diag
413719	BE439580	small inducible cytokine subfamily A (Cy	panc, lung, headnk, cerv, colon, uter, stom, esoph	diag
414577	A026548	hypothetical protein FLJ20992 similar to	angio	CTL+diag
414774	X02419	plasmaogen activator, urokinase	lung, blad, headnk, panc, stom, ovary, esoph	diag
414812	X72755	nucleoside induced by gamma interferon	breast, blad, lung, fibro, panc, angio, headnk	diag
414825	X05370	epidermal growth factor receptor (avian	glio	diag
414833	AA026960	OC28 protein kinase 1	blad, lung, renal, esoph, panc, headnk, angio	mAb+s.m.+CTL
414907	X30725	polo (Drosophila)-like kinase 1	blad, lung, ovary, stom, colon, cerv, headnk, test	s.m.
414945	BE076358	lymphocyte antigen 6 complex, locus E	meia	s.m.
415138	C18356	tissue factor pathway inhibitor 2	angio, panc, stom, lung, uter	mAb+s.m.
415311	A073267	ESTs	blad, ovary, renal	mAb+s.m.+CTL
415539	A0733881	BMP-1R18	breast, uter, pros	mAb+s.m.
415668	AW957684	Homo sapiens lysyl oxidase-like 4 (LOXL4	meia	diag
415669	NM_000528	serine (or cysteine) proteinase inhibito	lung	mAb+diag+s.m.
415817	U81867	protein tyrosine phosphatase, receptor-t	lung, glio, headnk, cerv, mea, esoph, fibro	mAb+s.m.
415910	U23050	hemelinase (CX-3-C) receptor 1	glio	mAb
415929	AA724573	Homo sapiens mucoglycin-3 (MUCOLG3)	meia	mAb+s.m.+CTL
415989	A0267700	ESTs	pros, ovary, blad, lung, headnk, panc, colon, stom	CTL+diag
416031	AF265370	interleukin, beta3	headnk, esoph, mea	CTL+s.m.
416039	AA260776	MAOCD (reticoid anast deficient, yeast, h	lung, testis, colon, uter, stom	CTL
416250	AA581386	Keremin 2	esoph, lung, cerv, ovary	mAb
416350	AF188625	phospholipase A2, group IID	test, mea, fibro	CTL
416530	U62801	Kallikrein 6 (neurosin, zyme)	ovary, uter	diag

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	423184	NM_004428	Hs.1624	ephrin-A1	pros, panc, renal	mAb+s.m.
	423242	AL030402	Hs.125783	DEME-6 protein	breast, renal, ovar, pros, colon	CTL
	423422	AC005175	Hs.128425	NY-REN-24 antigen	glio	mAb
5	423508	AW604297	Hs.125711	hepatitis A virus cellular receptor 1	renal, colon	mAb
	423583	AL122055	Hs.129536	KNA1020 protein	pros	s.m.
	423534	AW605908	Hs.1699	heparin-binding growth factor binding pr	lung, blad, headnk, panc	diag
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test	mAb+diag+s.m.
	423936	U77629	Hs.135639	achate-actin complex (Macrophage) homol	colon, stom, ovar	CTL
10	423991	Q13666	Hs.135348	serpinin (OGF-20)	breast, colon, blad, lung, fibro, panc, headnk, ovar, meli	mAb+s.m.
	424008	R02740	Hs.132555	active chemokine receptor, GTP-binding	blad, headnk, stom, cerv, esoph	diag
	424046	AF027866	Hs.138202	peptide (for cysteine) proteinase inhibi	headnk, lung, cerv	mAb+s.m.+CTL
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	colon, stom	mAb+s.m.
	424321	W74048	Hs.1785	lymphocyte-specific protein tyrosine kin	meli, fibro	s.m.
	424381	AA285749	Hs.146239	protein kinase Gm2 (CHEK2)	colon, lung, test, panc	s.m.
15	424411	NM_005020	Hs.146548	crystallin, beta A2	lung	s.m.
	424502	AF242388	Hs.145565	lengtin	lung	s.m.
	424533	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	panc, pros, argio, blad, lung	mAb+s.m.
	424620	AA101043	Hs.151234	kallistren 7 (glycomyric, stratum com	headnk, panc, lung, blad, uter, cerv, colon, stom, test, meli	diag
	424687	050770	Hs.151738	matrix metalloproteinase 9 (gelatinase B	blad, breast	CTL+s.m.
20	424735	U51875	Hs.172498	short-chain alcohol dehydrogenase family	meli	CTL+s.m.
	424825	AF207059	Hs.153357	procollagen-lysine, 2-oxoglutarate 5-de	ovar, blad, lung, headnk, panc, stom	s.m.
	424805	NM_002487	Hs.153704	INROR (involved in mitosis gene al-related	renal, fibro	mAb+s.m.
	424908	X58263	Hs.154151	protein tyrosine phosphatase, receptor I	pros, colon, stom, uter, cerv, headnk, esoph, panc	diag
	425071	NM_013889	Hs.154424	deiodinase, iodothyronine, type II	glio, meli	mAb+s.m.+CTL
25	425088	AA663372	Hs.163395	hypothetical protein FLJ12015	glio	mAb+s.m.
	425115	AA44664	Hs.123556	downstream ot G protein-coupled recept	breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph	mAb+diag+s.m.
	425247	NM_005940	Hs.159308	matrix metalloproteinase 11 (stromelysin	lung, headnk	s.m.
	425322	U58350	Hs.155837	protein kinase, DNA-activated, catalytic	meli, glio	mAb+s.m.
	425335	AB07937	Hs.158287	syndecan 3	lung, headnk, cerv, esoph, blad	mAb
30	425650	NM_001844	Hs.1525	desmoplakin 3 (pemphigus vulgaris antigen	blad, lung, headnk, cerv, esoph, blad	mAb
	425721	AC002015	Hs.159308	uropilin 1A	blad, lung, headnk	CTL+diag
	425723	NM_014420	Hs.155311	displek (Placopus laevis) homolog 4	endo, uter, colon	s.m.
	425734	AF056209	Hs.155396	peptidylglycine alpha-amidating monooxy	lung	diag
	425776	U25128	Hs.159459	parathyroid hormone receptor 2	ovar, uter, lung	s.m.
35	425842	A5874657	Hs.158623	HK-2 (Drosophila) homolog B	panc, glio	mAb+s.m.
	425852	AK001304	Hs.159583	death receptor 5, TNF superfamily member	blad, lung, headnk	mAb
	425883	AL137308	Hs.161031	Human sapiens mRNA: cDNA DKF4340K0322	(flad, blad, stom, panc	mAb+s.m.
	425921	NM_007221	Hs.162211	solute carrier family 6 (neurotransmitter	renal	mAb+s.m.
	425988	AU076629	Hs.165590	fibroblast growth factor receptor 4	renal	mAb+s.m.
40	426028	NM_001110	Hs.170205	a 4-strigatin and metalloproteinase doma	blad, lung, renal, colon, ovar, uter, panc	mAb+diag
	426215	AW504818	Hs.155220	steniolecin 2	panc, lung, colon, esoph, stom	diag
	426227	U67058	Hs.154279	Human proteinase activated receptor-2 mR	ovar, blad, stom	CTL+s.m.
	426322	JO5068	Hs.2012	transcobalamin I (vitamin B12 binding pr	glio	s.m.
	426344	H41821	Hs.322485	transcriptional activator of the c-fos p	ovar, lung, headnk, cerv, colon, uter, stom, test	CTL+s.m.
45	426427	M68699	Hs.168540	TTK protein kinase	blad, breast	s.m.
	426451	A908185	Hs.169946	GATA-binding protein 3 (T-cell receptor	ovar, colon, blad, lung, cerv	mAb+diag
	426514	BE516633	Hs.170195	bone morphogenetic protein 7 (osteogenic	meli	diag
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	lung, esoph, pros, uter, panc, colon, ovar, headnk	mAb+s.m.
	426761	AU157019	Hs.172689	PORCN (Pro-cerebrol side receptor inducing	renal	mAb+s.m.
50	426812	AF103365	Hs.172613	solute carrier family 12 (potassium/chlo	renal, colon, ovar, uter, stom	CTL
	426890	AA335167	Hs.41294	ESTs	lung, blad, test, meli	CTL
	427238	BC270447	Hs.356512	ubiquitin carrier protein	lung, headnk, blad, meli, esoph	CTL+s.m.
	427335	AA468542	Hs.251677	G antigen 78	colon, stom, panc	CTL
	427343	A930044	Hs.176877	protein kinase C binding protein 2	blad, lung, ovar, stom, test, esoph	mAb
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	panc	CTL
	427747	AW411425	Hs.180655	serine/threonine kinase 12	blad, lung	s.m.
	427923	AW274357	Hs.301406	FGFR3E3 predicted 11 TM protein	mel	mAb
60	427968	NM_001963	Hs.2220	epidermal growth factor (beta-agonist	panc	CTL
	428093	AW594506	Hs.194830	ESTs	ovar, panc	mAb+s.m.
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	glio	s.m.
	428179	AI127772	Hs.279696	serumglucocorticoid regulated kinase-II	breast	mAb+s.m.
	428187	AB067303	Hs.285529	protein-coupled receptor 49	ovar, colon, stom	diag
	428242	H55705	Hs.22550	leukemia inhibitory factor (chemokine	ovar, panc, lung	mAb+s.m.
65	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	renal	diag
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, meli, stom	mAb+diag+s.m.
	428368	BE440042	Hs.83336	matrix metalloproteinase 3 (stromelysin,	headnk, stom, esoph, colon	diag
	428382	H16233	Hs.2256	secondary granule, neuroendocrine prot	headnk, colon, lung, panc, stom, test, meli	s.m.
	428450	NM_014791	Hs.184339	KOA0175 gene product	lung, blad, colon, uter, ovar	s.m.
70	428479	Y00272	Hs.334562	cell division cycle 2, C1 to S and G2 to	lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, meli	mAb+s.m.
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	panc	diag
	428486	AK034497	Hs.184604	pancreatic polypeptide	mel	mAb
	428505	AL035461	Hs.2281	chromogranin B (proctodagranin 1)	ovar, cerv, panc, stom, headnk	diag
	428513	BE220806	Hs.184697	plein C1	ovar, EWS, uter	mAb+s.m.
75	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	blad, ovar, pros, lung, stom, test	CTL+s.m.
	428684	AK001666	Hs.189059	similar to SALL1 (sal (Drosophila)-like	breast, colon, lung, panc, stom, headnk, cerv, EWS	mAb
	428698	AA827713	Hs.324538	KIAA1615 protein	lung	diag
	428748	AW593206	Hs.98785	Ksp25 protein	ovar, cerv, lung, panc, stom, renal	diag
	428758	AA432888	Hs.98502	CA125 antigen, mucin 16	ovar	mAb+s.m.
80	428778	AK000030	Hs.183326	fibroblast growth factor receptor-like 1	glio, meli	mAb+s.m.
	428784	Y12351	Hs.183470	potentreg receptor P2X, ligand-gated ion	renal	mAb+s.m.+CTL
	428841	AA118430	Hs.104355	ESTs	cerv, panc, colon, stom, headnk, renal	mAb+diag
	428853	AA306610	Hs.348183	tumor necrosis factor receptor superfam	lung, cerv	diag
	428969	AF120274	Hs.194689	arner		

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	428970	BC275891	Hs 194691	retinoic acid induces 3 (RAIG1), metabo	stom, panc, colon, ovar	mAb-s.m.
	429149	AW193360	Hs 197962	Homolog of mouse ADP-ribosylation factor	glio	mAb-s.m.
	429211	AF052693	Hs 198249	lung protein, beta 5 (connexin 3)	lung, blad, headnk, cerv, esoph, stom, meli	mAb-s.m.
5	429263	AA019008	Hs 198396	ATP-binding cassette, sub-family A (ABC1)	lung	mAb-s.m.
	429276	AF055605	Hs 198612	G protein-coupled receptor 51	angio, blad, glio	mAb-s.m.
	429333	AL117406	Hs 1334891	ATP-binding cassette transporter MRP8	breast, pros	mAb-s.m.
	429547	AW009166	Hs 99376	FGFENSH predicted novel secreted protein	panc, headnk, lung, ovar	diag
	429610	AB024937	Hs 211092	LUXN protein: PLUNC (palate lung and nas	lung, fibro	mAb+diag
10	429903	AL134197	Hs 93397	cyclin-dependent kinase 5, regulatory su	lung, meli	s.m.
	429910	NM_000667	Hs 2597	5-hydroxytryptamine (serotonin) receptor	les	mAb-s.m.
	430147	R80704	Hs 234344	nary/nervous-of-split related with YRP	glio	s.m.
	430280	AA361258	Hs 237868	interleukin 7 receptor	meli, lung, panc, stom, esoph, headnk	mAb-s.m.-CTL
	430377	NM_001922	Hs 301965	dopachrome tautomerase (dopachrome delta	meti	CTL
	430486	BE062109	Hs 241551	chloride channel, calcium activated, fam	ovar, blad, headnk, cerv, esoph	mAb-s.m.
15	430822	AW053371	Hs 243017	glyceraledehyde 3-phosphate dehydrogenase	meti	s.m.
	430890	X54232	Hs 2699	glio, lung, cerv, blad, esoph	glio	mAb-s.m.
	431053	S40369	Hs 249141	Glutamate receptor subunit	glio	mAb
	431130	NM_005103	Hs 2719	HC4, epidermal-specific, whey acidic pr	ovar, utr	diag
	431462	AW583672	Hs 265311	granulin-like neuroendocrine peptide, pros	panc, lung, glio, test	diag
20	431515	NM_012152	Hs 258503	EDG-7 (endothelial differentiation, lys	ovar, pros, lung, blad	mAb-s.m.
	431620	AA126109	Hs 264981	2-5'-oligoadenylate synthetase 2 (69-71	esoph, cerv	CTL+s.m.
	431629	ALU077025	Hs 265827	interferon, alpha-inducible protein (clo	panc, utr, cerv, stom, esoph, meli	mAb+diag
	431630	NM_002204	Hs 263429	integrin, alpha 3 (panin) CD49c, alpha	ovar, panc, blad, headnk, meli, renal	mAb-s.m.
	431840	AA534908	Hs 2860	POU domain, class 5, transcription facto	test, renal, blad	CTL
25	431846	BE019924	Hs 271580	uropkin B	blad, headnk, utr, cerv, stom, ovar	mAb+diag
	431870	AW449902	Hs 103500	ESTs	renal	mAb-s.m.-CTL
	431939	AW008961	Hs 231994	ESTs	panc, blad, headnk, ovar, colon, pros, panc, breast, esoph, test, meli	mAb+diag
	431958	NX3526	Hs 2877	orchestrin 3, type 1, P-130 (hepatic placenta	renal	mAb+diag
	432196	AW200888	Hs 273230	hypothetical protein, FL20630	renal	CTL
30	432201	AIS38613	Hs 238241	Transmembrane protease, serine 3	breast, colon, ovar, stom, panc, utr, cerv, lung	mAb+diag+s.m.
	432579	AF043244	Hs 278439	nucleolar protein 3 (apoptosis repressor	renal	diag
	432596	AJ274741	Hs 278481	marlin 5	pros, breast	CTL
	432606	NM_002704	Hs 3066	granzyme K (serine protease, granzyme 3,	renal, breast, lung, stom, hepC, fibro	CTL
	432800	BE391046	Hs 278962	Aim-1 protein	meti, pros	mAb-s.m.
35	432829	W60377	Hs 57772	ESTs	blad	CTL+s.m.
	432867	AW016938	Hs 232384	ESTs	stom, colon	mAb-s.m.-CTL
	432874	W64322	Hs 279651	metastoma inhibitory activity	panc, stom, meli	diag
	432990	AL036071	Hs 279899	tumor necrosis factor receptor superfam	pros, renal	mAb-s.m.
	433001	AF217513	Hs 279905	clone H06310 PR00310p1	colon, breast, lung, blad, cerv, utr, test, meli	s.m.
40	433447	U28195	Hs 3281	neuronal pentamer II	blad, esoph, colon, renal	diag
	433448	AF055719	Hs 52384	carboxypeptidase AA	headnk, esoph, lung	s.m.
	433867	AK000596	Hs 3618	Hippocampin-like 1	renal	CTL
	434206	AW136973	Hs 362915	ESTs, Weakly similar to S66890 mitogen 1	stom, colon	CTL+s.m.
45	434216	AF123689	Hs 53605	lucase zipper, putative tumor suppressor	meti	s.m.
	435013	H19123	Hs 110024	NM_020142 Homo sapiens NADH ubiquinone	o renal, lung	CTL
	435472	AW972330	Hs 283022	triggering receptor expressed on myeloid	glio	diag
	435505	AF200492	Hs 211238	interleukin-1 homolog 1	lung, headnk	mAb
	435969	AF255910	Hs 54650	junctional adhesion molecule 2	angio, glio	mAb
50	436456	AW252677	Hs 245122	metastin-inducing hormone receptor (meti	mAb-s.m.
	436460	AJ271643	Hs 87469	putative acid-sensing ion channel	lung, blad, colon, ovar, utr, headnk, test	mAb-s.m.
	436481	AA739597	Hs 5199	HSPC150 protein similar to ubiquitin-con	renal	s.m.
	436576	A458213	Hs 77542	ESTs	renal, panc, headnk, lung	mAb-s.m.
	436608	AA828980	Hs 152371	down syndrome critical region protein DS	blad, lung	CTL+s.m.
55	436955	AF027325	Hs 156704	carbonic anhydrase XII	lung, blad, headnk, utr, cerv, colon	mAb-s.m.
	436961	AW075974	Hs 156704	ESTs	lung, panc, renal, utr, glio	CTL
	436982	AB018305	Hs 5378	spondin 1, (t-spondin) extracellular mat	ovar, fibro	diag
	437016	AW167616	Hs 5398	granin monophosphate synthetase	headnk, cerv, lung, cerv, esoph, headnk	s.m.
	437044	AL033864	Hs 59517	headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph	panc, renal	mAb-s.m.-CTL
60	437100	AT616073	Hs 14535	Homo sapiens cDNA: FLJ2314 fs, clone H	renal	mAb-s.m.-CTL
	437212	AT65021	Hs 210775	ESTs	renal, utr, ovar	CTL
	437789	AIS81344	Hs 127812	ESTs, Weakly similar to T17330 hypothel	blad	CTL
	437852	BE001836	Hs 266897	putative GPCR	lung, lung	mAb-s.m.-CTL
	437939	AIS50087	Hs 306828	gb.wg5G2.1 1 NCQ_CGad12 Homo sapien	blad, ovar, utr, cerv, blad, renal	diag
	438380	T06430	Hs 6194	chondroitin sulfate proteoglycan BEHABb	glio, meli	diag
65	438549	BE386801	Hs 21858	trinuclotide repeat containing 3	meti	CTL+diag
	438859	AIS5962	Hs 53522	Homo sapiens mRNA for KIAA1647 protein,	renal	mAb-s.m.-CTL
	439129	AW195515	Hs 253177	ESTs	renal	mAb-s.m.-CTL
	439366	AW979074	Hs 265311	gb. EST391184 IMAGE resequences, MAGP	renal	diag
	439318	AW300887	Hs 266338	membrane-spanning 4 domains, subfamily A	uter, stom, pros, fibro	mAb
70	439223	AW238299	Hs 250818	UL 16 binding protein 2	lung, headnk, cerv, esoph, blad, colon	mAb
	439477	W69813	Hs 58842	hypothetical protein FL10K30	lung	mAb-s.m.
	439569	AW602168	Hs 222399	CESP1 protein	breast, AWPC, pros, blad	diag
	439606	W79123	Hs 58551	G protein-coupled receptor 87	lung, blad, headnk, cerv, esoph	mAb-s.m.
	439738	BE246502	Hs 9598	sema domain, immunoglobulin domain (H)	blad, lung, cerv, renal	mAb-s.m.-CTL
75	439759	AL339555	Hs 617709	Homo sapiens mRNA full length insert cDN	colon, stom, panc, lung	mAb
	439979	AW602921	Hs 5823	hypothetical protein FL10K30	renal, cerv, pros, headnk, colon, test	s.m.
	440006	AK000517	Hs 6844	NALP2 protein; PYRIN-Containing A-PAF 1	blad, ovar, lung, headnk, test	diag
	440065	W03476	Hs 265331	Homo sapiens Fc receptor homolog express	meti	s.m.
	440225	BE295782	Hs 1519	tumor necrosis factor receptor superfam	glio, renal, colon, blad	mAb-s.m.
80	440304	BE195984	Hs 126395	hepatitis A virus cellular receptor 1	renal	mAb-s.m.-CTL
	440311	AT733079	Hs 125407	ESTs, Moderately similar to ALUE_HUMAN1	renal	mAb+diag
	440516	SA2303	Hs 161	cadherin 2, type 1. N-cadherin (neuronal	glio, ovar, utr, renal, hepC	s.m.
	440672	AF083811	Hs 7345	MAD1 (mitotic arrest deficient, yeast, h	meti	

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441362	BE614410	HE 23044	RAD51 (S. cerevisiae) homolog (E coli R	lung, blad, headkn, test, melia, esoph	s.m.
441392	AW551831	HE 222119	ESTs, Weakly similar to S30433 keratin 1	renal	mAb+s.m.-CTL
442006	AW975183	HE 372210	ESTs, Weakly similar to S72402 hypothel	fibro, angio	mAb
442171	AW664964	HE 128899	ESTs, hypothetical protein for IMAGE:447	breast, lung, blad, panc, headkn, stom, ovar, pros	mAb+s.m.-CTL
442133	AN874358	HE 129017	ESTs, type I transmembrane protein	ovar, uter	mAb+s.m.-CTL
442438	AA959596		gh-c25031.51 NC2_GGAP_Ku5 Homo sapiens	uter, ovar, renal	mAb+s.m.-CTL
443105	X95753	HE 9004	chondroitin sulfate proteoglycan 4 (mela	mela	mAb+diag
443211	AF128388	HE 143655	ESTs	blad, ovar, lung, headkn, stom	mAb+s.m.-CTL
443247	BE614387	HE 333693	E-myc target JP01	colon, lung, blad, panc	CTL
443426	AF081538	HE 23522	chromosome 20 open reading frame 1	renal	diag
443595	AF163132	HE 39613	PPAR(gamma) angiopoietin related protein	renal	diag
443646	AF065139	HE 164226	Thrombospondin 1	angio, panc, uter	diag
443785	AW449552	HE 190125	basic-helix-loop-helix-PAS protein	glio, uter, ovar	mAb+s.m.-CTL
443859	NM_013409	HE 39114	irisin	lung, cerv, headkn, blad, esoph	mAb+s.m.
443987	AW163123	HE 10071	seven transmembrane protein TM7SF3	renal	mAb+s.m.
444006	BE350285	HE 10096	type 1 transmembrane protein Fm14	panc, colon, lung, ovar, renal, esoph, melia, blad, stom, cerv	mAb+s.m.
444371	BE540274	HE 239	forkhead box M1	lung, headkn, blad, glio, test, melia	s.m.
444381	BE387335	HE 263713	hypothetical protein BCD14245	breast, colon, blad, lung, panc, headkn, ovar, stom, uter, renal, angio, blad, melia, esoph	diag
444488	AW192879	HE 359660	ancient conserved domain protein 4	renal	mAb+s.m.
444527	NM_005408	HE 11383	small inducible cytokine subfamily A (Cy	fibro, esoph	diag
444781	NM_014400	HE 11950	EGF-anchored metalloelastase-associated prote	lung, blad, headkn, cerv	mAb+diag
444783	AA001486	HE 52180	anilin (Drosophila Scars homolog), act	ovar, lung, blad, headkn, panc, cerv, stom, uter, colon, esoph	CTL+s.m.
444809	BE307568	HE 208219	opioid	mela	mAb+s.m.
445070	NM_000677	HE 258	adrenomedullin A3 receptor	renal	mAb+s.m.
445417	AA021028	HE 12680	a disintegrin-like and metalloprotease w	panc, headkn, stom, lung, esoph	diag
445537	AJ245671	HE 12844	EGF-like domain, multiple 6	ovar, blad, uter, breast, lung, headkn, renal, fibro, panc, cerv	mAb+diag
445881	AA031342	HE 199460	DCPR1 protein	stom, panc, esoph, omuc, esoph	mAb
445895	D29954	HE 13421	KIAA0056 protein	pros	CTL
446051	BE048061	HE 37054	ephrin-A3	colon, breast	mAb+diag
446163	AJ026880	HE 23522	protein receptor	breast, cerv, uter	mAb+s.m.
446232	AA281948	HE 194691	retinoic acid induced 3	stom, panc, colon, ovar	mAb+s.m.
446341	AA040763	HE 310735	FGENESH prediction similar to melittidin	mela	mAb+s.m.
446619	AW076643	HE 3113	secreted phosphoprotein 1 (osteopontin,	ovar, fibro, panc, headkn, lung, colon, blad, melia, esoph, uter	diag
446650	AB019665	HE 15913	solute carrier family 22 (organic cation	renal	mAb+diag
446921	AB012113	HE 157539	small inducible cytokine subfamily A (Cy	glio, blad, panc, headkn, lung, fibro, melia	diag
447004	AA026688	HE 157539	FGENESH predicted secreted protein	colon, panc, cerv, breast, ovar, lung, panc	CTL+diag
447033	AS37412	HE 157601	Predigoid gene: Eos cloned; secreted w/	renal	CTL+s.m.
447072	D61934	HE 17279	type I transmembrane sulfoxidase 1	renal	CTL+diag
447131	NM_024595	HE 237971	retinoic acid receptor response (baxaro	colon, breast, stom, lung, melia, ovar	CTL+s.m.
447208	BE315201	HE 237971	hypothetical protein MG65267	esoph, stom, colon	CTL+diag
447269	NM_004861	HE 17858	ceratroside (3'-phosphoadenylylthylate	renal	CTL
447342	AI193268	HE 19322	Homo sapiens. Similar to RIKEN cDNA 2010	colon, blad, pros, lung, stom, AWP, C	CTL
447400	AD030322	HE 18457	hypothetical protein FL20315	colon, pros, stom, uter	s.m.
447674	BE276940	HE 19192	cyclin-dependent kinase 2	renal, ovar, uter	mAb+s.m.-CTL
447835	AW561623	HE 164129	ESTs, Weakly similar to I36022 hypothel	mela	mAb+s.m.-CTL
447837	AL109716	HE 20034	Homo sapiens mRNA full length insert cDN	breast, panc, colon, lung, ovar, stom	mAb+s.m.-CTL
448105	AW591433	HE 298241	Transmembrane protease, serine 3	ovar, uter, lung, stom, headkn, glio, panc	mAb+s.m.
448243	AW369771	HE 367688	mygrin, beta 8	glio	diag
448321	NM_058883	HE 20912	adenomatous polyposis coli like	glio	mAb+s.m.-CTL
448499	BE613280	HE 77550	p53-regulated DDA3	glio	CTL+s.m.
448595	AB014544	HE 21572	KIAA0644 gene product	breast, glio	mAb+s.m.
448610	NM_006157	HE 21902	nei (chicken)-like 1	lung, renal	mAb+s.m.
448735	NM_005626	HE 187658	solute carrier family 6 (neurotransmitter	panc, lung, stom, omuc	mAb+s.m.
448844	AI581519	HE 177164	FGENESH predicted novel cell surface pr	panc, ovar, uter, glio, headkn, lung	mAb
449048	Z45051	HE 22320	solute to S68401 (cathe) glucose induc	renal, panc	mAb+s.m.
449444	AW181436	HE 351306	solute carrier family 10 (monocarboxylic	lung, panc, renal, stom, hepC, fibro, melia	CTL
449523	NM_000579	HE 54443	chemokine (C-C motif) receptor 5	colon	s.m.
449720	AA311152	HE 288708	hypothetical protein FLJ21592	headkn, blad, lung, panc, angio, test, melia, esoph	mAb+s.m.
449722	BE280074	HE 23960	cyclin B1	renal	mAb+diag+s.m.
450001	NM_001044	HE 406	solute carrier family 6 (neurotransmitter	colon	CTL
450375	AA009647	HE 325337	adenomatous polyposis coli-like protein	lung, headkn, panc, breast, stom, ovar, esoph, colon	s.m.
450531	AW001032	HE 203800	(BC017003) Similar to hypothetical prote	lung, renal	diag
450701	H39560	HE 288467	hypothetical protein XP_098151 (leucine-	blad, lung, ovar, glio, fibro, melia	mAb+s.m.
450726	AW024600	HE 355462	HUMPSPBA Human pulmonary surfactant-asso	colon, panc	CTL
450931	N25156	HE 25648	factor necrosis factor receptor superfam	renal	CTL+s.m.
450963	AA380394	HE 25740	EROT1 (S. cerevisiae) like	blad, lung, ovar, glio	diag
451039	RS7795	HE 25954	interleukin 13 receptor, alpha 2	colon, fibro, melia	mAb+s.m.
451310	AW050651	HE 26213	Human DNA sequence from clone RP3-447F3	colon, panc	CTL
451527	AF022813	HE 26518	transmembrane 4 superfamily member 7	renal	CTL+s.m.
451537	RS6631	HE 26550	retinoid X receptor, gamma	blad, ovar, lung, pros	mAb+diag
451668	Z43048	HE 326644	cartilage acidic protein 1	angio	CTL
451939	U80456	HE 27311	single-minded (Drosophila) homolog 2	renal	CTL+s.m.
451979	F06972	HE 27372	endothelial tyrosine kinase (ETK) (EMQ,	pros	CTL+s.m.
451988	AF633528	HE 27410	papillomavirus regulatory factor PRF-1	angio	CTL
452097	AB022364	HE 27916	a disintegrin-like and metalloprotease 1	renal	mAb+diag
452190	H26735	HE 31668	Homo sapiens clone PP1498 unknown mRNA	breast, stom, panc	mAb
452194	AI694413	HE 373599	olfactory receptor, family 2, subfamily	stom, panc, renal, colon, melia, fibro	mAb+s.m.
452203	X57522	HE 352018	transporter 1, ATP-binding cassette, s.1b	cerv, esoph, blad, stom, melia, renal	diag
452281	T33590	HE 262979	Homo sapiens cDNA FLJ11041 f6, clone PL	blad, headkn, panc, stom, lung, esoph, fibro	mAb+s.m.
452355	N54926	HE 25202	G-protein-coupled receptor 34	glio, fibro, panc	diag
452401	NM_007115	HE 23352	tumor necrosis factor, alpha-induced pro	blad, breast, panc, headkn, stom, lung, arth, renal, esoph	diag
452431	U88879	HE 29499	tol-like receptor 3	renal, hepC	mAb

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452747	BE153855	Hs.61460	Ig superfamily receptor LNR	breast, blad, lung, headnk, ovar, stom, uter, panc	mAb
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	renal, headnk, colon, lung, panc	mAb+s.m.+CTL
452838	U65011	Hs.30743	preferentially expressed antigen in melan	lung, ovar, breast, mela, test, esoph, renal	CTL
452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	headnk, breast, colon, arth, lung, blad, esoph, stom	mAb-diag
453195	BE241876	Hs.32352	hypothetical protein DKFZp34K1210	renal	CTL
453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	renal, pros	mAb+s.m.
453642	AK370936	Hs.34074	dispeptyl/peptidase VI	glio	mAb+s.m.
453837	AL138387	Hs.756126	baculoviral IAP repeat-containing 7 (liv	renal, mela	s.m.
453857	AL080235	Hs.33861	Ras-induced oncosome 1 (RIS1)	lung, lung, uter, headnk, cerv, panc, pros	mAb+s.m.
453988	AW076603	Hs.67711	High-mobility group (nonhistone) chromos	lung, uter, blad, test	CTL+s.m.
456546	AI690321	Hs.203845	KCNK15 potassium channel, subfamily K, m	ovar	mAb+s.m.
456662	NM_002448	Hs.1434	msh (Drosophila) homeo box homolog 1 (fo	uter, ovar	CTL
456759	BE259150	Hs.127792	della (Drosophila) like 3	glio, lung	mAb+s.m.
457133	AG5498	Hs.351271	v-Ki-ras2 Kirsten rat sarcoma 2 viral on	panc	s.m.
457489	AB93815	Hs.127179	cryptic gene	panc, pros, lung	diag
457561	AA331517	Hs.286055	chimerin (chimaerin) 2	glio	mAb+s.m.
458079	AT96870	Hs.54277	Homo sapiens similar to RIKEN cDNA 28100	mela, fibro	mAb
458435	AA187818	Hs.144121	ESTs, Weakly similar to T46916 hypothet	glio	mAb+s.m.+CTL
458527	AW088642	Hs.97984	SRY (sex determining region Y)-box 17 (S	ovar, uter, test	CTL

TABLE 66B:					
Pkey:		Unique Eos probeid identifier number			
CAT number:		Gene cluster number			
Accession:		Genbank accession numbers			
Pkey:	CAT Number Accession				
408745	MH1944_5	BC020987 A042187.4 AW188822 BG027862 AG41618 AG361453 A008754 AW207491 AA077391 BG012775 BG097382 AA286833 AA150722 B007625 B027864 B009100 B006275 B006270 B031000 B029864 B006277 B006727 B006266 B006391 B006990 B007762 B007762 BG099377 AA150780 B003518 B002718 B0015789 B0033802 AA341405			
438966	1242593_1	AW979074 AA834841 AA828690 AK022175 AU147222 AT124645 AU121400 F07756 AW979025 AA828695 AA82857 BE35573 AA82858 AT43616 BE153095 AB047365 AT161053 AW168660 AA833500 BG078419 BE171071 BF004368 BF754297 F61781 F08146 F07647 T77332 AA897461 AA829714 A337680 AB009391 AW961854			
442438	24990_1				

TABLE 66C:					
Pkey:		Unique number corresponding to an Eos probeid			
Ref:		Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.			
Strand:		Indicates DNA strand from which exons were predicted.			
N_positon:		Indicates nucleotide positions of predicted exons.			
Pkey	Ref	Strand	N_positon		
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,		
402075	8117407	Plus	121507-122035,122804-122921,124019-12416		
402901	8894222	Minus	175429-175567		
404287	2326514	Plus	53134-53281		
404682	9797231	Minus	40577-41150		
404875	5801324	Plus	96588-96732,97722-97831		
404917	3738341	Minus	43081-43229		
405035	7107731	Minus	142538-142546		
405547	1054740	Plus	124361-124520,124914-125050		
406400	9256298	Plus	15531-1712,1878-2140,4252-4385,5922-6077		

TABLE 67:					
Pkey:		Unique Eos probeid identifier number			
EosAccession:		Exemplar Accession number, Genbank accession number			
UnigeneID:		Unigene number			
Unigene Title:		Unigene title			
Seq ID No:	Sequence Identification Number linking the information in Table 67 to the sequences in Table 68				
Pkey	EosAccession	UnigeneID	Unigene Title	Seq ID No	
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No 1 & 199	
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No 2 & 200	
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	Seq ID No 3 & 201	
417886	AW067903	Hs.82772	collagen, type XI, alpha 1	Seq ID No 4 & 202	
444381	BE381335	Hs.281373	hypothetical protein BC014245	Seq ID No 5 & 203	
452281	T33500	Hs.28792	Homo sapiens cDNA FLJ11041 ff, clone PL	Seq ID No 6	
426698	AA852773	Hs.334838	KIAA1896 protein	Seq ID No 7 & 204	
452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	Seq ID No 8 & 205	
432021	AS38613	Hs.296241	Transmembrane protease, serine 3	Seq ID No 9 & 206	
434005	AW136973	Hs.362915	ESTs, Weakly similar to S69850 (malign)	Seq ID No 10 & 207	
427260	AA315993	Hs.105494	regenerating gene type IV	Seq ID No 11 & 208	
405041	AB013025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No 12 & 209	
443426	AF038158	Hs.93229	chromosome 20 open reading frame 1	Seq ID No 13 & 210	
443211	AT178388	Hs.143655	ESTs	Seq ID No 14	
428664	AK001666	Hs.180905	similar to SALL1 (sal (Drosophila))-like	Seq ID No 15 & 211	
413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	Seq ID No 16 & 212	
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No 17 & 213	
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No 18 & 214	
403890	AF123050	Hs.44532	dihydroquin	Seq ID No 19 & 215	
416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	Seq ID No 20 & 216	
409757	NM_001898	Hs.123114	cystatin SN	Seq ID No 21 & 217	

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425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter)
452194	A0694413	Hs.373559	olfactory receptor, family 2, subfamily
452194	A0694413	Hs.373559	olfactory receptor, family 2, subfamily
444783	AK001466	Hs.62180	snail (Drosophila Scraps homolog), act
422956	BE454072	Hs.122579	ECT2 protein (Epithelial cell transform
424955	NM_002497	Hs.153704	NIMA, member in mitosis gene a)-related k
415989	A1267700	Hs.351201	ESTs
415989	A1267700	Hs.351201	ESTs
424262	AK000520	Hs.143811	hypothetical protein FLJ20513
424252	AK000520	Hs.143811	hypothetical protein FLJ20513
423267	AW016936	Hs.233354	ESTs
437559	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN
428710	BE276891	Hs.194921	retinoic acid induced 3 (RAIG3), metabo
428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam
428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam
428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam
428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam
428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam
425203	X57522	Hs.320118	transferrin 1, A1P-binding cascade, sub
428330	L25254	Hs.7256	matrix metalloproteinase 7 (matrilysin,
436480	AJ271643	Hs.67469	putative acid sensing ion channel
407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,
425115	R44694	Hs.123566	downstream of G-protein-coupled recept
438472	AW972330	Hs.283022	triggering receptor expressed on myeloid
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
415511	AF132617	Hs.182362	ESTs
443304	BE159994	Hs.123535	hepatitis A virus cellular receptor 1
423161	AL045227	Hs.124776	downstream of cadherin 6 (by 3.3kb)
423161	AL045227	Hs.124776	downstream of cadherin 6 (by 3.3kb)
410153	BE311926	Hs.15830	hypothetical protein FLJ12691
410153	BE311926	Hs.15830	hypothetical protein FLJ12691
410153	BE311926	Hs.15830	hypothetical protein FLJ12691
410153	BE311926	Hs.15830	hypothetical protein FLJ12691
436895	AF037335	Hs.5338	carbonic anhydrase XII
436895	AF037335	Hs.5338	carbonic anhydrase XII
421471	U03545	Hs.327179	solute carrier family 17 (sodium phospho
428296	NM_003058	Hs.183572	solute carrier family 12 (organic cation
426990	AA363167	Hs.41264	ESTs
437212	AF195021	Hs.210775	ESTs
436896	AW972674	Hs.125407	glt-EST301184 MAGe resequences, MAGP Homo
443311	AF133075	Hs.14535	glt-EST, Moderately similar to ALUE_HUMAN 1
437100	AF167103	Hs.14535	Homo sapiens cDNA: FLJ22314.1c, clone H
437100	AF167103	Hs.14535	Homo sapiens cDNA: FLJ22314.1c, clone H
450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter
419080	AF155835	Hs.16878	hypothetical protein FLJ15620
443959	AF169312	Hs.9613	PPAR(gamma), angiotensin related protein
443959	AF169312	Hs.9613	PPAR(gamma), angiotensin related protein
410407	X86839	Hs.63287	carbonic anhydrase IX
453496	A4442103	Hs.33084	solute carrier family 7 (facilitated glu
420737	LC0636	Hs.9869	CD70; tumor necrosis factor (ligand) s
439579	AW600291	Hs.6823	hypothetical protein FLJ10430
420789	A1670057	Hs.199882	ESTs
420789	A570057	Hs.199882	ESTs
441332	AF045181	Hs.222119	ESTs, Weakly similar to S30433 heratin 1
452431	U08879	Hs.25499	tol-like receptor 3
431870	AW449902	Hs.105500	ESTs
431870	AW449902	Hs.105500	ESTs
445523	NM_005879	Hs.54443	chemokine (C-C motif) receptor 5
409745	A0077391	Hs.17558	glt-7B14E12 Chromosome 7 Fetal Brain cDNA
438859	AF595926	Hs.33522	Homo sapiens mRNA for KIAA1647 protein,
409637	AJ233948	Hs.55407	Homo sapiens mRNA: cDNA DKF Zp43K0521 (f
409637	AJ233948	Hs.55407	Homo sapiens mRNA: cDNA DKF Zp43K0521 (f
405348	A0401535	Hs.146090	ESTs
447269	NM_004861	Hs.17558	cerebroside (2-phosphoadenylthio)lactat
453195	BE241876	Hs.32362	hypothetical protein DKF Zp43K1210
428841	AJ181840	Hs.104535	ESTs
428841	AJ181840	Hs.104535	ESTs
428841	AJ181840	Hs.104535	ESTs
409653	AJ743750	Hs.96306	KIAA1862 protein
409663	AJ743750	Hs.96306	KIAA1862 protein
431339	AK002061	Hs.231258	ESTs
432056	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;
411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein
433867	AK000596	Hs.3618	hippocampin-like 1
433867	AK000596	Hs.3618	hippocampin-like 1
437338	A150307	Hs.352628	glt-wt0502-11 NO CGAP_Xgd12 Homo sapien
432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor
418526	BE019020	Hs.68538	solute carrier family 16 (monocarboxylic
432196	AW300888	Hs.273230	hypothetical protein FLJ10830
432196	AW300888	Hs.273230	hypothetical protein FLJ10830
438529	AF1955515	Hs.253177	ESTs
410055	AJ250538	Hs.58241	gene for serine/threonine protein kinase
446650	A0016625	Hs.15813	solute carrier family 22 (organic cation

Seq ID No 22 & 218	
Seq ID No 23 & 219	
Seq ID No 24 & 220	
Seq ID No 25 & 221	
Seq ID No 26 & 222	
Seq ID No 27 & 223	
Seq ID No 28	
Seq ID No 29	
Seq ID No 30 & 224	
Seq ID No 31 & 225	
Seq ID No 32	
Seq ID No 33	
Seq ID No 34 & 226	
Seq ID No 35 & 227	
Seq ID No 36 & 228	
Seq ID No 37 & 229	
Seq ID No 38 & 230	
Seq ID No 39 & 231	
Seq ID No 40 & 232	
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Seq ID No 44 & 236	
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Seq ID No 88	
Seq ID No 89	
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Seq ID No 97	
Seq ID No 98 & 270	
Seq ID No 99 & 271	
Seq ID No 100 & 272	
Seq ID No 101 & 273	
Seq ID No 102	
Seq ID No 103 & 274	
Seq ID No 104 & 275	

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	425812	AF105365	Ha.172613	solute carrier family 12 (glutassimilable	Seq ID No 105 & 276
	447131	NM_004585	Ha.17466	retinoic acid receptor responder (barzo	Seq ID No 106 & 277
	494444	AW818436	Ha.351306	solute carrier family 16 (monocarboxylic	Seq ID No 107 & 278
	492627	BE336567	Ha.118787	transforming growth factor, beta-induced	Seq ID No 108 & 279
	444488	AI156460	Ha.354689	ancient conserved domain protein 4	Seq ID No 109 & 280
	495931	N25156	Ha.254548	tumor necrosis factor receptor superfamily	Seq ID No 110 & 281
	405220	BE243323	Ha.51233	tumor necrosis factor receptor superfamily	Seq ID No 111 & 282
	405220	BE243323	Ha.51233	tumor necrosis factor receptor superfamily	Seq ID No 112 & 283
	425998	AD176229	Ha.163550	fibroblast growth factor receptor 4	Seq ID No 113 & 284
	425998	AD176229	Ha.163550	fibroblast growth factor receptor 4	Seq ID No 114 & 285
	425909	X58288	Ha.154511	protein tyrosine phosphatase, receptor I	Seq ID No 115 & 286
	434387	AW161323	Ha.10071	seven transmembrane protein TM7SF3	Seq ID No 116 & 287
	425950	AD103071	Ha.73989	tumor necrosis factor receptor superfamily	Seq ID No 117 & 288
	435676	AA58213	Ha.17542	ESTs	Seq ID No 118 & 289
	451527	AF022813	Ha.25518	transmembrane 4 superfamily member 7	Seq ID No 119 & 290
	448733	NM_005629	Ha.187958	solute carrier family 6 (neurotransmitter	Seq ID No 120 & 291
	410274	AA381807	Ha.61762	hypoxia-inducible protein 2	Seq ID No 121 & 292
	125218	HE1523	Ha.110024	Empirically selected from AFFX single pr	Seq ID No 122 & 293
	456961	AW375474	Ha.156704	ESTs	Seq ID No 123
	431630	NM_002204	Ha.255829	integrin, alpha 3 (antigen CD45c, alpha	Seq ID No 124 & 294
	431630	NM_002204	Ha.255829	integrin, alpha 3 (antigen CD45c, alpha	Seq ID No 125 & 295
	419508	AW097938	Ha.50786	ATP-binding cassette, sub-family C (CFTR	Seq ID No 126 & 296
	431840	AA334908	Ha.2390	POU domain, class 5, transcription facto	Seq ID No 127 & 297
	442438	AA395998		glucosyltransferase 1 NGL-OGAP_Ki6s Homo sapiens	Seq ID No 128
	478355	AW591623	Ha.184129	ESTs, Weakly similar to 138022 hypophos	Seq ID No 129
	429276	AF356895	Ha.198612	G protein-coupled receptor 51	Seq ID No 130 & 298
	448595	AB014544	Ha.215172	HA-0044 gene product	Seq ID No 131 & 299
	440516	SC4303	Ha.1161	cathepsin D, type 1, N-cadherin (neuronal	Seq ID No 132 & 300
	456759	BE258150	Ha.127792	della (Drosophila) like 3	Seq ID No 133 & 301
	447004	AW296968	Ha.157539	FGENESH predicted secreted protein	Seq ID No 134 & 302
	425988	AA630372	Ha.163550	hypothetical protein FLJ12015	Seq ID No 135 & 303
	401389	AB007075	Ha.301281	Homo sapiens mRN, chromosome 1 specific	Seq ID No 136 & 304
	448321	NM_005883	Ha.20912	adenomatous polyposis coli like	Seq ID No 137 & 305
	428344	H41821	Ha.322469	transcriptional activator of the c-fos p	Seq ID No 138 & 306
	419704	AA429104	Ha.45057	ESTs	Seq ID No 139 & 307
	412958	DE7458	Ha.76590	KIA0282 protein	Seq ID No 140 & 308
	448409	BE613280	Ha.77550	p53-regulated DDA3	Seq ID No 141 & 309
	458435	AI418718	Ha.144121	ESTs, Weakly similar to T46916 hypophos	Seq ID No 142 & 310
	443736	AA449952	Ha.193725	basic-helix-loop-helix-PAS protein	Seq ID No 143 & 311
	427343	AB80844	Ha.178977	protein kinase C-binding protein 2	Seq ID No 144 & 312
	416857	AA188775	Ha.292453	FGENESH predicted TM containing protein	Seq ID No 145 & 313
	429149	AW193360	Ha.197962	Homolog of mouse ADP-ribosylation factor	Seq ID No 146 & 314
	416030	BE207573	Ha.83321	neuromedin B	Seq ID No 147 & 315
	457561	AA331517	Ha.289555	chimerin (chimerin) 2	Seq ID No 148 & 316
	457561	AA331517	Ha.289555	chimerin (chimerin) 2	Seq ID No 149 & 317
	450147	R60704	Ha.234434	hair/hairless-of-spl related with YRP	Seq ID No 150 & 318
	453642	AI370936	Ha.34074	dipeptidylpeptidase VI	Seq ID No 151 & 319
	453657	AI380235	Ha.38861	Ras-induced oncosome 1 (RIS1)	Seq ID No 152 & 320
	449048	Z45051	Ha.22820	similar to 568401 (cathe) glucosyl induc	Seq ID No 153 & 321
	418506	AA054248	Ha.372951	Unknown protein for MGC-29643 (monomey	Seq ID No 154 & 322
	416636	NQ2536	Ha.42845	solute carrier family 16 (monocarboxylic	Seq ID No 155 & 323
	421508	NM_004833	Ha.105115	absent in melanoma 2	Seq ID No 156 & 324
	421379	Y15221	Ha.103882	small inducible cytokine subfamily B (Cy	Seq ID No 157 & 325
	428744	Y12651	Ha.193470	putative receptor P2X, ligand-gated ion	Seq ID No 158 & 326
	431958	X63629	Ha.2877	cathepsin D, type 1, P-cadherin (placenta	Seq ID No 159 & 327
	417542	JO4129	Ha.82769	progestagen-associated endometrial prote	Seq ID No 160 & 328
	419878	NM_001327	Ha.167373	carcinosarcoma antigen (NY-ESO-1)	Seq ID No 161 & 329
	419878	NM_001327	Ha.167373	carcinosarcoma antigen (NY-ESO-1)	Seq ID No 162 & 330
	420208	BE276065	Ha.95972	silver (mouse homolog) like	Seq ID No 163 & 331
	430377	NM_001922	Ha.301865	dopachrome tautomerase (dopachrome: delta	Seq ID No 164 & 332
	438549	BE368601	Ha.21858	tinucleotide repeat containing 3	Seq ID No 165 & 333
	412580	AA113262	Ha.17301	similar to CABLES (Homo sapiens)	Seq ID No 166 & 334
	417166	AA431323	Ha.42146	Paralox box protein Pax-3	Seq ID No 167 & 335
	428513	BE220806	Ha.184697	plexin C1	Seq ID No 168 & 336
	447937	AI109716	Ha.20034	Homo sapiens mRNA full length insert cDN	Seq ID No 169 & 337
	447937	AI109716	Ha.20034	Homo sapiens mRNA full length insert cDN	Seq ID No 170 & 338
	446341	AI040763	Ha.310735	FGENESH prediction similar to multidrug	Seq ID No 171 & 339
	446341	AI040763	Ha.310735	FGENESH prediction similar to multidrug	Seq ID No 172 & 340
	458079	AW096870	Ha.54277	Homo sapiens similar to RIKEN cDNA 28100	Seq ID No 173 & 341
	415668	AW957684	Ha.306814	Homo sapiens tyrosinase like 4 (LOXL4)	Seq ID No 174 & 342
	447674	BE270840	Ha.19192	cyclic-dependent kinase 2	Seq ID No 175 & 343
	447674	BE270840	Ha.19192	cyclic-dependent kinase 2	Seq ID No 176 & 344
	440065	W03476	Ha.266331	Homo sapiens Fc receptor homolog express	Seq ID No 177 & 345
	414945	BE073038	Ha.77667	lymphocyte antigen 6 complex, locus E	Seq ID No 178 & 346
	440672	AF603811	Ha.7245	MAOI (aromatic amine oxidase, yeast, h	Seq ID No 179 & 347
	412609	Z48804	Ha.74724	ocular albinism 1 (Netherlands-Falks)	Seq ID No 180 & 348
	453837	AI138387	Ha.256126	baculoviral IAP repeat-containing 7 (Iv	Seq ID No 181 & 349
	453837	AI138387	Ha.256126	baculoviral IAP repeat-containing 7 (Iv	Seq ID No 182 & 350
	434276	AF120659	Ha.93605	leucine zipper, putative tumor suppressor	Seq ID No 183 & 351
	408367	BE207588	Ha.44424	Homo sapiens orphan neurotransmitter tra	Seq ID No 184 & 352
	444809	BE207588	Ha.208219	oculoparasin	Seq ID No 185 & 353
	415929	AA724373	Ha.304950	Homo sapiens mucopolip-3 (MUCOLIP3)	Seq ID No 186 & 354
	421666	AI035250	Ha.1408	endothelin 3	Seq ID No 187 & 355

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424321	W/4048	Hs.1765	lymphocyte-specific protein tyrosine kin	Seq ID No 188 & 356
425535	AB007537	Hs.158287	syndecan 3	Seq ID No 189 & 357
451537	R56631	Hs.26550	retinoid X receptor, gamma	Seq ID No 191 & 358
430260	AA361258	Hs.237868	interleukin 7 receptor	Seq ID No 192 & 359
418664	BE387287	Hs.53384	S100 calcium-binding protein, beta (neur	Seq ID No 193 & 360
448610	NM_006157	Hs.21802	ret (chicken)-like 1	Seq ID No 194 & 361
432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No 195 & 362
415350	AF188625	Hs.185507	phospholipase A2, group IIO	Seq ID No 196 & 363
405545			Target Exon	Seq ID No 197 & 365
414812	X72755	Hs.77367	monokines induced by gamma interferon	Seq ID No 198 & 366
423874	W94322	Hs.279651	melanoma inhibitory activity	

Table 68 lists sequences as described in Table 67

15	Seq ID NO: 1 DNA sequence				
	Nucleic Acid Accession #: NM_002421.2				
	Coding sequence: 1..1409				
20	1	11	31	41	51
	ATGCACAGCT	TTCTCTCACT	GCTGCTGCTG	CTTCTCTGGG	GTGTGGTGTG
	CCAGCGACTC	TGAAGACACA	AGAGCAAGAT	GTGGCTTAGG	TCCGAAATAA
	TACTACAACT	TGAAGAAATGA	TGGGAGGCGA	CTTGAAGAGC	GGAGAAATAG
	GTGGAATAAT	TGAAGCAAAAT	GCAAGAAATC	TTTGGGCTGA	AAGTGACTGG
25	GCTGAARACC	TGAAGGTGAT	GAGCAGGCC	AGATGTGGAG	TGCTTGATGT
	GTCTCTCACTG	AGGGGAAAGCC	TGGCTGGGAG	CAACACACATC	TGACTACAG
	TACAGCGCAG	ATTTGCCAG	AGCAGATGTG	GCACATGCCA	CTTCCAACTC
	TGAGTAAATG	TCAACCTCTC	GACATTCACC	AAAGTCTCTG	AGGGTCAAGC
	ATATCTTTTG	TGAGGGGAGA	TCAATGGGAC	AACTCTCTCT	TTGATGGAGC
30	CTTGCTCATG	CTTTTCAAC	AGAGCCAGGT	ATTGAGAGGG	ATGCTCATTT
	GAAGAGTGA	CCCAAAATTT	CAGAGATGAC	GTGTTGGCGC	TGATGAGAT
	GGCCATCTCT	TGAGACTCTC	ACCTTCTACT	GATATCGGGG	CTTTGATGTA
	ACCTTCAGTG	GTGATGTTC	GCTAGTCTAG	GATGACATTT	ATGGCATCCA
35	GGACGTTCCC	AAATCTCTGT	CGAGCCCATC	GGCCCAAA	CCCCAAAGC
	AAGTCAATCT	TGATGCTGAT	AACTGAGATT	TGGAGAGAG	TGATGTTCTT
	TTCTACATGC	GCACAAATCC	CTTCTACCCG	GAAGTTGAGC	TCAATTTCAAT
	TGGCCACAAC	TGCGAAATGG	GCTTGAAGCT	GCTTACGAAT	TTGCGAGATC
	CGGTTTTC	AAAGGAAATA	GTACTGGGCT	GTTCAGGGAG	AGAAATGTGT
40	CCGAGAGCA	CTTACAGCTC	CTTTGGCTCT	CTTGAAGATG	TGAGATCAT
	CTTTCTGAGG	AAACACATGG	AAACAACTAC	TTCTTTGTTG	CTAACAAATA
	GATGAATATA	AACGATCTAT	GGATCCAGGT	TATCCCAAAA	TGATGACACA
	GGAAATGGCC	ACAAAGTTGA	TGCAATTTTC	ATGAAGATG	GATTTTCTTA
	GGAAACAGAC	AATCAAAATT	TGATCTTAAA	ACGAAGAGAA	TTTGTACTCT
45	AAATAGCTGT	TCAACTGCGC	GAATAATTAG		
	Seq ID NO: 2 DNA sequence				
	Nucleic Acid Accession #: NM_002421.2				
	Coding sequence: 1..1409				
50	1	11	21	31	41
	ATGCACAGCT	TTCTCTCACT	GCTGCTGCTG	CTTCTCTGGG	GTGTGGTGTG
	CCAGCGACTC	TGAAGACACA	AGAGCAAGAT	GTGGCTTAGG	TCCGAAATAA
	TACTACAACT	TGAAGAAATGA	TGGGAGGCGA	CTTGAAGAGC	GGAGAAATAG
	GTGGAATAAT	TGAAGCAAAAT	GCAAGAAATC	TTTGGGCTGA	AAGTGACTGG
55	GCTGAARACC	TGAAGGTGAT	GAGCAGGCC	AGATGTGGAG	TGCTTGATGT
	GTCTCTCACTG	AGGGGAAAGCC	TGGCTGGGAG	CAACACACATC	TGACTACAG
	TACAGCGCAG	ATTTGCCAG	AGCAGATGTG	GACCATGCCA	TTTGAAGAGC
	TGAGTAAATG	TCAACCTCTC	GACATTCACC	AAAGTCTCTG	AGGGTCAAGC
	ATATCTTTTG	TGAGGGGAGA	TCAATGGGAC	AACTCTCTCT	TTGATGGAGC
60	CTTGCTCATG	CTTTTCAAC	AGAGCCAGGT	ATTGAGAGGG	ATGCTCATTT
	GAAGAGTGA	CCCAAAATTT	CAGAGATGAC	AACTTACATC	GTGTTGGCGC
	GGCCATCTCT	TGAGACTCTC	ACCTTCTACT	GATATCGGGG	CTTTGATGTA
	ACCTTCAGTG	GTGATGTTC	GCTAGCTCAG	GATGACATTT	ATGGCATCCA
	GGACGTTCCC	AAATCTCTGT	CGAGCCCATC	GGCCCAAA	CCCCAAAGC
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Nucleic Acid Accession: NM_014244

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PCT/US02/29560

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PCT/US02/29560

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 TTTCTTGGG CTTGCTGAGT GTTGTGAATA ACCGACATGT CTCGAGATGT GATGTGCTCC 3120
 AATGGGATCT CAGTCTGAGT GTGGAATCTC AGGCTCTAC TGACGCTCTC CCGTAAGAC 3180
 AGTTTCTCTA CTCTCTGGA GAAGAACAAG TTGGGTCAG CTAAGGAGGA ACTTGGGTGT 3240
 AAGGAGCAAT CGAGACAGAG TGAATCTCTT AGAATCTGCT TTGTTTGTGA AGACTCATC 3300
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	ACAACCTGAG GCAAGTGCTA CATTACGAT TGTGCTATG CTGCTTTGCA AAAAGTTG 3418									
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	CGGCTGGGGG	AGTAGGCGCT	CAAGCCCGTG	AGCACCTGT	TCATGAATCT	GGGCTCGGGG	540			
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	CAGAGTGTGA	ATTTTTDTAA	ACTCCATATG	GCTTGACGGA	GCAGCGCGTG	TGTACCACAG	180			
	AGAAGCAGCG	CTGGCAAAAT	ACAAGGCTAC	CTACCGAGAA	GCTAAGCGG	TGTGTGAATT	240			
	TGAAGCGGCG	CATCTTCGAA	CTTACAGACA	GCTGAGAGCA	GCCAGAAAAA	TTGGATTCTCA	300			
30	TGTCTGTCT	CGTGGATGGA	TGGTAAAGGG	CAGAGTGTGA	TACCCCATGT	TGAGACGAG	360			
	GGCCAACTGT	GGATTTGGAA	AACTGGCAT	TATTTGATAT	GGAAATCTCT	TCATAGAGAG	420			
	TGAAGATGTG	GATGCTTATT	GCTACAACCC	ACACCGAAGG	GAGTGTGGTG	GGTCTTTTAC	480			
	AGATCCAAAG	CAATTTTATTA	AATCTCCAGG	CTTCCCAAT	GAGTAGAAG	ATACCAAAAT	540			
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	CCAAATCAAA	TATGTGCGAA	TGATCTCTGT	ATCCAAATCC	AGTCAAGGAA	AAATACAGG	840			
	TACTATCTCT	ACTGATGAGT	AAATGAGAGA	TTTATGCCAT	TATATAAAAT		900			
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	TAGGGAANAAT	TGAAAAATAT	AGGAAACCTT	AAAGAGGAAA	ATGAAACCTC	TCATAATCCC	1080			
	ACTGATGAGA	AAATGAGAGG	GTATACATTT	CTATATTTTT	TCTCTTCAGT	GATTTTCTTA	1140			
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45	TCATATGACA	GTGTTGTATT	ATACTTTTAA	AATCTTGAAC	TTTATAAACA	TTTTTCTGAA	1260			
	TCATTTGATTA	TTCTACAATA	ACATGATTTT	AAACAGCTGT	AAATATTTCT	ATGATATGAA	1320			
	TGTTTTATCG	ATTATTTTAG	CTGTCTCTTA	TGTTTGGAAT	TTCAAGTCTAT	TTTCTATAAT	1380			
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	ATAGAGTAC	TACTTCTACT	GGAAATAAAA	ACTTTTTCAG	TGAGAGATTT	AGGCACTATC	900			
70	AAAAAAGAAA	AGGATGATCT	AAAAACACA	GTGTTTATGT	TGGAATCTTT	TGGAATCTCT	960			
	TTGATCTCAC	TGTTATATTT	ACAAATTTAT	TATTTATTTT	CTAAATGTGA	AGGAATATCA	1020			
	TAAATTTAGG	AAATATGGGA	AAATATGGGA	ACTTTAATGA	AGAAATGAAA	ACTTCTCATC	1080			
	ATCCGCTGCG	ATGAAATGAA	CAAGGCTTAA	CATTTTGATA	TTTTTTTCTT	TCAGTCAATT	1140			
	TGTGATTTGT	GGTATATGTA	TATATGTACC	TATATGTATT	TGCATTTGAA	ATTTTGGAAAT	1200			
75	CTGCTCTAT	GTACAGTTTT	GTATTTATCT	TTTTAAATCT	TGAACCTTTT	GAACTATTTT	1260			
	TGAAATCATT	GATTTATCTA	CAAAAACATG	ATTTTAAATC	CGCTGAAAT	ATTTCTATGT	1320			
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AAGATCTTAA AGCCAAAGAG AAGGCTCTCA TCTTATGGCA TTGCACAAAG GAGAGCCATC 240
CACCTTATCC TGAAAGTGTG GAGGCGCAAT GATGAGGAGC TGCCCTTTGT TCTTGTGAG 300
TCAGTGTAGT AGGCGAAGAG GCACCTCTTC CAGTTCG3AA GGTCCAGCTC AGTGCGACAA 360
GTGAAAGCAA TGATGGAGAC TAAGAAGGAT ATATCCCTGT AGACCCAGAT TGTGACTTGC 420
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TCCCAAAATT AATGAAGATG AGATAGTAGT AGTAGATTG GGGTGGGATG GGTAGATAG 660
AGTATATTGC CCAACTCTAT GTTCTTTTGA TTCTACACA ATTAATTAGT TGACATGATT 720
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Seq ID NO: 20 DNA Sequence
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Coding sequence: 75..692

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GCATATATCC ATCTGAAGCC TTACTCGAG TCAGCAAAAT CCGACTCACC TTGCTGTATA 240
CTACTGATCT TGAOCTCATA AAATACCTAA ATATGTGTGT GGAAACAAGT AAAGATTGGT 300
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TCTGTGAAAG ATGCGAGTTT GATATGGAT GTGCGAGAGC TGCAAAAGAT GACGTGGC 420
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Coding sequence: 57..482

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ACTACAGACG ACCTTCGCTG CCGGTACTAA GAGCGAGATA ACAGAGCTCT GGGGGGGTGA 300
ATTACTTCTT CGAGTCTGGA CTGGGCGGGA CTATATGTAC CAGTCCCGC GCGCATGAT 360
ACACTCTTCT CTTCATGATA CAGCCAGAAC TCAGAGAAAG ACAGTTGTGC TCTTOSAGA 420
TCTACAGAT TCCCTGGGAG AACAGAAAGT CCGTGTGAAA ATCGAGTGT CAGAATCCT 480
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CGACCGCTTG ACTGTGGGCC GCGACACCTG GAGAGGCTCT CCGTGTGTC TGCGGACAGA 600
GAGAGACAGA GAGAGCTGGA GAGGCTCTTT GTTCTTCACG AGGAGGCTCT GCGCTCCCTC 660
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Seq ID NO: 22 DNA sequence
Nucleic Acid Accession #: NM_007231.1
Coding sequence: 89..2017

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TGAATATGAG GAGCTGTGTA ATGTGTCGAA AATGTGAGT TGACTTTTGT CTATATTG 240
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GCTTCCAGT GAGCAATATG GGAATAAAGT GCGCTCCCAA CGGTCAAGTG GATGAATGA 780
GACTGTAGTA ATGTGTTGGT AATTAGCAT TTGTCTCTT CTGGCTGTG TCAATATGG 840
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CCCTATGTG GTCTACTCA TCTGTATGAT ACGAGGTGCA ACTCTGGAG GTGCTCAA 960

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TGCTCTATCA TCTTCAAGTA AGTTCAAAAA CMACTGCTTC TCTGATGCCA TTGCGGTTTG 1140
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Coding sequence: 19..516

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CAATCTAACCC TGAAGATGGT GAGGCCAGAT GATGAGAGAC TGGCTTGTGT TCTTGTGTAG 300
TCAATGATG AGCAAGAGG GCACTCTCCG CAGTGTGCGA GGTGCACTC AGTGTGAAA 360
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Seq ID NO: 24 DNA sequence
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Coding sequence: 1..948

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15

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Seq ID NO: 26 DNA Sequence
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 GAGTATCAGS AATTATAGCA AATGTCATC AAACTTTTTCT TAAGCTTACC TAAAGTTATT 1380
 TCACTCGAAA ATTTCAAGCA ACTTTGTGCA ACATTAATAT GACATCTCAA ACTAGCAAGT 1440
 CTTTGAATTT TATGCACTGT AGTAAACATT CTCTCTATTA ACTTTATFAC CTAAAGCTAA 1500
 ACCTAAATTT TTTAGCAAAA ATTAGAAJAA TAGTCTTCAC TCATCAAAAA ATAAAGTTTG 1560
 TTACATTTAG TATTTTCCCA AT

Seq ID NO: 30 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: ..817

1 11 21 31 41 51
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 AGATATATCA TACGAAATG AATATTATA TTCTCTTGG ATTCTGGGA GCCACATTGT 60
 CAGCCCCAGT TTACTTCTTA ATCTTAATA TTGCTCACTT TTGCACTAC AGTCTCAGGG 120
 CCACTATTCT TCGATTTCTG TGGATTTTGA TGGTCAAGC AGCTCTCAGT 180
 AATTCCAGGA CTCCTCCAGT TCTCTTTATC AGCTCTAGAC CAGTTTGGTG GACTGCTCCC 240
 AATACAGATA CCGTTACACG GAGAGGCCAG TTTTGCCCAA GAGGCCAGCG CAGGCCAAGT 300
 TGATCCCTTA CAGCTCTCAA CAGCCGCTCA GACACACAGA GCGCCAGATC AGGTGATCGT 360
 CTAATGTATC TCGATGACGA CAGCTCTGGA AGCTCTGAGT GCAATGAGT CTAAGTCTG 420
 TCCATGGTTC CTAACCTGGG AACAACCTCA GCAAACAGTT CCAAGGTCAC CTCACCAAC 480
 AAGACAGCAA CAGTATGAGG AGCAGATACC ATTCTATGCT CATTGGAT ACATTCOCA 540
 ACTAGACAGA CTCGCTATAT CAGAGGAGCA GACGACACTA GCTTTGATC CCGACATAGG 600
 CACAGCTGCT GAAATATATA TGAATTCAAC AGGAGAGGG ATACTATATT TACGAAAGA 660
 AGCATCAAC TTTAGACATG ACAGTGCGAG AGTTTTCATG CCTCTAACTT CACCAAAAC 720
 CAGCACAACC AATGTTTTCA CTCTGCTGCT AGACCAAAC ATTACCCGAG AGCTCCOAGA 780
 AGAGAGGAC AGAGATGACA GCTTAGGGA ACCATAA 817

Seq ID NO: 31 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: ..917

1 11 21 31 41 51
 | | | | |
 AGAGAGAAA AGAACACAGA TCTCCGATGG TTGAGATTT TCTTTTAGG TCGAGAGTA 60
 AGATATATCA TACGAAATG AATATTATA TTCTCTTGG ATTCTGGGA GCCACATTGT 120
 CAGCCCCAGT TATCCACAGC CTTCTCATCT CTGACAGGAA TAGCACTAGT TTACTTCTTA 180
 ATCTTAATA TGTGATTTT TTGCACTAC AGCTCTCAGG CCAACTTAAT TATGATGATC 240
 CACCTTTCTC TGGATTTTAA CACAGCAGC AGCGAGCTCA AATTCCAGGA CTCCTCCAGT 300
 TCTCTTTATC AGCTCTAGAC CAGTTTGGTG GACTGCTCCC AATACAGATA CCTTACACG 360
 GAGAGGCCAG TTTTGCCCAA GAGGCCAGG CAGGCCAGT TGTCTCTTA CACTGTCAA 420
 CAGCCGCTCA GACACACAGA CAGCTCTGGA AGCTCTGAGT CTAATGAGT CTACCTCGG 480
 TCGCTCATGA CAGAGCAGAG ATGTTTCAAT ACTATCCAGT TTACATGGTC TCAACCTGGG 540
 AACACCTCA GCAACAGCTT CCAAGGTCAC CTCACCAAC AAGACAGCAA CAGTATGAG 600
 AGCATATCC ATTCTATGCT CAATTTGGAT ACATTCOCA ACTYACAGAA CTCGCTATAT 660
 CAGAGAGCA CAGCAGGATA GCTTTGATCA AGCTCTGAGT GAAATGATC TGTGATGATC 720
 TGTATGCAAC AGGAGAGAGT ATACCATATT TACAAAAGAA AGCATCAAC TTTAGACATG 780
 ACAGTGCGAG AGTTTTCATG CCTCAACTT CACCAAAAC CAGCACAACC AATGTTTTCA 840
 CTCTGCTGCT AGACCAAAC ATTACCCGAG AGCTCCGAGA AGAGAGGAC AGAGCTGACA 900
 GCTTAGGGA ACCATAA 917

Seq ID NO: 32 DNA Sequence
Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
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 CAAGATTTAG CACTTCTGAG CTGTTGTCTT TGTCTCCAGT CTACCCGTGAG CAGTTCTTAA 120
 GGTGTTTAAA CAGAGAGAA GAGAAAGAG GCTTAGGTTA TACTGCTTAG AGCTCTCTCT 180
 TCACTATACC TACGACACG CTCACCCGTA ATCTGATACC TAGACACAGA CCGCTTCTCT 240
 TTCTCTGCCC CTGTTTCTG CTGCGCTCTCT TTCAATTGCA CGTGTGTGGA GTATAGCTTT 300
 TCCCTCTGCC TACTCAGCTC CTTGAACTCA GGGTGAATTT GAGACCCAGA GGAATGGGAT 360
 TTAGCATGCT TTGCTTCTCT TCTGCTCTGT CTTAGAACTT AAGTACATA GGGGANGAGG 420
 TTTGATGAGG GAGAGCCCC ATCCAAAGAC ATCTAAGTTT CAGTGTGCAT AACGACGAC 480
 CAGTTTCA

Seq ID NO: 33 DNA Sequence

WO 03/025138

PCT/US02/29560

Nucleic Acid Accession #		Eos sequence					
	1	11	21	31	41	51	
5	CTCCCAAGT	GCTGATGAGT	CAGGCGATG	CCACTGCTCC	CAGCCTTCCA	GAGGAATTIT	60
	ACGCCCATGT	CCAGCAATTC	TGTTTGTATA	AACTAATCTT	ATTTTITAAA	TAATATAGTT	120
	CTACTTTTCT	GACTTTTATA	TTTTCCTCTG	CTAATAATGA	TTTTCATATG	CAGAAAGAT	180
10	TAATATAGTA	ATCATGAATT	GCTTCATATA	TTTGGCAGTA	AGTCAATGAA	ATAATAGGCG	240
	ACTTATATAC	CATCTTTTGC	ATCATATAAA	GTATCAAAAT	CCATTAACTC	AAAACCTCTT	300
	TAGCATTTT	GAGGACAGAA	AACTGTTTCA	TGGTCTCTTC	AGTTCCTCAG	GCCTTTTGTC	360
15	TAATATAGTA	GAATCTTTGA	TAGATTTTGA	ATTATGTCCT	CACCTGTGAA	CATATATATT	420
	TTTCTGTATA	GAAGACAGAT	CCTCTACCTC	CTTTGTGTTA	ANGCCTTTAT	ATGAAACAAT	480
	TAAGTAAAG	CATTCAATAG	TGTGTGATTA	ACTGTGCTATA	CTAATAAGAT	GATACAGCAC	540
20	ATTTTTCATG	CCGTAAATGT	AGACATCACT	ATATAAGATT	CTCAGCTTTG	GGATGATGAC	600
	GTTCCTGAGA	GGATATAGAT	ACTAAATGAA	TGGATGGGAT	TGGCTGTGAA	ACACTCTGCT	660
	CTACTATACA	GCCTTGAATG	TGTAATGTGA	ACATGCAAAA	GAGAACATGC	ATACACTCAA	720
25	ATTTGTACAA	TGCTATAACT	GGAAGTTGAA	GGACTTGAAT	TTTTTATTG	TGCTATTGTT	780
	ATGTTTCTTG	TAATGTTTTA	TATCTAAGGA	ATTTTGTAGG	TATATATAA	GAATAAGAGA	840
	ATATATACAA	ATGATGTGAC	TGAGAGTTT	TTACTATAAA	TTAGATATAT	TTTCTTCTTA	900
30	TTGCAATATA	TAATCTTAAT	CTTTAAGAA	TAATATTAAT	TTAATATTAT	AACTTCAAT	960
	CTTTAAGAA	TAATATTAAT	AAATTAATAT	TATAATTAAT	AACTCTTAAG	AAATTAATAT	1020
	ATAATTTAAT	ATAATTAATA	ATAATCTTAA	AGAAATTAATA	ATTACATTTA	ATAATTAATA	1080
35	AAATCTTAA	TCTTTAAGAA	TAAATTAATA	TCTTTAATG	CCATATGAT	CCGAGAGGAG	1140
	AGAACTAAT	CCCTCTCTCT	TCTGATATGA	CTTTTCTCTC	ACATGCTGCT	GTATGTGTTA	1200
	GTGAGATGA	AGTCTTAAG	AACATCAATA	TGATGTTGGG	GATAATCCAA	AGACATTTT	1260
40	TGAGATCAA	ATGGCATGTC	GAGAGTTTGT	TTCTTGCTATA	TGTATTACT	GTGCCACAGC	1320
	ATATATACAA	ATGATGTGAC	TGAGATGAGA	AGTGTGAAT	TGTACATATA	CAGCATCTGA	1380
	TTGCAATATA	TAATCTTAAT	CTTTAAGAA	TAATATTAAT	TTAATATTAT	AACTTCAAT	1440
45	CTTTAAGAA	TAATATTAAT	AAATTAATAT	TATAATTAAT	AACTCTTAAG	AAATTAATAT	1500
	ATAATTTAAT	ATAATTAATA	ATAATCTTAA	AGAAATTAATA	ATTACATTTA	ATAATTAATA	1560
	AAATCTTAA	TCTTTAAGAA	TAAATTAATA	TCTTTAATG	CCATATGAT	CCGAGAGGAG	1620
50	AGAACTAAT	CCCTCTCTCT	TCTGATATGA	CTTTTCTCTC	ACATGCTGCT	GTATGTGTTA	1680
	GTGAGATGA	AGTCTTAAG	AACATCAATA	TGATGTTGGG	GATAATCCAA	AGACATTTT	1740
	TGAGATCAA	ATGGCATGTC	GAGAGTTTGT	TTCTTGCTATA	TGTATTACT	GTGCCACAGC	1800
55	ATATATACAA	ATGATGTGAC	TGAGATGAGA	AGTGTGAAT	TGTACATATA	CAGCATCTGA	1860
	TTGCAATATA	TAATCTTAAT	CTTTAAGAA	TAATATTAAT	TTAATATTAT	AACTTCAAT	1920
	CTTTAAGAA	TAATATTAAT	AAATTAATAT	TATAATTAAT	AACTCTTAAG	AAATTAATAT	1980
60	ATAATTTAAT	ATAATTAATA	ATAATCTTAA	AGAAATTAATA	ATTACATTTA	ATAATTAATA	2040
	AAATCTTAA	TCTTTAAGAA	TAAATTAATA	TCTTTAATG	CCATATGAT	CCGAGAGGAG	2100
	AGAACTAAT	CCCTCTCTCT	TCTGATATGA	CTTTTCTCTC	ACATGCTGCT	GTATGTGTTA	2160
65	GTGAGATGA	AGTCTTAAG	AACATCAATA	TGATGTTGGG	GATAATCCAA	AGACATTTT	2220
	TGAGATCAA	ATGGCATGTC	GAGAGTTTGT	TTCTTGCTATA	TGTATTACT	GTGCCACAGC	2280
	ATATATACAA	ATGATGTGAC	TGAGATGAGA	AGTGTGAAT	TGTACATATA	CAGCATCTGA	2340
70	TTGCAATATA	TAATCTTAAT	CTTTAAGAA	TAATATTAAT	TTAATATTAT	AACTTCAAT	2400
	CTTTAAGAA	TAATATTAAT	AAATTAATAT	TATAATTAAT	AACTCTTAAG	AAATTAATAT	2460
	ATAATTTAAT	ATAATTAATA	ATAATCTTAA	AGAAATTAATA	ATTACATTTA	ATAATTAATA	2520
75	AAATCTTAA	TCTTTAAGAA	TAAATTAATA	TCTTTAATG	CCATATGAT	CCGAGAGGAG	2580
	AGAACTAAT	CCCTCTCTCT	TCTGATATGA	CTTTTCTCTC	ACATGCTGCT	GTATGTGTTA	2640
	GTGAGATGA	AGTCTTAAG	AACATCAATA	TGATGTTGGG	GATAATCCAA	AGACATTTT	2700
80	TGAGATCAA	ATGGCATGTC	GAGAGTTTGT	TTCTTGCTATA	TGTATTACT	GTGCCACAGC	2760
	ATATATACAA	ATGATGTGAC	TGAGATGAGA	AGTGTGAAT	TGTACATATA	CAGCATCTGA	2820
	TTGCAATATA	TAATCTTAAT	CTTTAAGAA	TAATATTAAT	TTAATATTAT	AACTTCAAT	2880
85	CTTTAAGAA	TAATATTAAT	AAATTAATAT	TATAATTAAT	AACTCTTAAG	AAATTAATAT	2940
	ATAATTTAAT	ATAATTAATA	ATAATCTTAA	AGAAATTAATA	ATTACATTTA	ATAATTAATA	3000
	AAATCTTAA	TCTTTAAGAA	TAAATTAATA	TCTTTAATG	CCATATGAT	CCGAGAGGAG	3060

Seq ID NO: 34 DNA Sequence

Nucleic Acid Accession #: NM_003979.2

Coding sequence: 254..1157

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	ACAAGTCTGC	AGAGTGGGAG	GGCGGGATAG	CTGTCCAAAG	TCTCCCGCAG	CAGTGAAGAG	180
65	CGCTGCTGCT	GCCTCTCTGC	GCGCGGGGAG	CAGCAACGAG	TTCAAGGCCA	ACGCTCTGGC	240
	ACTAGAGGCT	AGAAATGGCTA	CAACAGTCCC	TGATGGTGGT	CGCAATGGCC	TGAAATCCAA	300
	CTACTACAGA	CTTGTGCTCT	CTCTGAGGTA	CTTGGGATAT	CTTGGGATAT	CGCTGGCCAG	360
70	AGCCCGGCTT	GTAGCTCTGG	TGGCTCTCAT	GTCTCACTCT	CGAATCTGG	CTCTGAGGCT	420
	CGAGGACTCC	AACAGAGGGA	AAATCTCTGC	TACTCAATTT	CTCTCTCTCC	TGGTGTGTTT	480
	GGGACTCTTT	GCCTCACTCT	TGGCTCTCAT	CATGCGAGTC	GACGCGAGCA	CAGGCGCCAC	540
75	ACGCTCTCTC	CTCTTGCTCT	GTCTCTCTCT	GTATCTCTCT	TCCTCTCTCT	TGGTGTGTTT	600
	TCTGCTCTCT	ACCAAGCTGG	TCCGCGGGAG	GAGCGCCCTT	TCCCTCTCTG	TGATCTCTGG	660
	TCCTGCGCTG	CTCTCTCTCT	TAGTCTCTCT	TGTTATGCTT	ATTTAATATA	TGCTCTCTCT	720
80	CATGATAGAG	ACCAAGCTCTA	ATGCTCTTTC	TGAGCTCTCT	GTCTCTCTCT	GCAATGAGGA	780
	CTTGTGCTCT	CTGCTCACTCT	AGCTCTCTCT	CTTGTGCTCT	GTCTCTCTCT	TCATCTCTCT	840
	CTTGTGCTCT	CTGCTCACTCT	AGCTCTCTCT	CTTGTGCTCT	GTCTCTCTCT	TCATCTCTCT	900
85	GTATCTCTCT	TGCTCTCTCT	TCTGCTCTCT	CTGCTCTCT	GTCTCTCTCT	TGCTCTCTCT	960
	TGCTCTCTCT	TGCTCTCTCT	TCTGCTCTCT	CTGCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1020
	TGCTCTCTCT	TGCTCTCTCT	TCTGCTCTCT	CTGCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1080
90	TTATCTCTCT	GAGCTCTCT	TCTGCTCTCT	TGCTCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1140
	GAGCTCTCT	TGCTCTCTCT	TCTGCTCTCT	TGCTCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1200
	CTATCTCTCT	TATCTCTCT	CTGCTCTCT	GTCTCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1260
95	CATCTCTCTCT	TATCTCTCT	CTGCTCTCT	GTCTCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1320
	CATCTCTCTCT	TATCTCTCT	CTGCTCTCT	GTCTCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1380
	CATCTCTCTCT	TATCTCTCT	CTGCTCTCT	GTCTCTCTCT	GTCTCTCTCT	TGCTCTCTCT	1440
100	AGATGTTGCC	TCTCTCCGAG	CTCTCAACAC	ATTTCTTCTA	TCTCTGGGCT	GATGCTGGCT	1500
	AGTAAAGACT	CAGTCTCTAG	AGGCGCTGTA	GTATTTTCTT	TTTCTTCTCT	CATCTCTCTG	1560

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5 ATACTCTTTT TAAGTGGAG TCTCAGGCAA CTCAGCTTTA GACGCTTACT CTTTGTGTTT 1620
 GTTTTCTTGA ACAAGATCTT GCTCTGTGAC CAGAGCTTGA GTGCAGTGTT GGGATCAACG 1680
 CCGAGTGCAG CCTGCACAC CTTGTGCTCAA GGAATCTCTC CATCTCCATC TCCAAAAGTG 1740
 CTGGATGAC AGGCGTAGCC CACAGCTCCC AGGCTAGGCC CTTAATCTTG CTTGTAATTT 1800
 CCGTGGACTA AAGGCTGGTT CATCTGAGCT AGGCTGGCTT CACAGAGCTC TAGGCGCTTG 1860
 CTCTCTTAAG TCACTGAGG TTTGTGTGAG CTTGTGGGCT CAGAGCAGAG CTCGATATCT 1920
 GAGCAAAAT AGCAAAAGCC TTCTCTGACC CACTGGGCTG AATCTACACT GGAGGCGAAC 1980
 TTGCTGGCAC CCGCGCTCCC CAACCTCTCT TGGCTGGTGA GGAGAGGCTA AAGATCACCC 2040
 TAAATTTACT GTATCTCTTA GTGCTGGCTC ACATTGGGCT TGAAGAGCTC CCGGACCAAC 2100
 ATTCAACAGAT CAGCTCTCTC TTCTGTGACT GTCCGCAAC TTGCTGTGCA TCCGAGATC 2160
 TAACTCTCCC CTACTCTGCT CCGAGGATCT TTTGAGACT CACTACACCA ACCCGGGTGG 2220
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 CTCATCTTGC ACCCGAAGCT CTGTAAATAG ATTTACGGCA TTTACGGGCT CATTTCTGAA 2340
 GTGGGCAATG TCTGTAATG GAGGATGTTT ATTATATATA TAAGTTATTT ACCTGAGTAT 2400
 15 GCAATAAAGA TGTGTGTGCC ACTCTTTACT GGTGTGTGCC GCAAAAAAAA AAAAAA 2456

Seq ID NO: 35 DNA Sequence
 Nucleic Acid Accession #: NM_032957.1
 Coding sequence: 1..4203

20 1 11 21 31 41 51
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 25 GACACCTCTC GAGACAGGCT CTCTGCGGCC AGAATTTGCG AGAGGGCGCA AGAGAGGCTT 240
 TTCCCGTACT GGGCTCTGTC ATCTCTGGGG AAGCTCTGCT CTCTCTCTGT AGACCCCAAT 300
 GCTTCTACAC CGGATCTCTC AAGATATATT TACGCTTCCA GGCATCTCTC GCAATGATCA 360
 CAGGTTCATCA ACAGGCTTGTG GAACACTCTC TACCGGCTTA AGGTGTGTGT GCTGGGCTCC 420
 30 GGGGAGCAGC TTGTGATCCA TCTGTAGGTC AGAAACGANG AAGGTAAACA TCTACAGATC 480
 CACTTGTGCT GTAGAGAGGT GGCAGATGCT TCGCTTCATT TCTACACAAA GGTAAAGAGA 540
 AAAAGGCTCT AGAGGAGGCT GTCTGTGAGA CTGAGGACTT TTAGAGGACTT GAGACAGAGC 600
 GGAAGACAGC ACAGGGGTGTG CCGCTTACTC CTGTCCGGBA ACCGTGAAGA CAAAGCGCAC 660
 CATCATTTCA TGCCTGTACA TTACTTTGTC GATGCCAGAG CCDCGAGAGC ACACAACATT 720
 35 GACTGTAAAG GAGACAGTGT GATCTTTTAC GAACTACACA AGCTGGAGAA GATTTGTGGA 780
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 CAGTGTCTGG AGAGAGCGAC CAGAGCAGCG CAGCCGGGTG AGCCGCAACC GAGGTTCAAG 900
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 40 ATCTCTGTGC GCGTGTAGGG GCGCATATGT GCTGTTTGAG TGGCTTGAGA GACACAGGTT 1020
 CTGCAACAGC CAGACAGGAG CACTCTTGAG CATCTCTGAT CAGAGCTGAT CAGCTTGTCA 1080
 ACCAAGGCTT GATCTCTGGA CTGCTGGGAC CAGATCATCC AGCACTGGC AGGACGTGCT 1140
 GAGTGTTCAC CAACACAGCC CGAGCTGCGG AAGCTGGGGC ACATTATCCA GATTGTGTTT 1200
 45 AGTGTGAGCC CCGTCCAGGG CAGGCTCTGG TCCCGACAGG GCGCTGGGGG CTTACAGTCC 1260
 TATAAGTGTG ACATCTGATC TGATGCTGGT CAGCGAGGCA CGCTCAGGCG GTCTGATGCC 1320
 TGGGACACA CTGCAACCGG AAAGGAAAGG AAGTGTCTGA GCTATCGGTG TCTCAGTCCC 1380
 50 GGCACAGACA TGCAGAGCTC GGTTCGCGAG GGGGTCCGCT CCGTCACTCT TACCAGGGCC 1440
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 GGAAGACCAA ACATCATGCA CAGACGACAG ATCTGGTGGT GGGTCTCTCC CAGAGGCTCC 1560
 GATGAGGCC ATTTAGGCTC CGCTTTGAC AGAGCGTTTT CGAGAGAGTG TATTATCTCC 1620
 55 CTGGGGAAGG CTCTGGGACA CATGCCGCCG GTGGTGCCCT ATGGGCTCTC GATCTCTTTC 1680
 CCTCTCTATC CTGTATGAGA GAGAGGCTTG GAGTCTGAG GGGCCGCGGA CTGGGCGGAG 1740
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 60 GTGATGTACA CGGGCTCTCC GTACCCCACA CGCATAGAAC CCGGGGTTGT CCTCAAGATG 1980
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 75 CTCTCTCTG AAGAGAGGCC GCGACAGAAA CCGCGAGGAG GAGAGAGAAA ATGCTCCCTG 2640
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 80 AAGCAGCAGT TTGAGGAGGT CTGTATCCAG CTGACAGGAG GAGGCTGTGG CTATCGGCT 2940
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CGGAGACGCA  GAGACAGGGG  AGGCGCTGGT  GTGTGTCGAG  TGCCTCCCGA  GACATCTTGT  4080
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TTTTCTAATA  ACTGGTGTGA  GTTGC  4945

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Seq ID NO: 16 DNA Sequence

Nucleic Acid Accession #: NM_016434.1

Coding sequence: 828..4487

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1      11      21      31      41      51
|      |      |      |      |      |
AGTCAGCCCT  GCTGCCAGCC  AGTGCCTGGT  GCTGGGAGCT  CAGGAGAGCC  CCGCGGAGCC  60
ACTGCGGGAC  AGTGAACGGA  GCGAAGAGCT  GAACCGAGGA  GAGGAGAGAT  ACGGCGCGGT  120
CAGGCGCTCT  AGTGAACGGA  TCGTGGGCAA  GCGCGACGCG  TTTCAAAATT  TCGAGAAGG  180
CGGTGGCTCT  ACATCTGAGC  AGTAAAGAGA  TGGCTCTGGG  GAGAGAGAGT  CAGGAGCTCT  240
CGGGCAATCT  GTGTGTCGAG  GCGTAAAGAG  GAGCTGACTG  GAGCTGTGAG  CTTGTGGTGG  300
GATGACGATC  AGAGGAGAGC  AGCGGCGGGA  CCCCAGATT  CTGCGTGTGG  GCGATGAGG  360
TGAGGTTTAC  TGGCCAGCGG  AGCGGAGAC  AAGACGCGCA  AACCGCGGT  TAGCGCTGGA  420
CGAGCGAAG  AGGAGGCGGA  CGCCCTCCG  GGGGAGACAG  TTTCCGCGG  GAGCACAAGG  480
CAGCGAGGAG  GAGCGAGAGC  GAGGAGAGTC  GGGGAGAGAG  GAGGAGAGAG  GAGGAGAGAG  540
CCCGCGAATA  CTTGTAGCTG  GCTTACAGCT  GGGGAGGGGT  GGCGCGCTC  GATCTGAGTC  600
GGTTGAGTTC  CTGAGGAGCC  CGGTTCTGG  AAGGTTTGCC  GCGGAGACAA  GTGAGCAGTC  660
TGTGCTAGAG  GATGTTCTGA  AGAGAAGAGC  GTTGTGTGCC  AGTGCAGATG  CTGCGATCGG  720
TTACACAGAG  GATGAGAGCT  GATGAGAGCT  CTGAGAGAGC  AGACCGAAT  AGACCGAAT  780
AGCTCTGCC  TCAAGCAGGC  TCTGTGCGCT  TCGAGAGACA  GCGTGATATG  CCGAAGATAG  840
TGACGAATGG  TCGAGCGGTA  GACTTCCCT  TCGAGCCCTA  CAATGCGCAA  CAGGAGATAG  900
TGACCAAGGT  CTTGGAATTC  CTGAGAGAGA  AGTGAATGAG  GATCTGAGAG  GCGGCTTACG  960
GTACAGAGAG  GAGCGAGAGC  CTGCTGTGCA  CAGAGTGTGG  GATCTGAGAG  GAGCTGTGCA  1020
AGGCACTCT  TGGCCCGAG  ATTGCGAGGA  GCGCGCAAGG  AGAAGCTTTC  CCGAGTCGCG  1080
CCTGTGATC  CTGGGCGAAC  GCTGCTGCTG  CTGCTGAGGA  CCGCATAGCT  TGTCTACGG  1140
ACATCCCAAA  GATTATTATC  GCGTCAAGGA  CCGACTGTGA  ACTACAGAGC  GTATCAAGG  1200
AGCTTGGAGA  GACTCTCTAC  CGGCTTAGAG  TGTGTGTGCT  GCGCTGCGCG  GAGCAGACTG  1260
GCATCTCTC  TGAAGTGAAG  AAGAAAGAGA  GATCAACTCT  ACAGATCCAC  TGTGTGCGTA  1320
AGAGAGTGGC  AAGTGTCTCC  TGTATTTCT  ACACAACGT  AAGAAAGAAA  AGCTCGAGAG  1380
AGAGAGTGGC  CAGCCCAATC  CTGACATTG  AGGACTTGGT  CAGAGCGGGA  AGCAAGGACA  1440
GGGTGTGCC  TTACTACCTT  TCCCGAGACC  TGAAGGAGCA  AGCCGACATC  ATAATTATCG  1500
CTTACAATA  CTTTGTGAT  GCGAAGAGCC  CGAGAGGACA  CAACATTTAG  CTBAAGGGGA  1560
CAGTGTGAT  CTTTGAAGGA  GCTCACAGC  TGGAGAGAT  GTGTGAAGAA  TCGCATCCT  1620
TTGACCTGAC  TCCCATGAGC  GCGCTTTCAG  GACTGCGGCT  CATAGACAGC  GTCTGTGAGG  1680
AGACGACGCA  GCGAGGCGAG  CAGGCTGAGC  GCGACCGGGA  GTTACAGCGG  GAGTCCCGCA  1740
CGCCAGGCT  GAGTCAAGAG  CTGAGAGAG  TTGCAAGCT  GATGTGAGCT  GTGAGCCCT  1800
TGGAGGGGCG  CATGATGCT  GTTGAAGTGC  CTGAGAGACA  CAGCGGTGTC  ACCAAGCGAG  1860
GGAGCTACAT  CTTTGAAGCT  TTTGCTGAAG  CCGAGATCAC  GTTTCAGAGC  AAGGCGTCGA  1920
TCTGTGACTC  GCTGAGACAG  ATCATCTCAG  ACCGTGCGAG  AGTGTGTGGA  GTTGTACCA  1980
ACAGCGAGC  ACTGAGAGAG  GTGCGGACA  TTATGACAGT  GATGTGAGCT  GTGAGCCCT  2040
CGGAGGCGAG  CCGCTGTTC  CGAGCGAGGC  TGGGGCGGCT  ACGTCTCAT  AGATGTGACA  2100
TCACTCTGTA  TGTCTGTGAC  CGGAGGACCG  CTGACCGCTC  TGAATGCTGG  AGCACACTG  2160
CAGACAGAAA  GCGAGGAGAG  GTGCTGAGCT  AGTGTGCTT  CAGTCCCGGC  CAGAGATGTC  2220
AGAGCGGCT  CGGCGAGGCG  GCGCGGCTCT  TGAAGCTTAC  CAGGCGGAG  CTGGGCGCG  2280
TGTCTCTCT  TGTCTGTGAG  ATGCAATCC  CTTTCCCAAT  CTGCTGTGAG  AAGCCACACA  2340
TCATCGACAA  GCACAGATC  TGGGTGGGG  TGCTGCCGAG  AGGCCCGAT  GAGGCCCAAT  2400
TGAGCTCCGC  GTTTGACAGA  CGGTTTTCGG  AGAGATGCTT  ATCTCCCGCT  GGAAGAGGCT  2460
TGCGCAACAT  GCTCTCTGTA  GCGCTGTATG  GCGCTCTGAT  CTTCTCTCT  TCTCTGATG  2520
TCATGAGAGA  GAGCTGTGTA  GCGGCGGAGT  CCGCGCACT  GCGGCGGAG  ATGAGGAGGC  2580
TGAGCGGCT  GTTGTGTGAG  CCGAGGAGCA  AAGCGCACT  TCTCGAGACC  ATCAGTGGCT  2640
ACATGATGAG  GTTGTGCCCG  CCGAGTCCA  CGCGGCCAC  CTTCTGGGCG  GTTGTGCCGG  2700
GCAAGGCGAG  CGAGGCGGCT  GACTCTTCAG  ACAGAGATGG  GCGTGTGTGT  ATGTGACGTA  2760
GCTCTCGGTA  CCGCTCAAGC  ATGAGCCCTC  GGTGTGCTCT  CAGATGTCAG  TCTGTGATG  2820
AGATGAGGG  CAGAGGTGG  GCTGAGGCC  AGTCTCTCT  TGGAGAGAGT  GTGATAGCG  2880
ACGAGGCTC  CAGGCGCTGT  AACCAGCGCA  TCGCGCGAGT  GATCCGCGAC  CGCGAGACT  2940
ACGAGAGCT  CTTCTCTGT  GACACAGGT  TGCGCTTTC  GAGAGAGGA  GCGCACATCT  3000
CCTCTTGGT  GCTCTCTGAG  ATGAGGCTCT  ATGACACTT  TGGCTGTGTC  ATCCAGAGC  3060
TGGCGAGTT  CTTCTGTGT  GCGAGCGAAA  CTAATCCAGC  GCGCGCCCC  CGGCTACAG  3120
CACCACTGT  GCTGTGAGAA  GATGCTGTCA  GCGAGGCCAA  GTGCGCTGGC  CCGTCTCTCT  3180
CACACAGAAA  AGCTAAGAT  GTGAGACTGC  ATGTCCCGAG  CTTGAGAGAG  AGGTCTCTAG  3240
GTTCACTGAG  TGTCTCTGAG  CCGAGAGAGT  GCGTGTGTTT  GAGATGTGAG  CAGAGGAGC  3300
TTCTCTGAG  GAGAGAGGCC  ACGGCGCTGC  TGGCGCGGCT  GAGAGCACAG  CAGAGAGGG  3360
ACGAGGCGCC  TGGCGAGGAG  CAGGCGCCAA  GCTGCTCCAC  CCGTCTCCCT  CTTCTGTGAG  3420
CGGAGCGCG  AAGAAGAACT  CGAGGAGGGA  GAGAGAGAT  CCGGCTGGTC  AGCCACTCG  3480

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	AGGAGCCCTT	GCTCTGTGCA	CAGACGACCA	GGGCCAGCT	CTTCAATGCT	GCCCTGAGAC	3540
	AGGAGTTGGG	CCAGGCGAAC	TTTGCACACT	TCACCCAGCC	CCTCGAGCAG	TACAAGGGTT	3600
	CCGATGACCT	CGCGCCGCTG	GGCGCTGTC	TCGGCCCCCT	CTTGTGTGAG	GACCCGAGGA	3660
5	AGACACAACT	GTCCTCAGGC	TCTTCAACGT	TTTGTGGGCG	CCACCATAG	CGACGATTTG	3720
	AGGAGTCTTG	TATCCAGCTG	ACAGGACGAG	GCTGTGGCTA	CTGCGCTCAG	CACAGATHTC	3780
	CCCGAGACAG	CGCGCTCTGG	ACCCGACTGG	AAAGACGSGS	CCGATATCCA		3840
	AGCTCAGCST	GTCCACGGCT	GGGGCCGAG	AGCTGGACCC	CCAGAGGCAC	CTGAACCAAG	3900
	GCAGGGCCCA	CTCTGTGCC	AGGCCACCC	CACACAGAGA	CCCTGGCAG	CAACACACGT	3960
	GGGGTCTCTG	AGTGGCCAGA	GGGGGAGCC	AGGGCAGGA	CCCTGTGAG	GCTTACCTGG	4020
10	CTGATGTCCG	CAGGACCTGT	GGTCCGCGG	GCTTATGCGA	ACTCTTGCGA	GCCCTGGAG	4080
	CTTATAGACA	AGATGACAGC	CTCGACAGG	TGCTGTGCTT	GTTTGGCGCC	CTGACACTGT	4140
	CAAGGCGAGA	GGACTTCCCC	CTCTGTGACA	GTTTCAAGAT	GTTTGTGGCT	CCACACACCA	4200
	AGGAGGCTCT	CTCAGACAGG	TGCACAGACC	TGACCGGCGG	GCCCTATCCG	GGGATGGAGG	4260
	CACCGGACG	CGACGCTCTG	AGGCTCTGCT	GCTTAGACCA	AGGGATCCCC		4320
15	AAACCGGCC	CTCAGGTCCT	AGGAAGACCG	GGAGAACCCA	GAGCAGACTT	TGCTCTTCCC	4380
	TTAGACAGAG	GCGCAGGAG	ACTGTGGGG	GCGGGGTGGA	GGATCGAGT	CCAGGCCAGT	4440
	CTCAGAGACC	TGCCACGCG	CCTGCAGCAT	CTGAGTGGGG	CCTCTAGAGT	GTGCCGAGCC	4500
	TGCCACAGCC	CCTCAGAGAA	GCAGAGGCTC	ATCGACGCTT	TCTGGCAGGA	GCCCGAGTGA	4560
20	GTGCGCAGG	AGGCCGCCAG	CACACCGAG	TGCGCTTGAT	CACCTGCTCT	TCCAGCTCTG	4620
	GTGGGCGAAG	AAACCGACCA	ACAGATAGG	CCAGCCCATG	CCAGCCGGCT	TGGCCCGCTG	4680
	CAAGGCTCAG	CGAGGGCGGG	CCCATGGTTG	GTCCCTGGGG	TGGGACCGGA	TCTGGGCGCT	4740
	CTCTTGAGAA	GCCCTGAGCT	ACCTTGGGCT	GTGGGTTGGG	TTTCTTGAGAA	AAGTCTCTCC	4800
	CAGATCTCC	CTGCTCTCTG	CCCTGTGGT	GGTGGACAG	GGGACACCCA	CCGTAACCCC	4860
25	TCAACCGGAA	GGAGGAGACG	CCGCTGGGCA	CGTCTCCACT	TTTATACAG	GGACACGGCT	4920
	CTCTAATAAA	GCTGCTGGCA	GTGCCC				4946

Seq ID NO: 37 DNA Sequence
Nucleic Acid Accession #: NM_015647.2
Coding sequence: 246..1893

30	1	11	21	31	41	51	
	AGCCTCTCCG	GCTACTCGGG	GTACGGCTGT	GGCCCCGACA	CGAGATGAGG	GTCTTCACTT	60
	CGGTGAACTC	AACCTCTGAA	CGCGCTGTGG	CGAGGGCGAG	AGGGCTATGG	CCACCCCCCA	120
35	GGTTGTCGCT	TGCGCCAGCGA	AGAGGCCAAC	GCTGCTCTGG	GGTGGTCCC	CAGCTGAGAG	180
	TGTATGAGCA	CTTTCGCGAT	CTCTCCGAG	CTGCTGCTGG	CTCTCTCAGG		240
	GAACTATGCC	AGGCGCGCGC	CCGCCGGCTA	CAGCACCCAG	TGTGGCTGGA	GAAATGCTGT	300
	TCAGCAGGCG	CAGTGTGCTT	GGCCCTCTCT	TCTCCACGAG	GAAAGCTAAG	AATCTGGAGC	360
	TGCATGTCCC	CAGCTGTGAG	CAGAGGTCCT	CAGGGTCAAC	AGCTTCCGCG	GAGCCCGGAG	420
40	TGCTGCGCTG	TGTGAGGAGG	CACTTCTCCG	CCGCGACGAG	CGCTGCGGAG	CGAGCGGAGT	480
	TGCTGCGCGC	CTGTGGACAG	AGGCAAGGAC	GGGCGGGGAG	CCCTGTGGCG	GAGCAGCGGC	540
	ACAGCTGCTC	CACCTCTGCC	CTCTGTCTGT	AGAAAGGGCC	CGGACGAAGA	CCGCGAGGAG	600
	GGAGGAGAAA	GATCCGGCTG	GTACGACCCAC	CGAGAGGAGC	CGCTGCTGTG	GCACAGAGCG	660
	ACAGGGCCAA	GCTCTCTCAT	GTGGCGGTGA	AGAGGGTGT	GAAGCCAGC	AACCTTGCCA	720
45	CCTTCAACCA	GGCCTTCCG	GACTACAGGG	GTTCGATGTA	CTTCCGCGCC	CTAGCCGCTCT	780
	GTCTCGGCC	CTCTTCTGCT	GAAGACCCCA	AGAAAGCACA	CTCTCTCCAA	GGCTTCTAAC	840
	AATTGTTGCG	GGCCACCATC	AAGCAGCACT	TGTAGGAGGT	CTGTATCCAG	CTGACGGGAC	900
	GAGGCTGTGG	CTATGGGCTC	GAACACAGCA	TTCCCGCAGG	GCAGCGGGCA	CAGCGGGTCC	960
	TGGACCCGAC	TGGAGGAGCT	GGCTGGGATC	CCAGACTGAC	CTTTGTCCAG	GCTGTAGGCC	1020
	AGACGCTGGA	CCGCCAAGCG	CACCTGAACC	AGGGCGAGCC	CCACCTGTGC	CCGAGGCCAC	1080
50	CCCCAACAGG	AGACCTCTGG	AGCCAAACAC	AGTGGGGGTC	TGGGTTGCC	AGAGCAGGGA	1140
	AGACAGGGCA	GCACGCCGTG	AGGCCCTTAC	TGGCTGTATG	CCGCAAGGCC	CTGGGTTCCG	1200
	AGGCTGTGTA	CGACTCTCTG	GAGCGCTGTA	CAGGCTATTA	GCAGAGCGAC	GACCTCTGGA	1260
	AGGCTGTGGC	TGTGTTGGCG	GGCCTGACCA	CTGCAAGGCC	AGAGGACTTC	CCCTCTGCTG	1320
55	ACAGGTTCAAG	CATGTTTGTG	GTCCACACCC	ACAAACAGCG	CTTCTCACAG	AAGTGCACAG	1380
	AGCTACGGCG	GGCCGCTTAC	CGCGGACATC	ACCCCAACGG	ACCCCAAGAG	GAGAGGGTTG	1440
	GTGCTGTGCG	TGTGCTTACG	CGACGGGCTC	CCCAACAGG	CTCTGACG	TCTGTAGAGA	1500
	CGGGAGAGAC	CCAGAGGAGG	ATCTCTCTCT	TCTTTAGACA	GAGGCGAGCA	GGGACTGTGG	1560
	GGGCGGGCGG	TGAGGATGCA	GGTCCAGGCC	AGTCTCCAGG	ACCTCCCCAC	GGGCTGTGAG	1620
60	CATCTGAGTG	GGGTGAGCTC	CATGGGAGAG	ACATCTGCTG	GCAGCAAGCC	ACGAGAGCTC	1680
	CGAGCGGCGC	CCCTCTCTCT	CTGCTGAGTG	CTGAGGGCTC	TGAGGCGAGG	GAGCTGGTGC	1740
	CTCTTCAAGC	CGCTGCTGCT	GACTTCCAGC	GCTCCGAGCG	CTGCTGAGCA	GGGCACTTCT	1800
	AGGCTCTTAG	GATGTGCGCA	GCTCTGCCCA	CCGCTGCCAG	GAGACGAGCT	GTCATCGAGG	1860
	CTTCTGTGCG	AGAGCCCGAG	TGAGTGGCCA	CGAGGGCCCG	CAGCACACCC	AAGCTGGCTT	1920
65	GATCACTCTG	CTGTGCTGCA	GGTGTGGGCT	AGAACAGGCT	AGGAGGAGAG	GAGCTGGGCT	1980
	ATATCCGCGG	GCTTGGGCGG	CTGACGGCTC	CAGGCGAGCG	GGGCCCAATG	TGTGGTCTGT	2040
	CGGTGGGACC	GGATCTGGGG	CTGCTCTTGA	GAAAGCTTGA	GCTACTTTGG	GGTCTGGGGT	2100
	GGGTTTCTCG	GAAATGCTCT	CCCGAGAACT	TCCCTGGGTC	CTGGGCTGTG	AGTGTGGTCA	2160
	CAGGGGACCC	CCMGCTGAGC	CCCTCACCGG	GAGGAGGAGG	ACCCGCTGGG	GCAGCTGTCC	2220
	ACTTTTATCT	AGGGGACAGG	GCTCTCTAT	AAGGCTCTGT	GCAGTGGCCA	GGAAAJAJAA	2288
70	AAAAAJAA						

Seq ID NO: 38 DNA Sequence
Nucleic Acid Accession #: NM_003823.2
Coding sequence: 101..1003

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	TCCTCAGGCG	GGCCCGGGCG	AAAGGAGGTT	CGATGTGCGT	CAGGCAAGCC	AGGTTCTCTT	60
	GTCCGGGCTG	AGCCCGGCTC	TCCCTGTCTC	AGCAAGAGCC	ATGAGGGGCG	TGGAGGGGCG	120
80	AGGCTGTGCG	CTGCTGTGCG	TGGTGTGGCG	GCTGCTGGCG	CTGCTCGGG	TGCCCGCTGT	180
	AGCTGAGGAT	GCAGAAACAC	CCACTTACCC	CTGGCGGAGC	CCAGAGAGAG	GGAGGCGGCT	240
	GGTTGGGCGC	CACTGCGGCG	CAGCGACACT	TGTGACGAGC	CCGTGCGCGC	GAGAGACGCT	300
	CAGCACTGTT	GGCCGCTGTC	CAGACGGCCA	CTACACCGAG	TCTTGGAACT	AGCTGGAGCG	360
	CTGCGCTCAT	TGCAACGCTC	TCTCGGGGGA	GCTTGGAGGAG	GAGGCAAGGG	CTTGGCCAGC	420
	CACCCACAC	GTGGCTGGCC	GCTCGCGCAC	CGGCTTCTTC	GCGGACGCTG	GTTCCTGCTT	480

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Seq ID NO: 40 DNA Sequence
 Nucleic Acid Accession #: NM_00593
 Coding sequence: 165..2591

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WO 03/025138

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CTGAGCTCCG TCAGGGCTAT GACACAGAGG TAGACGAGGC TGGGAGCCAG CTGTGAGGGG 2240
GTGAGCGACA GGGAGTGGCG TTGGCCCGAG CATTGATCCG GAACCGTGTG GTACTTATCC 2260
TGATGATGTC CACCACTGCC CTGGATGACA ACAGCGACGT ACAGGTDGAG CAGCTCTCTG 2280
ACGAAGCCG TGAGCTGTAC TTGCAGCTCAG TCGCTTCTAT CAGCCAGCAC CTGAGCTGCG 2300
TGAAGCGGCG TGACCAATCT CTCTTCTCG AGCCAGGCGC TATCCGGGAG GGGGGAACCC 2320
ACCGAGGCTC CATGAGGAAA AAGGGGCTGCT ACTGGGCCAT GTTGCGAGCT CTGCGAGTC 2340
CTCCAGATG AAGGCTCTCT GAGACTGCTG CACTTCACTC CCCTCCCTTT TCTTCTCTCT 2360
GTGGTGAGGA ACAGAGACTG CAGAGTAGAC CTGCTCTACT GCTATGATTA CTCTAAATTT 2380
GCTTTGAGTA TGTATCTCT TTTCAGAGCT CTCTCTGATA ATCGACATCT CCGTAGATAC 2400
AAACAGGGA TTGTTAATTC CTACTGTAACT GAGATTAGG GCGAGGCGTA ATGCTTTGGT 2420
GTGGCCAGCA CTCTGAACT GAGAAATGTT CAGAAATGAC GGAAAGATTA TCAGCTATTT 2440
TCAACATACG TGAGGACATA TGCTGGCCCA TAAACACCTT GGAAGTTCTT GATATTATTA 2460
ATAAAATTGG TGTTTTGT

Seq ID NO: 41 DNA Sequence

Nucleic Acid Accession #: NM_002423.2

Coding sequence: 48..551

20 1 11 21 31 41 51
ACCAATCAA GATAGTCC AAGACAAAT GTCTCTGAC GGCACTATG GCACTACCG 60
TGCTGTGTC TGTGTGCTC TGCTGTGGA GCTTGCCCTT GCGCTGCTT CAGGAGGGG 120
GAGCGCTAG TGAGCTACG TGGGAGCAGG CTCAGGACTA TCTCAGAGA TTTTATCTCT 140
ATGACTCAG AACAAAATAT GCGACAGT TTGAAAGCAA ACTCAAGG ATGCAAAAT 160
CTTTTGCGCT ACCATAACTT GGAATGTGTA ACTTCCGCT CATGAGAAAT ATGCAAGAGC 180
CGMAGTATG AGTGAAGACT GTTGCGAAT CTCTCATATT TCTCATAGC CMAAATGA 190
CTTCAAGT GTCACTACT GTGAGTATG CATATCTCG AGCACTAAGC CATATTACAG 200
TGATGCTAT AGTGTCAAG GCTTTAAACA TGTGGGCCAA AGAGATCCCC CTGCATTTC 480
GGAAAGTGT ATGGGACTAC GCTGACATCA TGATTGCTTT TGCCCGAGTA GCTCAATGGG 540
ACTCTCAACT ATTGATGG CTGGAGAACT GCTGCTACTA TGCTTTGCTC CTCTGGAGC 600
GTCTGGAGG AGATGCTCTC TTGATGAGG ATGAAAGCTG GAGGAGTGT AGCACTTAG 620
GGATTAACTT CTGTGATGCT GCACTCATG AACTTGCCCA TTCTTTGGT ATGAGGACT 760
CCCTGATCCA TAATGACGT ATGTATCCAA CXTATGAGAA TGGAGTCCC CAAATTTTA 780
AACTTATCCA GGAGTATAT AAGGCACTC AGAAACATTA TGGAAGAGCA ACTATATAT 840
GAAAGATA GAACTGCTAG GCGAAGACTT CATCTATCA TTCACTATA TGTATATCAT 900
TGTGACAAA TCAGATTGTA TAGACATGT TCCCTCACTC CATTTAGCAA TTAATGCAAC 960
CTTTTATAT GGAATGGT TTGAAATGCT TTTCACCTCT TTATATGGT AAACCTGCTT 1020
ATGTTGACG TGTGCTTAT TCAATCTATG ACCTTTGTG GTGCGGGTAG ATGTCAATAA 1080
ATGTTACATA CACAAATAA TAAATGTTT ATTCTATGAT AAATTTA 1127

Seq ID NO: 42 DNA Sequence

Nucleic Acid Accession #: NM_018674

Coding sequence: 390..1099

45 1 11 21 31 41 51
CGAGACATC GCTGAGCGGA GCGGCTGGGG CTGCGCGGCG TGGCGGAGGA GCGCTGCTCT 60
CTCTGCTAC TGCTGCTCT GCGAGGACAC AGCGAGGGCG TGACACTGT GCTGTGCTG 120
ATTAGGGAAG CCACAAAGAG ACGATGAGG AGAGAGACAA GGGGAGCAG AGGACGAGC 180
GGGACAGGCA GCACAGGGC TGCGAGGCTG TGCGGAGTGG GAGTGACTCC CCCACTCGG 240
GCCCCAACCC TGTCCCTGTC CTCTTCCCG TGCCCTCGAG TTTAGAGAG CAGCGCTCGT 300
CAACGATGCC ACTCGGAGCG GACGACGGCG TGCTGCTGTA GGAAGACAG GCGACGGAGG 360
GTCTGCGAG TCCGAGGAG GGGGACAGA TGCCGATGGA GATTGTGTG AAATCAAA 420
TTGTCAGGA GAGTGGGAAA CCGAAGGAGA AGGAGGCGAG GGATGAGCAG AGCTCTCTCG 480
GGGCTGTTGC CCGTGAAGCA GCGCCGCCAG ACCTGGGCCA CTTTGGCAGC ACCAGCACCC 540
TGCTGAGACT GGGCGGGGCG TGTGGGCCAG GCGCCGACAG ACTTCAGACA ACCTTGTGGG 600
CACTGCTGCT ACTGACTC CTGGTGGCT TCTGTACGA CACTCTGAG CTGGGCGGG 660
GCTACTGAC CCGGCTCAC CTGTGAGCAA TGAGCCCGCG TGCCCGAGCC CAGTGGGCG 720
GCTTCCGCG TGTCACCTC TGCAATATCA ACCGCTTCC GATTTCGCA CTGAGGATG 780
CGGACATCT CCACTGTGCC AATTCAGAG GAGTGCGCCC CAAAGAGCG ATGTGGCAC 840
GTGGGCGCT CTTGCTCTAG CAGAGGCTG ACGATGTGGA CATCTCAAC CCGATGGAG 900
ACAGCTGCG CGACATGCTT AAGAGCTGCA ACTTCAATG TGATCACTG TCGCACAGA 960
AGCTTCTGT GTCTATACT GCTATGGA AGTGTATAC CTTCAAGCG GACCCGCGA 1020
GCTGCTGCC CAGCGCGGGA GGGGCGATGG GCGATGGCTT GAGATCATG CTGAGATCT 1080
ACGAGAGGA GTACCTGCG ATCTGTGAAA TCTGTGAGG GAGGCTGTT GAGGAGATA 1140
TTGCGGTGCA GATCCAGAG CAGAGGAGAC GCGCTATCAT CCACGAGCT GGGTGGGG 1200
TGTCGCCAGG CTTCCAGACC TTGTGTGCTT GCGAAGACA GGGGCTGACC TACTGTGCC 1260
AGGCTGGG CAACTGTCCG CAGAGAGGTG AGCTCAGGGA GCGTGAAGTT CAGGCTCAT 1320
GGCTCTACG TGCTCTAC GCTGTGAGAA TCTGTGAAA GAGGCTGCT CTTCAGGCT 1380
GCGACTGCG GATGTGGAC ATGCCAGGCA ATGAGACCAT CTGCCACCA AATATATCA 1440
TCGAGTGTGC AGACAGCA CTGAGCTCCC TGAGTGGGG CCGTGAAGGG CCGTGTCTCT 1500
GCGCCACCCC CTGCAACTG ACAGCATATG GGAAGAAGAT TCTCATGTC AGATGTCOA 1560
ACAGGGGCTC AGAGGCTAC CTGGAGGAGA AGTACAGACA GAGGAGGCG TACTATGG 1620
AGACTTCTT GCTCTAGAT GTCTCTTTTG AGGCTCTGAC CTCTGAAGCG ATGAGAGAG 1680
GAGCAGGCTA TGGCTGTGCA GCCCTGCTGG GAGACTCGG GGGACAATG GCGCTGTCCA 1740
75 TCGGGCAG CATCTCTAAG TTCTGTGAGA TCTCTGAGTA CATCTATAG GTTCTGTGG 1800
ATGACGTAAA GCGGATGAG AGGCTGCECA AGACCCCTCT GCGGACCTCC AGTGGAGGCA 1860
CTCTGCTTT GGGGCTTAG GAGTGTGAGA ACAGAGTCC CTGCGGAGC CTGAGCTAG 1920
CGAGAGTGGG GGGGCTCAZ AGTGTCTTCC CAAATACCA CACCCCCAC GTTCCCCAC 1980
GAGGTCTCTT TGAAGATTTT GCTTCTAAG ACGTGTGCT GACTGAAAG ACCAGAGAT 2040
80 CTGAGACCTC TCTGGGATC CCGAGCAGAT TCTCTGTCT CTGGAGAGAT GCTGTGGGAG 2100
TGTCTCATG GAGAGGCGC GAGTGTGATG TCTCTCAT CTCTCCCTC CTGATATCA 2160
GCTCTCTT TCTAAGAGTC TTCTTCTCCA CACCCTTAT CCGAGAGCTG GTGCCGCCAG 2220
AGGCTGGAG ACCAGCCAT GGGGCCCTAC GAGAGAGGAG GAGAGGAGAG AGGAGGGAG 2280
GAGGAGTAGA GCCCATCCA GCGCGGAGAG GGGAGGCTC TGATCATTTG TAAATATTTA 2340

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PCT/US02/29560

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Seq ID NO: 43 RNA Sequence

Nucleic Acid Accession #: AK091016

Coding sequence: 201..2291

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 GATCTCAGCT CTTTTCAGC TAGTGGTGG ACCCCAGGA GGGGAAACTC AGGGAAGCCC 60
 AGGAGGAAGT GAAATATCCC CATGGAGTGA AGCTTTGTGT CTAACCTGGT TCCGGGCGAG 120
 TGATCCAGCT CCTGGGGGGC ATCAGCCAGC GCCAGCCAGG GGGGCACTG CCACCAAGAC 180
 TGAGAGTCTT AGAGGACTTG ATGGAAGTCA GCTCAGCCTC ACCTGCCGAG AGCCTCAAGA 240
 GGAAGGAAGG GCCCATGGTG GAGGCGGCTG CTGGTGGCCA GOTTTTCCAG CTTTCTCCTT 300
 CAGAGGACAG AGCAGGGGAC CTTGGTGGCC TCTCTGACCC CTCTTCACTT CCAGAGAGGG 360
 GTTCCCTGGC CTTTGGGCAC CCGAGCTGCG ACCCTGCATG TTTCCAGAGT GGCCCAATGG 420
 AGGCTGAAGA GGATTCTCTT CCGGAGAGAC AGGAGAGCTC AGCTCAGCTC CACAGAGAGA 480
 AGGCATCCTT GTATTATGGG GTGGGGAGCA CTGTGTCTGG TTCTATAGAG GAGGTACTAT 540
 GGAATCCTCT TGGGAGGCTC CAGACCCAGC TGTGTATGTT GGAGGTGTGG GAGGCGATTG 600
 CTCTCGGCAT TGAAGGACCC CTCTGGACCC TGACACAAGG CACCAATGGC CGGTACAGAA 660
 CCAAGTATCG CAGCCTCTGT TTCAACTGTC GGGACCCGAG GAACCTGAGC TTGTTTCTCA 720
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 TGGAGATTCA GCGGAGCATG GACGAGACAC TGACCTTGGA GGAATCTGGT GACACCGAGA 960
 TGTCTATGTA CTGCAACCCA CAGGCGCTGC CATCTGCATC AGAGGACACC ACAGGGACAG 1020
 ATGACACACT CTTTATGAG CCGAATGCTC ACATCTGAAA GGAATCTGAG CTTCTCAATG 1080
 AGCTCTAAG AGTCTTGAA GCGCGCAGAA GCTCGGGGGA CMAATCTTC CAGAAAAGCC 1140
 TAAGCMAAC TCTATTGCTT GCTCCAGAGA TGCCCAAAAC CAGGGAATTT TCTCCAGAGT 1200
 AAACCAAGGA CAGGTTCCCT CCAATGGGTC TCGATGTGGC TGCTGACACC ACAAGAGCCG 1260
 TCCGCTCTCT CAGCTTATGG GAGGTGCTTC TGAGCATGTT CTCCATAGAG CGGTTCGAG 1320
 CCAGGGCCCA GCTGTGTCTG GAGACAGACT GTGCGCTTGT CTAAGCTCTG CCACCGTGA 1380
 TCCGCTGAG AGGCTGCATC CCGTCCAGCA TGTCTTGGGA CTTCTAGGCC AGCATCTGCC 1440
 CAGCCAGAGC CAGGAGGCTC GTTGTGGTCA GACTGTGCCC ACATGGGGCC GGGGACACCC 1500
 AGAATCTGCC CTTGATGAG TGAATAGTCA ATATAGAGCT GCGACAGCT CCGTCTGAT 1560
 TGGCGCATAT GCGGATGCTC CTGCTGCCCC TGCTGTGCTT CAGGCCCTTG CCGACCGAGC 1620
 TGCGCCTTTT GGGGGGCCCA GGTCTGAGGG TCACTCACTC AAGTCTGTGG CTGGCTGTGC 1680
 TGCTCCCGAA GAGAGGGCTT CCGAGACAAG CAGGCTGCAG CCGCTGGTGT GGGAAAGTTC 1740
 AAAAGATGAT CTCTCTCAAC AGTAGAGTGG AGAGAGAGCA CTATCAAGC GATGAGACA 1800
 GCGGAAATGT GCGCTGAGAG GGCACTCTTC CCGCAGAGAG TGCTGTGGAG CAGAGCCAGG 1860
 CGAGGGGAGC ATAGCTTCCA AGGGAATCTC CTGCTTGGCA GAGGCCGCCC AGAGGCGAGG 1920
 GGAAGCTCTG GCGAGAGCCT GAAATCTGCC AGCATCTCTG GCGAGGGAGC TGCCCGCCAG 1980
 AGCAGAGGTT GCGCCAGTGC CAGCATGCTT ATTCAATAGC ACCAGCTGCT CATGGCTTGT 2040
 GCTGTGGCCA GCACTTCCAC AGGAATCTCT GTCCGACCA AGCCTCTCTC CGGCACTGCT 2100
 AATCTCTGCG GACCATGAGT CAGCAGCTCC AAGCTTACTC GTGCCCGAG ACCAGAGACT 2160
 CGATCCCCCG CCGCTCTGAG CTTTGTGTCA GCGCCCTTGC AGTCCAGAG CCGCTGTGCC 2220
 CAGCCCGTGA CTCTCTTTTG GAGCTACAG ATGAAGCTGG CTCTGAGTGT CTTTCTCTTA 2280
 GAAAGAGCTG ACCCTCTTA CCGACAGAA CAGGGGTTTT GATGCTGACA CTAGTTTGA 2340
 AGCCTTCTCC AGAGAGAGGT GGAATCTGAA GAGAGAGATG GTACGCGCTA CCGACTGCC 2400
 CTGTTGAAAC TTCTCTTTTG ACAATGTFTG CTGTGATTTT TTGTTCTCAT AAGAAATTTG 2460
 GT

Seq ID NO: 44 DNA Sequence

Nucleic Acid Accession #: NM_005291

Coding sequence: 75..1178

60
 65
 70
 75
 80

1 11 21 31 41 51
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 CCGACAGCTA GAGCATGTCC AAAAGAGATT GGTGGGCTGT ATCCAGAAAG CCGCCAGAGG 120
 AGATGCTGAA ACTCTCAGGC TCTGACTCCA GCGAGAGACT GAAATGCTCT GAGATGGCTC 180
 CCGAGGCTGT GATCAACAGC TTCTCTCTGG CCGACDCAAG GGAATGTGGC CAGGACAGCC 240
 CACTGCGAGA CARGCTGTTC GCGCTCTTCT ACCTTCTGGA TTTTATCCTG GCTTTAGTTG 300
 GGAATACCGT GCGCTCTGCG CTTTTCATCTC GAGACACAGA GTCCGGGACC CCGGCAACG 360
 TTTTCTTGAT GCATCTGGGC GGGCCGCACT TGGTGTGGCT GGTGCTGCTG CCGACCGCC 420
 TCTGTTACCA CTTCTCTGAG AAGCACTGSC CATTTGGGA AATGTATGCT GCTCTCACCG 480
 GCTTCTCTCT CTACCTCAAG ATGTAGGCCA GATCTCACTT CTTCACTGCG ATCAGGCGCG 540
 ACCGTTTCTT GGCCATTGTG CACCCGGTCA AGTCCCTACG GCTCCGAGCG CCGCTCTCAG 600
 CACACTGGGC CAGTGGCTTC CTGGTGGTGG TGGTGGAGTT GGGCATGGCC CCGCTCTGAG 660
 TGAGCCAGCA GACTCTGAGC ATCAACACCA CAGTGTGCTG CTTCCGAGCG TACCGGAG 720
 AGGCTCCCCA CCGTGGCTGC GTGCCCTGGC CAGTGGCTCT CAGCTTCCCG TTATCACCCA 780
 GCGTCACTGT CTACCTGCTG ATCATCCGCA GCTTGGGGCA GGGCTCCGCT GTGGAGAGCT 840
 GCGCTAGAAC CAGGACAGTC CCGATAGCTC CCGATAGGCT GCGCATCTCT CTGGTCTGCT 900
 TCGTGGCTCA CCACTCTGAG CCGTCTGCTT ACCTCTGCTC AGCTCTGCTC CATGGAGGCT 960
 CTTGCGCCAC CAGGCGCATC TCGCCCTGGC CMAAGCCGAT CAGCTCTGCG CTACAGAGCC 1020
 TCAAGGGGGC ACTGCAACCC ATCATGTATT TCTCTGTGCG TGAGAAGTTC CGGCAACGCC 1080
 TGTGCAATCT GCTCTGTGGC AAAAGGCTCA AGGCGGCCCC CCGCAGCTCT GAAGGAGAAA 1140
 CACACAGAGC CTGCTCTGAT GCGCTCTGCT ACCTCTGAGC GGGGAGGCTC GTCCAGGCC 1200
 AGGCGAGACT GTTTAGACT CAGCAGACCC AGGAGAGGCG ATCTGCTGCT TCCCGACCCA 1260
 CTTCCGACGC AAGCAACTCT AAATCTCAGC AGATGCCCAC CATTTCTCTA GATCCGCTAG 1320
 TCTCAACCCA TAAAGAGGGA GAACTGACAA AGGGGATCCA TCGCGCACCC CTTCTGAGGG 1380

PCT/US02/29560

60	Seq ID NO: 47 DNA Sequence									
	Nucleic Acid Accession 3: Bos sequence									
	1	11	21	31	41	51				
	GTGTGTAGTC	GGGATGATGA	ACGATTACAA	GCAGAAACAG	CTGTGGAGAC	CTGTTCACAG	60			
	AGTAAGTCTA	GTACAGCAAG	CTCCAAATAT	TTGAGAAAGC	AAAGATGTGC	CCCTTGTCAG	120			
65	CGAGAGGTTT	TAGACATGCT	GAGCTGGTGT	GTCTCTTGCT	AGGCTCCAGA	TTGTGGCCCA	180			
	ACTACTATCT	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	240			
	CTGCTGCTGC	TAGCTCTCTG	GGAAGAGACT	TATGTGATAT	ATCTCAACCTA	CATCTCAGAT	300			
	AAAGAGACAT	CTACACACAG	AGGAATAAAG	TTGCTGATAG	TGAGTCTGAT	ATCTCCATCT	420			
	CGACATCTAC	CTCTCTTACT	TCCAGAAAGG	TCTGTCTACG	AGAGATGAGC	TTTATTTCTC	480			
	CTGCTGCTGC	AGGAGAGAGC	CTGCTGCTGC	CTGCTGCTGC	GAGTATCTAT	GAAATATCAG	540			
	GTCTCTCGGA	AAAGGCTACT	GAGGCCCCCT	TGTGATTTTC	TGCTATTTAGC	TGCTCTCTCTG	600			
	GCAGACAGCT	AAGCTCATCA	GAGAGATAGC	CCAGGAAGAG	CTTTTAATAG	GAAGTTTGTC	660			
	AAAGAGAGCT	GAAGACGATT	AAAAGTGTCT	TGCGAGCGAT	GAAGATGCTT	GATGTGAGAA	720			
75	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	780			
	CAGCAGAGTT	ATTTCCATCT	CTAAATATAA	TGCGAATAGT	GTACTTTCTG	ACACAGCTAG	840			
	CAGGAGGCTG	CTGTGGATAT	TTCAATGAAA	ATCCATTTAT	ATCTTGAGAT	TGAGATATCT	900			
	AAAGAGACAA	GGATCATGAT	GAAATGATAT	TTGCTCTGTA	ATATTTCATG	CTTATATCTA	960			
	AAAGAGACCT	CTATTTTATG	CTGCTGCTGC	GAGATATATG	TTGAGAAAGC	CTGCTGCTGC	1020			
80	CTGCTGCTGC	CTGCTGCTGC	GAGATATATG	TTGAGAAAGC	CTGCTGCTGC	GAGATATATG	1080			
	ATACAGTGTG	AGTTTGACAG	CAGGACACGA	CTACATAGAG	TGAGATGTTT	TTTGTGATAT	1140			
	ATCTTTTACA	ATGATGTTCT	TACAGTGTCT	AHAGACAAAC	CAATTCTCTG	CAAGGTGCTG	1200			
	TTCAATAGAG	AAATGGTTTAT	TGCCAATATG	TGACATCTAT	CTGCTGCTGC	CTGCTGCTGC	1260			
	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	CTGCTGCTGC	1320			

WO 03/025138

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5

CAAAAAGTAA TGGAGGGATA GACTGAAGTT AAATGGGATC AGTATGTGA TGAGATCTCA 1380
 GAAGTGTGTC CACAATAAG CAGATACTCA TTTTAAACAG AGTCAATAGG ATTGAAGCTA 1440
 ATAAAAATAA TAGAATAAAA TACCGATCAA GAATGTGTCC TCGTGGTAT CTGGGTTTTG 1500
 AATTCTGGCT CCACAGAAGT TGTCAGATAT ATGACATTAA AC 1542

Seq ID NO: 48 DNA Sequence

Nucleic Acid Accession #: Bos sequence

Coding sequence: 52..1131

10

1 11 21 31 41 51
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 TGTGTAAAGT TTGTGTGGAGA GGCAGGTGCA TCTGTCAAGC TACCCTGCCA CTACAGTGGG 120
 CTGTGTCAAT CAGATGTGGTG GATGAAGAGG TCAATGTCTG TATTCAGATG CCMAAGTAT 180
 ATTGTCTGGG CCAATGAGAG CCACGTCAAC TATCGGAGGG ACAACAGTGA TAACTATTGT 240
 GGGGACCTTT CAAAGAAAGGA TGCTCTTTTG ACCATAGAAA ATACAGCTGT GTCTGACAGT 300
 GGGCTATATT GTTGCCGTGT TGAGCAGCCT GGGTGTGTTCA ATGACATGAA AATCACGTTA 360
 TCAATTGAGA TTGTGTCACC CAGGTCAAGC ACTACTGCAA TTGTGACAGC GTTCTCACCC 420
 GTCAAGATG TTGGAAGAGG CACCACGTT CCAACGAGAA GCACTGTTCG AACCAACACT 480
 GTTCCAAACA CAATGAGAGT TCCAAGACAA AGCACTGTTT CGAGCAAGAT GACTGTTTCA 540
 ACGACAACGA GCGTTCCCAAC GACAAGAGCG ATTCCACAAA CAAACAGTGT TCCAGTGACA 600
 ACAACGCTCT CTACCTTTGT TCCTCGAATG CTTTGTGCCA GCGCAAGCAA TGACCAAGTA 660
 GGCATCTAC GATCTTGACC TGAGCGAGA GAAACGCAAC CTATGKATCT GCAAGZGAGA 720
 ATAAAGAGAG AACCCACAGG CTCACCAATG TACTCTTACA CAACAGATGG GAATGACACC 780
 GTGACAGAGT CTTGACATGG CTTTGGGAT ACAAATCAAA CTCAACTGTT CCTAGAACAT 840
 AGTCTACTGA GGGCCAAATC CACTAAAGGA ATCTATCTGT GAGTCTGTAT TTCTGTCTGT 900
 GTTCTCTTGT CTCTCTTGTG TGTCAATATG ATTTCTTCCA AAGAGAGTGT 960
 CACAACAAAT GATGATTTT TACTGAGCTCT CAAATTAAG CTTTGCAAA TGCTGTTGAA 1020
 AAGGAGTCC AAGCAGAAGA CAATATCTAC ATTTAGAATA GTCTTTATCG CACGAGCTAA 1080

30

Seq ID NO: 49 DNA Sequence

Nucleic Acid Accession #: NM_004932.2

Coding sequence: 327..2699

35

1 11 21 31 41 51
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 ACTTCATTCA CTTGCAAACT AGTGTGTGCC CACAAGAGCC AGCTCTCCG AGCCCGTAAC 60
 CTTCGACATCC CAGAGCTGCG AGTTTCAAGCC GCGACAGCAA GAGCGGAGA GCCCGCAACC 120
 CGCGCGCGCG GCGCGCGCGA GCGCAGAGCA GCGTGGGCGG GTGCGAGGTT CTCGCGGAGC 180
 CGCAGGAGCC GACCAAGATAT AGCAATCTGAG ACCAGATATTA GCAAGAGGAA 240
 AGCAATGAG CTGATGATCC TGCGTGTGAA AAGGCACTTC CAAAGATGGG GCATCACTA 300
 CCGACAGACT CGAAGGTGCT ATCAGCATGA GCACTTACCG CTACTCTGT CTGCTCTTGT 360
 GGGTGGGCGC GCGCTACCCA ACTCTCTCAA CTCCACTATC AAGAGCAACT AGTGGTTTTC 420
 CAGCAAGAAA AAGGGCGCTG GACTGATATC TTGACCATGT GAACAGAGTG AACGCTTGAT 480
 AAGAGAGCTG GATTCAGATC CAGTCTCTTC TCTGSGAGA ATACAGAGGA TCCGATAT 540
 AGTATGTGGG CAACTTACAT TCAGACAGG ATAGAGGAGA TGATCACTT AAATATATCC 600
 TTTCAAGGGA TGGACAGAGA GATCTCTTCA TTATTAATGA AATCAGAGCG GACATACAGG 660
 CCACACAGAG GCTTGAGAGG AAGAAAACCG CGTGTTCAT CTCTGAGACT CAAGCTATAA 720
 ACAGAGGAG AAGGAGAGCC GTGAGCGCCG AGTCTGATAT CATCATCAG ATCATGCA 780
 TCAATGCAAA TGACCAATA TTCAACAGG AGGTTTACAG AGGCATGTC CCGAATATGT 840
 CTGATGTGGG TAACTTTGTT GTCCAAGTCA CTGCGAGCGA TGCAATGAT CCACATATGT 900
 GGAACAGTGG TAAAGTTGTC TACGATATTC TACAGGGACA GCGCTATTTT TGAATGAT 960
 CAGAAACAGG TATTATCAG AGCTCTTTC TCAACATGTA TCGAGAAAC AAGGAGGAT 1020
 ACCAAGTGT GATTCAGACC AAGGATATGG CGCGCCAGAT GGGAGATTA TCTGGGACA 1080
 CCACTGTGAA CATCAGACTG ACTGATGTCA ACGACAACCC TCCCGATTCT CCCAGAGTA 1140
 CATACAGATT TAAACTCTCT GAATCTCTCC CACCGGGGAC ACCAATGGG AGAATCAAG 1200
 CTACAGAGCC TGATATGGA GAAATGCTCA GAATATGATTA CATCATGCA GAGGTGAG 1260
 GCGTGGATAT GTTTGATGTC ATCAACGACC AGGAACCCA GGAAGGATAT TAACTGTCA 1320
 AAAAGCTTCT GCACTTTGAA AAGAGAAAG TGTATACCT TAAATGGA ACGCTCCAATC 1380
 CTATATGTTA GAGCTGAGTT TCTCACTGTT GCGCTTTCGA AGATTACGCC ACGTGTAGAA 1440
 TTGTGTGGA GATATGATG GAGCAAGCTT GATCTGAGCA ATCTGAGTAT ACTTACAAA 1500
 TAAAGAGA TGTGAGATTA AACAACCA TACGTCTGCT CACAGGCCAA GATCGAGATG 1560
 TCGCAGGAA TCTGTCTNAG TACTCTGTAG ATGACACAC AGATATGAC AGAATATCA 1620
 ACATGTATTC TGGAAATGGT TGGATTTTA CATCAAACT TCTTGACGA GAACACTGT 1680
 TATGGCAGCA CATTAAGGTG ATACAGACAG GACCAATTA TCGAATGAA ACTGATGAG 1740
 TACCTTATA TATTAAGATT CTAGATGTCA ATGACAGG CCGAGATT CTGAGTGTCT 1800
 ATGAAATCTT TCTCTGTCAA AAGCAAAGG CAGATCAGTT GATTCAAGCC CTGACGTCTG 1860
 TTGACAAGCA TGACCCTTAT AGTGGACACC AATTTTCTGT TTCTCTGGCC CTTGAGCAG 1920
 CCAAGTGGTC AACTCTTACC ATTACAGACA ACAAAGACA CACCGGGGA ATCTTACTCT 1980
 GGAATATGG CTATTAAGTA CAGCATATGA GCACTATCT CTCTCTGTG GTCATTTCAG 2040
 ACAACACTTA CCGAGTTCAA ACGACAGCTG GGCACATGAC TTGCTGGGCT TGTCTATGTT 2100
 ACACCAAGG GAACATCAA TCTCGCATG GGGAGGAGCT GATCAACCCC ACGGAGTGT 2160
 CACAGGGAGC TTGTGTGCC ATCTCTCTGT GCKTGTGAT CTACTAGTGT ACGATGTGTC 2220
 TTTTTCGCG CTATTAAGTA CAGCAATGA AAGAGGCT CTCTCTGCT AAGAGAGCA 2280
 TCAGCATATA GATCTCTGCT TACACGAGG AAGGTGTGTG AAGAGAGGAC ACCAGAGCTT 2340
 TTGATATGG CACCTCGAG AATCCTGAAG CATAAGAGA CAACAATTA CGAAGGAGCA 2400
 TTGTGCCGGA AGCCCTTTTC CTACGCCGAC GCACTCTAAC AGCTCGGAC AACAAGATG 2460
 TATGAGATT CATTAGCA CAGTATAGG AATATGAC GAGGCCACT GCGCCGCTAT 2520
 ACCACTCTT GCGCCATCTG GCGTATGAG GCACTGGCT CTGGGGGCT TGTCTGATCT 2580
 CCGTAGATCT AGTACAGCG GATOCAGCT AGCACTATGA TTAOCTTAGT GACTCGGGAC 2640
 CTGATTTCAA AAGGCTTGA GATATATGT GAGAGTGGA CAGTACAAA GACTCTAT 2700
 CTGTCTCTCT TTGATATTC CAGGATCTCT GTTCTACCC TTCCAAAAT CAATGGCTC 2760
 ATTATCTGAC TACTCGTGA AGGCTCTCT GTTCTACCC TTCCAAAAT CAATGGCTC 2820
 AGTCCGTGTG GATCCAAATG TAGAGACTTT TTTCTACTAC ACTTTATCA CTTCAAGG 2880
 GAGCAATTTT TATTTTATG TGATCAAGT TAAACAAGTC AGGCCAAGG CGAGTGCCG 2940
 GAGGGAGAGA CAGGGAACAG TATTTCACAT TGTCTCAGG CAGGCTGCC GCTTCTCCCT 3000

PCT/US02/29560

Seq ID NO: 50	DNA Sequence						
Nucleic Acid Accession #1	Eos sequence						
	11	21	31	41	51		
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35	ATTTTCTTCA	ATTATTAGAC	TCTTAGAAGA	CAAAACCAAC	AAAAGAGAC	CTATTCAGAG	180
	ATGCGTGAAT	CTTTTGTGA	AGAGCGGGCC	ACCTCTGAGC	AAAGATGTAT	AAAGATGTAT	240
	ATGCAATGAC	ATGCTGATG	ATGCTGATG	ATGCTGATG	ATGCTGATG	ATGCTGATG	300
	ATACCCCTCA	ACTAGAAAT	TTGTATGGGA	CTGACATGAT	CTCTTGCTTA	TGAGTGTTCC	360
	TTGTGTCCAA	AGACATGAT	GATCTAGTAG	ATAATGCTGA	GAGTGTATAT	TCCCGCCAGT	420
40	AAATCTCTCA	GGGCGTGATC	CTGCTCAAT	TAAATGCTGA	AGGTGTATTA	ATAATAAACA	480
	AAATCTCTCA	AAATCTCTCA	AAATCTCTCA	AAATCTCTCA	AAATCTCTCA	AAATCTCTCA	540
	GCCTAATGCT	TTTAGTGTG	AMCATCTGA	GAGGCCATCA	CACTTATATA	TAAAGCTGCT	600
	CTTTAGGAGC	TCTACCTCTA	AGCTATAGAA	ATATATCTCA	AGGAAATTTA	TACAGTGCGT	660
	TTGAGAGGCT	CTCATGCTG	TTCCGACGAG	GTGACTTTTA	CAFFTGCTAC	ACAGCATGCT	720
45	ATGAGTAAAT	AAAAGCTTAG	AGAGGTGGTC	TCCGACATCA	TATCTAATA	TAACTGAGCC	780
	TCCACAGAAA	GACGACATCT	TCATTAAGTG	GGAGATCTTG	TTCCGACAGC	CTGGGTCGCT	840
	GCCTCTATTC	CTAGATTATC	CCCTATTAGG	GAGAAATTTG	AGTTTGGTGT	TGCTGGTGT	900
50	TTGAAAAAAA	AAAAATAAAA	AAAAATTTAG	AACTTTTGAC	AGCCTCTTGG	CTGCTATATC	960
	TCGCTCTCTG	TCGCTCTCTG	TCGCTCTCTG	TCGCTCTCTG	TCGCTCTCTG	TCGCTCTCTG	1020
	CTGCTCTCTG	CTGCTCTCTG	CTGCTCTCTG	CTGCTCTCTG	CTGCTCTCTG	CTGCTCTCTG	1080
	ATTTTCCCCA	ATAATAAAT	AAATTAAGAC	ATAATTAAGG	TATTTACAAA	AGGGGGATAG	1140
	ATTTAAGAT	CTGTGACGA	TAAGTGGAA	AAATTTGACA	TGCGAGACAT	ATAACTCTG	1200
	ATTTAAGAA	ATTTTATGAA	ATTTTATGAA	ATTTTATGAA	ATTTTATGAA	ATTTTATGAA	1260
55	CTTTCTTAGA	AGGGTTATAG	CTCTCCAACT	AAATATGGTC	AGGGTCTGAT	ATTTTATGTA	1320
	GAGAAATAC	CTTTATAGAA	TATTTATCAA	AGATATGGTC	AGGGATAGTA	AAATATGCTG	1380
	GACCTATAGA	CTGATCTAAG	ATTTAGAGAG	ACCAATATAT	ATCTTCTATAT	TCCTCTGGAA	1440
	CTGATCTCTG	CTGATCTCTG	CTGATCTCTG	CTGATCTCTG	CTGATCTCTG	CTGATCTCTG	1500
	TTGTTATTTT	TTCTACTCTA	TATCTGATCA	AGAGATGGTG	TGGTGTATTT	TAAACAGCAT	1560
60	TAGACTCTGT	GAATTTTITG	GTCCCTCTTT	ATTAATATAC	ATTTCGACAA	AGATTCTGAT	1620
	TGTATGAAGA	TAATTTATGA	GATTACATCA	TAAATGATCT	TGTATGAGGA	TACATTTCCA	1680
	ATAGTGGGGG	ACTATATATG	ATGATGATAT	ATGATGATAT	ATGATGATAT	ATGATGATAT	1740
	ACTATATATG	AGATTAATAT	ATTTATGAT	GTGCTGTCTT	CCGCTGGAAA	ATGAAATTTG	1800
	CTGATAGAG	TAGATTAAGT	ATTATGAAT	TTAGTGTGTA	CCGAGAGTAT	ACTCTTGAT	1860
65	TTCTCTTTCA	CTGATCATAT	TTTATGGTGT	TGTAGTATTA	AGAAATCTTC	AGATCATGAT	1920
	TTCTCTTTCA	CTGATCTCTG	TGGGATATCT	ATTTATAGGC	AGATCTGCTG	ATCTGTGATG	1980
	ATATAGAGGC	ATATAGAGGC	ATATAGAGGC	ATATAGAGGC	ATATAGAGGC	ATATAGAGGC	2040
	TTCTAAGAT	ATTATTTGAT	TATATAAAAT	GGATGGGCTA	AGCAGACATG	TCATTTATTT	2100
	AGGCGGGGG	CGGTGTGCTA	CCGCTGATAT	CCGACATGAT	TGGGAGAGAT	AGGGGGGAGA	2160
	ATGCGTTGTA	CGGCGGAGGC	GGAGCTGTGA	GTGACGAGAT	ATGCGCGAAC	TGCGTCTCAT	2220
70	AGGCGGAGGC	AGAGCGGAGC	TTCTGCTTCA	AAAAAATAAA	AAAAAATAAA	TTTATGATAT	2280
	CCC						2340

[illegible]

PCT/US02/29560

Seq ID NO: 52		RNA Sequence		Nucleic Acid Accession		E: Eos sequence		Coding sequence: 641..2299	
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	GAGCTGGCCG	GAGCGCTTGG	CGTGGGCGCG	CGGCGGTCAG	CCAGCGAGAGT		TCGGTGTCGG		620
	GGGGCGCGCG	AGGCGCCCTCT	CTCAGAGCCG	CGCTCATCGC	CGATCGGGCT		GCCTCCGAGT		180
50	AGCGCTCTCT	AGCGCTCTCT	ATTCTCTCT	CGCTCTCTCT	CGCTCTCTCT		CGCTCTCTCT		240
	AGCGCTCTCT	AGCGCTCTCT	ATTCTCTCT	CGCTCTCTCT	CGCTCTCTCT		CGCTCTCTCT		300
	CGCGCGCGCG	AAAGCGCGCG	CGGCGCGCGG	CGGCGCGCGG	GTGGCGCGCG		GGGGAGCATC		360
	TCGGCGCGCG	CGCGCGCTCT	CCCGCGCGCG	CGCGCGCGCG	CTCTGGCTCT		CTCTGGCTCT		420
	CTCTGGCTCT	GTCTCGCGCG	GGCGCGCGCG	CCCGCGCGCG	CGCTCTCTCT		CTCTGGCTCT		480
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		540
55	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		600
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		660
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		720
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		780
60	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		840
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		900
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		960
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1020
65	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1080
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1140
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1200
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1260
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1320
70	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1380
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1440
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1500
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1560
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1620
75	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1680
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1740
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1800
	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG	CGCGCGCGCG		CGCGCGCGCG		1860
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PCT/US02/29560

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WO 03/025138

PCT/US02/29560

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Seq ID NO: 55 DNA Sequence
Nucleic Acid Accession #: NM_001218

Coding sequence: 1..1080

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Seq ID NO: 56 DNA Sequence
Nucleic Acid Accession #: BC000278

Coding sequence: 113..1144

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PCT/US02/29560

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Seq ID No: 57 DNA Sequence

Nucleic Acid Accession #: NM_06632.1

Coding sequence: 377..1582

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Seq ID No: 58 DNA Sequence

Nucleic Acid Accession #: NM_003058.1

Coding sequence: 145..1812

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PCT/US02/29560

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 CTGAGGCCCTA TCAACTTAGG TCTAGGCCCA GTGAGTCTTA TTGTCTACGT TGGAAAAATA 1980
 CCGATGGGAC CAGTCTCTCG CAATCTCTG CAGCTCACTT TATCTACAGT ATTCCTAGGA 2040
 CATTGACATC TGGTTTTCTG GAGGTTTTTT TTTCGATCT TTGTATTTTT TTAATTTTGA 2100
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Seq ID NO: 59 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 227..2311

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 30 GTCAAGGGGCG TGTGGAGCCG GCACAGATTG AGCGAGGHTG TCGCCCGGCTG GGGGAAGTG 60
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 TGGCACATA GAGCAAAAA TTTTACATT TGAATAAGGA GTTCTTAAAT AAGTGTGCC 1140
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TTAGCTTTTC CANTGCGAAG TAGACAGGAT ATGTTCCAGG TTTCTCGAC TGTAGGCACA 3420
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 40 GCCACGCTA TTTGTATCCA ATTTAACTT AGGTTTGTGT TCTTGAG 5687

Seq ID NO: 60 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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 AGCATTCCC AATGCTGAT AGAACGNTCC CAAKACATAA TGCCAGTGTG CAAAGCATGG 240
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 50 AATTACTTGT GATCATAGTA GTAGTGTGAT TGCCAAATGT GCTAAAGGCC AATGAATAT 360
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 TTTATGACA AATTAAATC CCAATATGCTT GAATATGATA ATGCTGTCAAT TTTAATCT 540
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 55 AAATTATTAC TGTGAAATTT TTTTATTTGT AGTAAACGGA GTATGCAATT TTAATTTCCT 660
 GTACACA 667

Seq ID NO: 61 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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 GGTAAAGAAA ATGGGTGATG TTTATAGCTT TTTGTCTCCA ATGATATGTT CCGGACAGA 420
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 70 GCGCAAAAG TCAAGGTGTC AGTGAGCTGT GATGTGCGCA CTGTATCCCA ACTCAT 537

Seq ID NO: 62 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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 80 GTTGTCAGAT AAACAGGTT GGACCAATAT AAAGGAAATA TAAATTAAGG TGGTTTATTT 240
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 TAGACAGTAT TGAATGTGTA ATAAATATTT GAAGTGACAT GTGGTGGGAC ATAAATCAAG 480
 ACTCAGTAAA TTTGAAJAGA TTCAATATCA TAAAGGATAT ATGATCCAGC CTTAGTAGAGA 540

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GTACAGGAAA TTTAAAAAAT GTAACATAAA TATCTTTAAT TTGTGAAATT AGAAAAATAC 600
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 ACCACCATGT CCAGCCAAATT TTGTAATTAT AGTAGAGACA GG 702

5 Seq ID NO: 63 DNA Sequence
 Nucleic Acid Accession #: AK025967

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 15 AGCATATAT ATGACCCAGG AGGTGGACAA CAACTGCCCT TGGTGGAAAC TCTGTCTTTT 420
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 AAATTGMAAA AAAAAAAA 1390

35 Seq ID NO: 64 DNA Sequence
 Nucleic Acid Accession #: Bos sequence

1 11 21 31 41 51
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 GCTCTTAATT TAAATAAAAA GCTTACATTT AAAAACTTGA AAAAAAAA AAATAAAAAA 2700
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 CTG

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PCT/US02/29560

Seq ID NO: 65 DNA Sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 1..1863

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	CAGCTCACCA	CGCTTCCACCT	CAGCAACCCCT	CGCGAGAGCC	CGGTGGAGCC	CCAGAGATCG	180
10	GAGACTCTGT	GCAAGAGAT	GGACTTTCTC	CTGTCCCGTA	TTGGTCTGTG	TGTGGAGCTG	240
	GCCAACGCTCT	GGGCGTCCCT	CTACCTGTGC	TACAAAAATG	GTGGCGGTGC	CTTCTGGATC	300
	GGCCAGCTGC	TCTTTCATGT	CATTGCTGGG	ATGCCAATTT	TCTCATGGA	GCTGGGCCCT	360
	GGCCAGTTCA	ACAAGGAAG	GGCCGCTGGT	GCTCTGGAGA	TCTGCCCAT	CTGGAAGAGT	420
	GTGGCTTCA	CGCTCAATC	CACTTCAGTC	TATGTGGAGT	TCCTCTGAT	CGTATGATC	480
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	AACAATCTCT	GGAAAGGCC	CAACTGCTCG	GATGCCCATC	CTGTGTACTC	CAGTGAGAGC	600
	AGCTCGGCGC	TCAACACAC	TTTGTGGAGC	ACAGCTCTGT	CCGAGTACTT	TGAAGTGGC	660
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	ACCTCAAGGA	AGGTGTGAT	GATCAACGCC	ACCATGCCAT	ACGTGTGCT	CACCTGCCCT	840
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	AACCTGTACA	GGGACGGAT	TGTCAACACC	TCCATCACT	CCCTGACGAG	CTTCTCTCTC	1080
25	GGCTTGTCTG	TCTTCTCTCT	CCTGGGATAC	ATGGACAGA	AGCACAGTGT	GGCCATGGGG	1140
	AGCTGTGGCA	AGGACGGCTC	AGGGCTGATC	TTGATCATCT	ACCGGAGAGC	CATCCACAG	1200
	CTCTCTGGTG	CTTGACAGCT	GGCCGTGCTC	TTCTTCATCA	TGTCTGCTAC	CTTGGGTATC	1260
	GACAGGGCCA	TGGTGTGAT	GGAGTCACTG	ATCACCGGGC	TATCATGATG	GTTCACAGCT	1320
30	CTGACACAG	ACCGTGAAGT	CTTCAACGCT	TTTCATCTGC	TGTGGCATCT	CTCTCTGTCC	1380
	CTGTTTCTGG	TACACAGGG	TGGATCTAC	GTCTTCAAGC	CTCTGGAGCA	TTTGTGAGCG	1440
	GGCACTGTCA	TGCTCTTTT	AGTGTCTCAT	GACATCACTG	GAGTGGCTCG	GTTCATAGTG	1500
	GTGGGCGAGT	TCAACGACGA	CATCCACAGC	ATGACCGGGC	AGCGGCGCAG	CGCTACTGCT	1560
	GGGCTGTGCT	GGAGCGTGGT	AGACCCCTGC	TTTCTCTCTG	TGGTGGTGGT	GGTCAAGTCT	1620
	GGGACTTCTA	GGGACCCCCA	CATGCGAGCC	TAGACTCTTC	CCGATCGGCG	CAGACCGCTG	1680
35	GGGCTGTGCT	GGGACCGCTG	AGGCTGTGCT	ATGATGCGCT	CTATTGCGG	CTACACAGCT	1740
	TGCAACCTGC	CTGGGTCCTT	TCCAGAGAAA	CTGGGCTAGC	CCATTGCGAC	CGAAGAGAGC	1800
	CGTGAAGCTG	TGGACACAGG	GGAGGTGGCG	GAGTTCAAGC	TCCGCCACTG	GCTCAAGGTG	1863
	TAG						

Seq ID NO: 66 DNA Sequence
Nucleic Acid Accession #: NM_022073.1
Coding sequence: 327..1046

45	1	11	21	31	41	51	
	GAGTCTGGCC	CGAGTCCCGG	CAGTGGTGGC	TTCCCATCCC	CAAAAGGCGC	CCTCCGACTC	60
	CTTCTGGCCG	ACTCTTCGCG	GGGCGAGTCC	GGAAACGGGT	CGTGGAGCTC	CGCACCATCT	120
	CCGCTGGTTC	CCGAAAGCAG	ATCCCTTTCT	CCGAGAGGTG	CCGAAACTCT	TCCCTTGTCC	180
	CCGACGCTGC	AGCGGTGGTG	GTACGTTGGC	AGCGCGACTG	TTCTCAAGCC	GGGCGCACGC	240
	TCCCGCGCCG	TGGGCTTGGC	GCTGCTGTAG	ATGCTTCCCT	CTCTGGTTCG	AGCCTGGGGA	300
50	TCCCGGACCT	CGATTCTCGG	GGCGAGATCC	CCCTGGAGCA	CATCATGAGG	CTGAGCTGGG	360
	AGAAATTTGC	CTCTGGAGTAC	ATCGTGGCCT	CTGTGCAGCA	GGTGGGCTTC	TGTCTAGCTG	420
	ACACCTTCTC	GGCGGGGTGT	GTGGGCGACT	GGTCTGTGGA	GGCGGTCAAG	CAGCTGGACT	480
	CGACCCGGGC	CTCGCGGGAC	GGCGAGCTGG	CGGGGCGCGG	CGCGGGGCTC	TCCAAAGGAC	540
	GGCTTCTCTC	GGTCCATCAT	GACAGCATGG	GGGGCGCTCG	GGAGCGCTCG	GAGGCCATCAT	600
55	ACTCATCTCA	GGATGAGTGT	AGGACATGTC	TGGTCTGTGA	TCCGCGAAAT	GGAGAGAGTG	660
	ATGTTTCCCA	CTGTGCACAC	CCCAACGGTG	ATGGTCCGTG	CATCACTGCG	ATCTACTACT	720
	TGAACAGAAA	TGGGATGGCC	AAGCTACATG	GTGGGATCTC	GGGGAATATT	CCAGAGGGGA	780
	AATCATCATC	AGCAGATGTG	GAGCCCAATT	TTGACAGACT	CTGTGCTTTC	TGTGAGACTC	840
60	GTAGAGAGCC	ACGAGATGTC	CAGCGCTCTC	AGCGACAGCG	CTATTGCGGG	ACTGTGCTGT	900
	ACTTTGATCG	TGAGAAAGAG	CGAGAAAGCA	AAAGAAATTT	CAGGAATTTA	ACTGAGGAAA	960
	CTGAATCTGC	CCTCACTGAA	GACTGACCGT	GCTCTGAAAT	CTCTGGGCTC	TGTTCAATTT	1020
	AGTAAAGGTT	CTGGAATTTCT	CTTAAATTTCT	TTGAGATCTG	AMAGTGGCTC	CTTCAGTGAC	1080
	AGTAACTTCC	CTCTCTACTCT	TGGATCTCTT	CAGATCCGCT	TCTGTGTGCT	GGTACTCAT	1140
65	GTTTTCTTCC	GAGACCTGTG	TGATCTTCCA	GATACTCTCT	TTCCCGATGG	AAGTATTTTG	1200
	CTAACTCCAG	AAATCTCTGC	AGACATCTCA	CTGGGCGACG	GGTTTACTGT	ATAGATTCGG	1260
	TAAATATATC	AAGAGAGAGG	CTAGAGAGCA	CAGCAGGGGA	ATGAACCTTT	CTGTGACTTT	1320
	ATGTATATCT	CCGATTTTGA	AAGAGAGGAG	TTGTGAGAGA	AAAGAAATGA	GGTGTGATAT	1380
	GCACACAGGA	GGATCGCCGG	AGGCTTTAAC	ACGAGGAAGC	AGAGAAATTT	GTGTCACTGT	1440
70	ACAAATTTCC	AGATCTTCTT	AATCCAGGGC	TGTTTGGGTT	TCTGGAGAAAT	TATCAACACC	1500
	TAAATGACAT	AATACCTCTA	GAAGGGGCTG	CTGTCACTAT	GAAACAATTTA	TAAAGTCTCC	1560
	ATGGGGGAGA	CAGTCTCTTT	TTGCCAGTCC	TGGAACTTGG	ATTTTCTGCC	TGACGTCCAC	1620
	TTTCTTGAAA	ATATGATGAT	TTCTGAATAA	GATGCGACAA	CAATTTTCTT	TGCATTTTCA	1680
	GCTTCTAACT	GGGAAACTTA	TTTCCCGAAA	ACTTAAAGAC	TAGACATTAG	TGTTTGTGGT	1740
75	TGTTTGTGTT	GAATGGAAAT	TAAATTTAAA	TGAAGGAGAA	AATATATCCC	TGGTATAGTT	1800
	GGTGTAAACCA	GTATATATAT	TGGAAGAGAG	TAGGTTCTACT	GATATACAAI	AAAGATGTGT	1860
	GACTCTTGAA	CATTATGATG	GGGAGTAAAG	TTGGGCTGTCT	CTTGTTTTGT	CTCTTTTCTT	1920
	TTTTTTTTTT	TTTTTTTTTT	AGTTTCTCTT	TTTAAATGAG	TCAACCTTTA	ACACAAAAAA	1980
	AGCAGGGTGA	TGTATTTTAA	AAAGGAAGGT	GGAAATATAA	AAATCTCAAA	GCTATTTGAG	2040
80	TTCTCTCTGC	TGCTTAGCAG	CTTTTCTTCA	GCTCAACTTG	CTCTCTAGAT	ACAGTGTGTT	2100
	TGGGCTGATC	ACGAGAGTGA	TGGAACTTGT	TAGAACTTGT	GAACTCTGAT	CTCTCTGAGT	2160
	AGACAGAGAT	CGACCTGCTC	GATTAACCTGT	GTATTGAGCA	CGTATTTTGC	AAAGCTGAGT	2220
	TGCTTAGTGT	TTCAAGTATTA	CTTTCACTAT	TTAAAAATCC	CTTTAATTTT	TTGCTTGAAA	2280
	ATCCCATGAA	CATTAAAGAG	CAGGAATAT	TTTCTCTTGT	TATGTACGGA	TATATATATA	2340

WO 03/025138

PCT/US02/29560

5
TATATAGTCT TCCAGATAG AAGTTTACTT TTCTCTCTTC TGGTTTGGG AAATTTCAG 2460
ATAGACATG TCACCATTA TTCTCAACGA CTGCTCTATT TTGTTGTACG GTAATAGTTA 2520
TCACCTTCTA AATTACTATG TAATTACTCT ACTTAATTATG TTATTTGTCT TGATATCTTT 2580
CTCTGGAGTG TAAACCAAT GAAGACAGGA ATTTTGTTATA TTTTTAACTA ATGCACATTA 2640
CTCTGACAC CTAATTAAGT GCGGCGACGA TAGTAAAGCG TGGTAAATA CTGTGTGAT 2700
AAATCTGATC TCTCATTA CTATTCTAA AAAAAAAAAA AAAAAAAAAA 2760
AAAAAAAAAG 2770

Seq ID NO: 67 DNA Sequence
Nucleic Acid Accession #: NM_139314.1
Coding sequence: 196..1416

10
1 11 21 31 41 51
| | | | |
15 ATAAAAACCG TCTCTGGGCG CGGCGGGGAG AAGCCGAGCT GAGCGGATCC TCACACGACT 60
GTGATCCGAT TCTTTCCAGC GGCTTCTGCA ACCAAGCGGG TCTTACCCCC GGTCTCTCCG 120
GTCTTCAGTC CTCGACCTG GAACCCCAAC GTCCCCGAGA GTCCCCGAAT CCCCCTCCCC 180
AGGCTACTTA AGAGAGTAGG GGGTCTCCG ACCGCGGGGG CAGCCTTGAT GCTCTCGAGC 240
GCCACCGCG TGTAAGTAGG GGTCTGAGGG GAGCCGCTCG AGTCCAACTG GCCTGCTTT 300
GGTCTCTGGG ACGAGATGAA TGTCTCGGCG CACGACATCC TGACGCTCGG CCAAGGGCTG 360
CGCGAACGCG CGGAGCGCAC CGCAGATCAG CTGAGCGGCG TGGACGGGCG CCTGAGCGCG 420
TGGCGGTCCG CCTGTGAGGG AACCGAGGGG TCACACCGAC TCCGTTAGC CCTGAGAGAC 480
CGGTTGACG CTGAGGCTCT TCACAGCTCT GACGACAC TCGAGGCTCA GACGACGAG 540
ATCCAGCGAC TCTTCCACAA GGTGCGCCAG CAGCAGCGCG ACCTCGAGAA GCAGCAGCTG 600
GGAATTGACG ATTCGCAAGG CCAAGTTTGG CTCTCGAGCC ACAGACACT AGACATGAG 660
GTGGCGAGC GTGCGCGAGG AAGAGGCTG CCGAGATGAG CCGACACGAG TGACCGGCT 720
CACATGTCG GCGGCTGCA GGGCTGCC AGGATTTGCG AGAGCTGTT CAGGTTGG 780
GAGAGCGAGA GTGACTATT TGAATCCAG CTTCAAGGGT TCTCCGATT TTTGTTGAC 840
TGCAATGATG CCTCAGTAGG AGGCTGACGA GTAATTTCAGA GCGCGCAGGA TGCTCAGTG 900
TGACTAACG GGGCTTGAGA AGCTCAACAG CGGGGGTTTG GGGATCCCGA CGGGGAGTTC 960
TGGCTGGGTC TGGAGTAGG GATGAGTAGG ACCGAGACCG CTGAGCGGCT GACCTCGAGC 1020
CAGCTCGTGG ACTCGGATGG CAGCGCGGAG TTGCTGGAGT TCTCCGTGCA CTTGGGTGGC 1080
GAGGACGCG CCTATAGGCT GCAGCTCACT GCACCCGTGG CGGCGAGCT GGGGCGCAC 1140
ACGCTCCAC CAGCGGGCTC TCTCGTACCT TTCTCCACTT GGGACAGGCA TCAGACACTG 1200
CCGAGGACCA AGACTTGCGC CAGACGCTCT TCTGAGGCT GGTGTTTGG CAGCTCGAGC 1260
CATTTCAAC TCACCGCGCA GTACTTCCGC TCCATCCCA AGCAGCGCA GAGGCTTAG 1320
AAGGGAATCT TCTGAGAGC CTGGCGGGGG GGTACTACG GCTCGAGGC CAGCACAATG 1380
TTGATCCAGC CCATGCGAGC AGAGGCGAGC TCTTATGGTC CTGCTGCGGC CTGTTCCAG 1440
GCCCGAAGA GAGGTTGACT CTGCTCTCTG CCGAGAGATG TGGCTTTCTC CTCTCTGGG 1500
AGGCTCTCA AGGATGAGC ATCTGGAATC TTGATCGAGG AGAGAGAGCA GAGACTCGGA 1560
GAGCGCCCTT TTCTGAGTGG AGGGGGGCTG CATGGTTTGC CTCTGAGAT GAGGCTGCA 1620
GGATATGCTC AGACTCTAGA GGCCTGAGCC AAGGGGCGAT GAGCTTCACT CTTCTCGAG 1680
CAGGAGTTTG GGGACTCAGA GGGACCACTT GGGGCGAGCG AGACTGGCTT CAATGCGGA 1740
CTGATCACA TTGATCGAGG GAGACCGGCG CTGTGTTGGG TCGAGAGGC CCTCATGTT 1800
CTGGTCTGT TTGTTGTAGG TCCCTTGGGG ACGACAGGAG GGGCCAACTG TATCTGGGG 1860
GAGTCAAG AGTTCTTGGG ATAAAGGCAA CCTCAGAAC CTTAATAAAA AAAAAAAAAA 1920
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 1967

Seq ID NO: 68 DNA Sequence
Nucleic Acid Accession #: NM_016109.2
Coding sequence: 196..1416

50
1 11 21 31 41 51
| | | | |
55 ATAAAAACCG TCTCTGGGCG CGGCGGGGAG AAGCCGAGCT GAGCGGATCC TCACACGACT 60
GTGATCCGAT TCTTTCAGAG GGCTTCTGCA ACCAAGCGGG TCTTACCCCC GGTCTCTCCG 120
GTCTTCAGTC CTCGACCTG GAACCCCAAC GTCCCCGAGA GTCCCCGAAT CCCCCTCCCC 180
AGGCTACTTA AGAGAGTAGG GGGTCTCCG ACCGCGGGGG CAGCCTTGAT GCTCTCGAGC 240
GCCACCGCG TGTAAGTAGG GGTCTGAGGG GAGCCGCTCG AGTCCAACTG GCCTGCTTT 300
GGTCTCTGGG ACGAGATGAA TGTCTCGGCG CACGACATCC TGACGCTCGG CCAAGGGCTG 360
CGCGAACGCG CGGAGCGCAC CGCAGATCAG CTGAGCGGCG TGGACGGGCG CCTGAGCGCG 420
TGGCGGTCCG CCTGTGAGGG AACCGAGGGG TCACACCGAC TCCGTTAGC CCTGAGAGAC 480
CGGTTGACG CTGAGGCTCT TCACAGCTCT CAGACACAC TCAAGGCTCA GAGACGAGG 540
ATCCAGCGAC TCTTCCACAA GGTGCGCCAG CAGCAGCGCG ACCTCGAGAA GACACACTG 600
GGAATTGACG ATTCGCAAGG CCAAGTTTGG CTCTGAGCC ACAGACACT AGACATGAG 660
CGGTTGACG CTGAGGCTCT TCACAGCTCT CAGACACAC TCAAGGCTCA GAGACGAGG 720
CACATGTCG GCGGCTGCA GCGGCTGCC AGGATTTGCG AGAGCTGTT CAGGTTGG 780
GAGAGCGAGA GTGACTATT TGAATCCAG CTTCAAGGGT TCTCCGATT TTTGTTGAC 840
TGCAATGATA CTTGATGATG AGCTGACGA GTAATTTCAGA GGGCGACGA TGCTCAGTG 900
GAGTTCACG GGGAGTAGG GAGGCTGCG AGGATTTGCG AGAGCTGTT CAGGTTGG 960
TGGCTGGTCT TGGAGTAGG GATGAGTAGG ACCGCGGAGC GGAACAGCG CTTGCGCTG 1020
CAGCTCGGGG ACTGGGATGG CAGCGCGGCG TTGCTGAGAT CTCTCGTGA CTTGGGTGGC 1080
GAGACAGCG CCTATAGGCT GCAGCTCACT GCACCGTGG GGTGCGAGCT GGGGCCAC 1140
ACGCTCCAC CAGACTTGCG CAGACGCTCT TCTGAGGCT GGTGTTTGG CAGCTCGAGC 1200
CCGAGGACCA AGACTTGCGC CAGACGCTCT TCTGAGGCT GGTGTTTGG CAGCTCGAGC 1260
CATTTCAAC TCACCGCGCA GTACTTCCGC TCCATCCCA AGCAGCGCA GAGGCTTAG 1320
AAGGGAATCT TCTGAGAGC CTGGCGGGGG GGTACTACG GCTCGAGGC CAGCACAATG 1380
TTGATCCAGC CCATGCGAGC AGAGGCGAGC TCTTATGGTC CTGCTGCGGC CTGTTCCAG 1440
GCCACAGAA GAGCTGACT CTGCTCTCTG CCGAGAGATG TGGCTTTCTC CTCTCTGGG 1500
GAGACGCTCT TTCTGAGTGG AGGGGGGCTG CATGGTTTGC CTCTGAGAT GAGGCTGCA 1560
GGATATGCTC AGACTCTAGA GGCCTGAGCC AAGGGGCGAT GAGCTTCACT CTTCTCGAG 1620
CGGAGGTTTG GGGACTCAGA GGCACACTT GGGGCGAGCG AGACTGGCTT CAATGCGGA 1680
CTGATCACA TTGATCGAGG GAGACCGGCG CTGTGTTGGG TCGAGAGGC CCTCATGTT 1740
CTGGTCTGT TTGTTGTAGG TCCCTTGGGG ACGACAGGAG GGGCCAACTG TATCTGGGG 1800
GAGTCAAG AGTTCTTGGG ATAAAGGCAA CCTCAGAAC CTT 1843

WO 03/025138

PCT/US02/29560

Seq ID NO: 69 DNA Sequence

Nucleic Acid Accession #: NM_001216.1

Coding sequence: 43..1422

	1	11	21	31	41	51	
5	GGCCGTACAC	ACCGTGTCT	GGGACACCC	ACAGTCAGCC	GCATGGCTCC	CCTGTGCCCC	60
	AGCCCTCAGC	TCCCTCTGTT	GATCCCGGAC	CCTGCTCCAG	GCTCTACTGT	GCAGTCTGCT	120
	CTGTCACTGC	TGCTCTGAT	GCCCTGCTAT	CCCGAGAGAT	TGCTCCCATAT	GCAGAGAGAT	180
	TCCCCCTTGG	GAGGAGCTTC	TCTGGGGGAA	GATGACCAAC	TGGGCGGAGA	GGATCTGCCC	240
10	AGTGAGAGAG	ATTACCCACG	AGAGAGAGAT	CCACCCCGAG	AGGAGGATCT	ACTTGGAGAG	300
	GAGGATCTAC	CTGAGAGGGA	GAATCTACT	GAATTTAAGC	CTAAATCTGA	AGAGAGAGGC	360
	TCCCTGAGAT	TCCAGGATCT	ACCTACTGTT	AGGCTCTCTG	GGATCTCTCA	AGAGCCCTCA	420
	AATATAGCC	ACAAGACATA	AGAGGCGGAT	GACCGAGCTC	ATTGGCTCTA	TGGAGGAGAC	480
	CGCCCTGTC	CCGCGGTGTC	CCAGAGCTGC	GGGCGCCGCT	TCCAGTCCCC	GGTGATATTC	540
15	CGCCCTCAGC	TGCGCGCTCT	CTGCGCGGCG	CTGCGCCCCC	TGGAACTCCT	GGGCTTCACG	600
	CTCGCGCGCC	TCCCGAGACT	GGCGCTGCGC	AACATGTGCC	ACAGTGTGCA	ACTGACCTGT	660
	CCTCTCTGCC	TGAGAGAGAT	CTGGGTGCC	ACCGGCTCTC	GCAGCTGCTT	GCAGCTGCTT	720
	CTGCACTGCG	GGGCTCGAGG	TCTCTCGGCG	TGGAGGCACA	CTGTGGAGAG	CCACGCTTTC	780
	CTGCGCGGAA	TCCAAGTGGT	TCACTCTCAG	ACCGGCTTTC	CCAGAGTTGA	CGAGGCTCTG	840
20	GGGCGCGCGG	GAGGCGTGCG	CGTGTGTGCG	GCCTTTCTGG	AGGAGGGGCT	GGAGAGAAAC	900
	AGTGCTCTAT	GAAGGATGCT	GTCTCGTTTG	GAAGAGATCG	CTGAGGAGAG	CTCGAGAGCT	960
	CAAGTCCCAAG	GACTCGACAT	ATCTGCACTC	CTGCGCTCTG	ACTTCGACCG	CTACTCTCAA	1020
	TATGAGGGGT	CTCTGACTAC	ACCGGCTCTG	GCCCAAGGTT	TCATCTGGAG	TGTGTTAAAC	1080
	CAGACAGTGA	TGCTGAGTGC	TAAAGCACTC	CCACACCTCT	CTGACACCTT	GTGGGGACCT	1140
	GGTGACTCTC	TGCTGAGACT	GAATCTCTCA	GGACAGCTCT	AGAGGCTGCT	TCTGTAGAAA	1200
	GAGGCTCTCT	TCCCTCTGCG	AGTGAACAGC	AGTCTCTGGG	CTGCTGAGCC	AGTCCACGCT	1260
	AATTCTTGCC	TGGCTGTGGG	TGACATCTCA	GCCTTGATTT	TGGGCTCTCT	TTTTGCTGTC	1320
	ACCAAGTCTG	CGTCTCTTGT	CGAGATGAGA	AGGAGCGAAC	GAAGGGGGGT	CAAAAGGGGT	1380
	GTGAGCAACC	CGCCACAGCA	GGTACCGGAC	ACTGAGGCTCT	AGAGGCTGCT	TCTGTAGAAA	1440
30	TGTGAGAGAC	CA GCGAGAGC	CA TCTGAGGG	CG AGCCGGTA	ACTGTCTGCT	CTCTGCTACT	1500
	ATGCCACTTC	CTTTAACTGT	CGAGAAATTT	TTTTAAATAA	AATATTTATA	AT	1562

Seq ID NO: 70 DNA Sequence

Nucleic Acid Accession #: NM_003039.1

Coding sequence: 107..1612

	1	11	21	31	41	51	
35	CTTCTCTCTC	CATTCAAGTC	ACCGCTTACT	TGGCTAAAAA	GGAGGTGAGC	GGCAGCTCTGC	60
	CCTTCCAGAG	CAGCAATGGA	GCACCAAGAT	CAGAGCATGA	AGGAAAGGAG	GCTGACGCTT	120
40	GTGCTGTGCC	TGGCAACCCG	GATAGCTGCG	TTTGGGTGAT	CCTTCCAGTA	TGGGTACAAAC	180
	GTGGGCTGCT	TCAACTCCCC	AGACGCTCTC	ATGCAACATAT	TTTACATAGA	GACTTACTAT	240
	GTGTGAGAGC	GTGATCTGAT	GAATGACCTT	CTCTTACAGT	TTTGAACCTG	TTTGAACCTG	300
	TCCATCTTTC	CATTTGAGGG	GTTTATCGGA	TGCCCTGCGG	TGGGCGCCCTT	GGTGAATAAA	360
	TTTGGAGAAA	AGGGGGCTTT	GCTGTTCAAC	AACATATTTT	CTATGCTGCC	TGGGATCTTA	420
45	ATGGGATGCA	GCAGAGCTGC	GCATCATTTT	GAGCTTATCA	TTATTTCCAG	ACTTTGGTGT	480
	GGAAATCATG	CAGGTGTATC	TTCAGACGTT	GTGCCCATGT	ACTTAAGGGA	GGTGGCCCTT	540
	AAAGACCTCC	GGGGGGCTTT	CGGGGTGAGT	CCCCAGCTCT	TCATCACTGT	TGGCATCTCT	600
	GTGGCCGAGA	CTTTGGTCTC	TGGGAATCTC	CTTGCACAGC	TAGATGGCTG	GCAGTCTGCT	660
	GTGGGGCTGA	CCAGGCTCCC	CGCGGGCTGT	GACCTCTCTC	TGCTGCGCTT	CTTCCCGAGG	720
50	AGCCCTGAGG	CGTGGAGCTG	TGTGGACAGG	GACGAGGCGG	CGCGCCAGAA	AGCCTTACAG	780
	CGCAGAGAGG	CCGCGGCTCT	CATCTCCGTT	CTGAAGCTGT	TCCGAGTCGG	CTGCTGGGCG	840
	TGGCAGCTCC	TGTCCATCAT	CGTCTCTCAT	GGGCGCCAGC	AGCTGTGGGG	GCTCAACGCT	900
	ATCTTACTAT	ACCGCGACCA	GATCTACTCT	ACCGCCCGGG	TCCCGGAGGA	CGACTGTGGG	960
55	TAGCTGAGCG	CGCGGCGGCG	GGGCTGTGAC	CGTCTCATGA	CCTTCTGCGC	CGTCTTCTGG	1020
	GTGGAGCTCC	TGGGTCGAGG	CGTGTCTGCT	GTGCTGGGCT	TCTCTCATCT	CCCTATAGCC	1080
	GTCTCGCTGC	TCACTCGACG	CTCGGAGCTG	CAGGACACAG	TGCTCTGAGT	GCCATACATC	1140
	AGCATCTGCT	GTGTGATCTC	CTAGCTGATA	GGACATGCCC	TGGGGCCGAG	TGCATATACC	1200
	GTGCTGTCTA	TCTATGAGAT	CTCTCTCGAG	TGCTCTGGGC	CATCTGTGCT	CTAGTGGGG	1260
60	GGCAGTGTGC	ACTGAGCTCT	CACTTCCACC	GTGGGCTTGA	TCTTCCCTGT	CATCCAGAGG	1320
	GGCCTCGGCG	CGTACAGCTT	CATTGTCTTC	GGGTTGATCT	GCTCTCTCAG	CACATCTTAC	1380
	ATCTCTTTGA	TGTGCCCGGA	GACCAAGGCG	AGAGGCTTCA	TAGAGATCAA	CCGATATTTT	1440
	ACGAGATGA	ATAGAGTCTC	TGAAGTGTAC	CGGAGAAAGG	AGGACTGTGA	AGAGCTTCCA	1500
	CCCTGTCACT	CGGACAGATG	ACTCTGAGCA	GGAGGCCAGT	CGAGCTGGTC	TGCCAGGGGC	1560
65	TTCCTCATTT	GCTATTTTGT	AGCTGTCTCT	AGATATCTCG	GAATATCCAG	AAATATAACA	1620
	ACTCTGATGT	GGAAATCGAT	CGCTCATCTC	AGCTCTCCCA	CCCGAGTGGG	AGAGTGTGAA	1680
	AGGGCGGCTG	TGCTTTCTCT	GAGACTGGGC	CGATCTGGCT	GATGTGGGCG	TGTGACAGAA	1740
	CCGAGTCAAA	TTAAAGCTAG	GGTCTCCGAC	TTTGCTGGTT	CGAGCTTCTG	GTGGCTCTCG	1800
	GTAACTGTGC	TCCACTCTGA	TGGGCTCAAC	TTTGTGTGGC	TGCTGGTAAAC	ATAACAGCAA	1860
70	CAGTACTACT	AGTGTGTAGA	TGGAGGAAT	CAAAATTTTC	CGAGAGAACT	AACTGGTGGG	1920
	CCGACACAGG	CTTCTCGGCG	CGATGGGAGT	TTGTTTAGAG	CGAAATCTAT	CCTCTTACCG	1980
	GATCTCTTTC	CAGAAATAC	TGTGTAGAAA	GGTGTGATGT	CGAGAAACAT	GACATCCAGA	2040
	AGGCTGAGGA	ACAGGTTCTG	GTGGAGACAC	TGAGTCAGAA	TTCTTCACTC	AAATATTTT	2100
	GTTAGTGAAA	AATGGAATGT	CTTCTGTGTA	GTCAATAAAA	TGAACCTGAT	CACATTTT	2160

Seq ID NO: 71 DNA Sequence

Nucleic Acid Accession #: NM_001252.1

Coding sequence: 138..719

	1	11	21	31	41	51	
80	GGCTGTGCCC	CTGACAGGTT	GAGCAGAGTA	GAGCGCCAGG	AGCCCCCGGA	GGGGGCTGCA	60
	GTCTTCTCTC	TCTCTCTCGC	GCAAGGCTCC	GGCGGCGCAT	GGCCCTCTCT	GGGCTAGGCG	120
	AGGTGATCCG	CGCGGAGATG	CCGAGAGAGG	GTTCGGGCTG	CTGGGGGCGG	GGAGAGCCCT	180
	ATGGTGTGGT	CTTGGGCGCT	GCTTGTGCTC	CATTGGTGGC	GGGCTTGGTG	ATCTGCTCTG	240

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TGGTGTGCAT CGACGGCTTC GCACAGGCTC AGCAGCAGCT GCGCTCTGAG TCACTTGGGT 300
 GGGAGGTAGC TGAGCTGCAG CTGAATCACA CAGGACCTCA CGAGGACCCC AGGCTATACT 360
 GGCAGGGGGG CCGACGACTG GGCCTCTCTT TCGTGATGG ACCAGAGACTG GACACAGGGC 420
 AGCTACATCT CCACTGGTAT GGCATCTTCA TGGTACAGAT CCAAGGTAGCT CTGGCACTCT 480
 GCTCTCCGAC GAGGATCTTC AGGACACACT CCGACACCTT GCGCTCTGGA ATCTGCTCTC 540
 CCGCTCCCGG TAGCATGAGC CTCTGCTGTC TGAGCTTTCA CCAAGGTGTG ACAATTGGCT 600
 CCGTGGCCCT GACGCCCTCG CCGCGAGGGG ACACACTGCT CACACACACT ACTCGGACAC 660
 TTTTGGCTTC GCAAAACACT GATGAGACTT TCTTTGGAGT CGAGTGGGTG GCGCCCTGAC 720
 GACTCTGCTT GATGATGCTT TTTTAAATTT TATTTAAGTT CAAGAGAAAT 780
 AGTGTACACA CAGGGSGCCA CCGGGGTTGG GGTGGGAGTG TGGTGGGGGG TATGTGTGCG 840
 AGGACAAGAG TAGAGCATTA GCTTTTCTTT TCAATTTCCT ATTTAAAAA 888

Seq ID NO: 72 DNA Sequence

Nucleic Acid Accession #: NN_018092.2

Coding sequence: 13...618

1 11 21 31 41 51
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 AGCAGGTTTT GAATGCTCTT TACTTCTTCT GTGGAGCAAA AGAAAANGC AGGAGTATTT 60
 GAAACAATCA CTAAGACTCA TGGACAATTT ATTGGCATTAT CTTGGGAGAT TGTCTTGGTC 120
 CTCTCATTTA TTTCTATTTT AGTACAANGT AAACAGGCTC GAAAAAAGST CATGGCTTGC 180
 AAAACCCGCTT TTAATAAAGC CCGGTTCCGA GAAGTGTGTG ATCCCTCTGA TATAGAACCT 240
 TTTTCACTAA GGGACAAAGA GATTTCTGGA GAGCTGGGAG ACTTGTCCGA AGAATTGGAC 300
 AACTACCGAG GGATGGCGGG CTCTCCACCC GCGCTCCGCT GCATCAACGA CACACACTGT 360
 GGGTCCGAGG CCTCCAGGCT CAUACAAAGC AGACCAACAC TCAGTTCCAT GMAGCTTCT 420
 CTCGGAATGT ACTTTGGACA ACCACAGCCA ATGAAGACAT TTAATAGTAC CTTCACAGAA 480
 ACTATTGACA CTCTTAACGA GGGACATGAG TCGCTGGAGC GCGGCTCTGA CCAAGAGATA 540
 ATGGAGAGAG TTCCCTGTGA AATTATATGT AGGGGGCGAG AAGATTCTCG ACAGACTATC 600
 ATATCGATTT ACTCTTAATC TTTCTGTAAT GGTGATGTGA ATTCTTAGGG TGTGTACCTA 660
 CCGAGCTCTC AGGACCAACT ACTGTTTTCG GAGGCAACAC CTTTCTCCCT ATCGACACTA 720
 CGAAGAGACT GATTTCATCT GATCTCATATG TATGTGGATG TATTATAGTT CTGAGGGT 780
 CTATATATGT TAAACCAATC AAGGACCTTA CTCATTACCG TGGAAACAA ATACTCTCT 840
 ATTGCTTGGT GTCATTTATA GGAAGCACTG CCAGTAAAG AGCATATGAA GAGTGGTGT 900
 GATGAGGCGA GCGTCAGGCT GCGTCTTGST TTTAGCAACA AGAGAGCTCG TCTTGACATA 960
 TAACGCTCT GTCATATTTT TATGGACGA ATAAACTTGA TTTTCTTCT CATCTCTTT 1020
 ATTTTCTCTT TCTCTAAATT TAAITTTTCT TATAAGCTA TGGTITTACC ATTTCAATTT 1080
 CTTACATAAG TACAGTGGT TAAITGACCA CATACTTCAG TATAGGCATT TGTCTTGGAG 1140
 TGTGCTCTGA TACAGTGGT TACTGTGCCA ATTAAGACCC AGTTGATATT CACCACATGT 1200
 TTTCTCTCTG GCTATCTCTT GACTCTCTCT TTTTAAFTA CTGGGCCCTT ATTCCTTATT 1260
 TTCTTGAGGA AATAATAGAT GATATGATT ATTACTTTC AATTATATT TCTCGATTA 1320
 TACTAGAAAA TTTCAATATC CTGGGATATA TGTACCATTO TCGAGTATGA CTAATAATTT 1380
 GAAUAGATGA AAATTTCTCA CCAAGCCCTT GAAGTTTACC AGATATATGC ACATTCACTG 1440
 AGAACCCATC TCTTCAAGTA GATTAATCAT TGTACAGACT CCGCATATGT TGGTTTGTG 1500
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 CTTACAGCAT ATGGTAACCA AGGTTAGATG CCAAGTAAAA TTCTTAGAA ATTGGATGAG 1620
 CCTTGAGATT GCTCTTAAAC TGGGACATGA CATTTTCTCA GCTCTTATCA AGATACAAA 1680
 CTTCCGACTT TTTTAAATC GGCATTTTGA CTTTTTATAT GTATATAAAA CATATATTA 1740
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 TTTATTAATC AAGATGAAGG ACCTACAGGA CAGATTCCIT TCAAGTGTCA CATCAGTGGC 1860
 TTTGTATGCA AATATGCTGT GTTGGACCTG GAGCCTATAA CTTATTGTAA AGACTTGGG 1920
 AATGTGGACA TATGCTCTTT CTCTCTCTTT GTTACTATGT TATGTTTGTG ATAAATTTTT 1980
 CACTGTGTGA TATTATCTGT CTAATACACT ACAGAAATCC CATATTAAAA ATATCATGT 2040
 ACCTGACCTC TTAATCATGT TATTTATGCC ACCAAGGTTG TGGATCTTAA GTATGTATG 2100
 GAAAGGAACCT CATTTATCAA ATTGTAGTA ATACAGACAT GCCATTTAAA AGAGGTAAAT 2160
 TCTGTCTTTC TATATTTTGT TAGTAATATC TCAATAGAAAT AAGTGGAGAT TTACATGAGT 2220
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 TAAATTTAAT AGCAATATAC TGCCTCAG

Seq ID NO: 73 DNA Sequence

Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 GCTGAATGTT TTTTTCATTT TCTGTAGAGA TGCAAAATGTT CATTCATTTCA TCTCATTTA 60
 CAAACAGATA CATAAATGTA GCTGTAGAGC GTATTATAGT CTTTATATCA CAGTGTG 120
 CTGTGTGGA CAGGTGTAGT TCGATTATGAG CCGCAAAATG GGTGTGTGAG GGTGTGTGAG 180
 CTTAGGCTCT TTAATATTGT GTTGTGTGCA TGTCAAGAG CTGAGCCAC ATGTTGCTA 240
 CGACAGGGCC TGAATGTTT AAACAGCGCTG GCGTTTCTCT GCTCTGGGGC CTTTCCCGG 300
 GGGTTCGGGT GAATCCCTCC CCAAGTGGGT CCGCCCCAC CCGTGTGGGG GGGATTAGT 360
 CCGAGGGCT GCGCAGCGCT CACCTGGGAG AGCTCTGAGG GCGAGGCCCC AGGCTGAG 420
 TTCAGGCTTG GGGAGAACGA GCGAGAAAGA GACCCGTATC GCAAGGTGAG CGGGGAGAGC 480
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 AGTCTGACTT AGTGTGAGC TCGACAGATG GAGCACTGGA GTTGGTGTAT TTTAGACAG 600
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 CAAACAGATT TTTCTCTTA ACATTTTACC CTTCAAGGAT GATTTCTCTT TGTTGGCAT 840
 TGTACGGAAA TGTGAGTACC CATGTAAAGT ACTTTGAGT TCGAATAGAT GTTCTCATCT 900
 TAACCTCTTA ATTAAGAAAA AAAAAAATAA

Seq ID NO: 74 DNA Sequence

Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 TTTTTTTTT TCTTTAGGA AGTTAAAGTA GAACACATAT TTGGAACTCA AAGTCATTT 60
 GAATGATACA TCAATTTCCC TGAACATGCC AAACAAAGGA GAATCACTCC TGGAGTGA 120

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664

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TTGACTTAAT TTTACCCAAA ATAAACGATA TAAGCACGTA AAAAAAAAAA AAAAAA 3057

Seq ID NO: 77 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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	ATCAAGGAGG	ATCAAGGAGG	TATGCTTAAG	ACTGGAGGGA	GAGGACCCAG	TTGAAAGACG	60
	TCTGGCTATA	ATCAAGGAGG	GCATACATAT	GGGCTGGTTT	GUTGCGAGTA	GAGGAATGTC	120
	CAATTTGGAG	ATCAAGGAGG	TTAAANATCG	CCGCTGTTT	GAACTTAGGG		180
10	GUTTTGAGG	GAGGACGAC	TTTGAGATAA	ACACCAAGCT	TGCGATTGTT	TTGGGAATAT	240
	CCAATTCTGC	TGTAGGAAGC	AGGAAAACAA	TAAACTCAAA	AGAAGTGTTA	CACATAGATA	300
	ACTAATTATG	TGATCTGTAG	ATAGTACAC	ATATTGTTGT	GTACAGAGAT	CAAAAGGGAC	360
	AGAAAGACCA	AGGACGACAT	AGCATTCAC	GSTACCTATA	ATATGCTGGA	CATGGAGACA	420
	TCAGATGACA	GAGATGTTCA	ATTTGACAG	ATGGATGAC	ACTCGATGAC	CCACGATCTA	480
15	GCTGGTGTGA	TGATTCACCC	CAACTGCCC	CCTCTCCGCT	GTGTTGACCC	ACCCGACGAC	540
	CTGCTCTGCT	CTTCTCAGAA	TGTGTTTAT	ATTATTATTA	TAAAGATGTT	TATTTGAGCA	600
	TTTA						604

Seq ID NO: 78 DNA Sequence

Nucleic Acid Accession #: Eos sequence

20	1	11	21	31	41	51	
	TTTTTTTTTT	TTTTTTTTTT	AATGCTCAAA	TAACTAGGTT	TATTAAATTA	ATGTAAACAA	60
	CATTTCTGGA	AGCAGAGGCG	AGGTTGCTGG	GTGGGCTAAC	ACACGGGAGA	GGGGGCAAGT	120
25	TGGGTGGAA	GATCGATCAC	ACGAGCTGGA	CTGTGGGTCA	TGCAGTGTGC	AGCTATCTGT	180
	TCAATTATGA	ACCTGATGCT	GAGCGAGGCT	CTGATTTTGT	AGTACCTTAT	GTTACAGTGA	240
	ATATTAGTGT	CCTCTGCTGT	CTTCTGCTGC	CTTTTGATCT	CTGTACACAG	GATATCGTTG	300
	TACTATCTAC	AGTAGACTAA	TTTAGTATAT	TGTGTGTAA	ACTTCTTTTG	AGTTTATGTT	360
	TTTCTGCTCT	CTACAGACG	AATTGGATAT	TCCCAACAAA	TCTGCAAGTC	TGGGTTTAT	420
30	CTTGAGATGT	TGCTGCTGCT	GAGCAAGGCT	AGTTGTATAC	AGTGTGACAG	CCTGCTCCAT	480
	TTTAACTTCT	CTGGTTTCTC	AATCTGAGCA	TTCTCTTACC	TCCAGCAAGC	GAGCCGATAT	540
	TATGGCTGTC	TTGGATTATA	GCGAGAGTCT	TTCTAACTGG	TCTCTCTCCC	TCCAGTCTTA	600
	AGCTTAAAT	CGTCTCCTTG	ATT				623

Seq ID NO: 79 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 315..1416

40	1	11	21	31	41	51	
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	CTGTGTAGTG	GGATGAGCAG	AGAAACAAAA	CAAAATTAAT	CAGTGAAGAA	AGCCCTATAA	120
	TAAACTTTCA	GACGACGAT	CTATTCTCTA	GCTTATTTTA	AGCTCAACTT	AAAGAAAGAG	180
	ACTGTCTCT	GATCTTTCTT	GCTTCAATA	CATTAATAGA	TTTAACTCCA	CCCTCCCTCA	240
	AAAGAAACAG	CNTTTCCTAC	TTTATACTG	TCTATATGAT	TGATTGTGAC	AGCTCATCTG	300
45	GCAGAAAGAG	CTGAGACATC	GTTTCCCTCA	CAAGAAACCT	TCCCGGGGTG	GAAACAAGATG	360
	GATTATCAAG	TGTCAAGTCC	AATCTATGAC	ATCAATTAAT	ATACATCGGA	GGCTGCGCAA	420
	AAATTCATG	TGAAGCAAT	GGGAGGCCG	CTCTCTGCTC	GGCTCTATAC	ACTGGTGTTC	480
	ATCTTTGGTT	TTGGTGCCAA	CATGCTGGTC	ATCTCTATCC	TGATAAACTG	CAAAAGCGCT	540
	AAGAGCATGA	CTGACATCTA	CTGCTCTCAC	CTGGCCATCT	CTGAAGCTGT	TTTCTCTCTT	600
50	ACTGTCCOCT	CTTGGGCTCA	CTATGCTGCG	GGCCAGTGGG	ACTTTGGAAA	TACATTTGTT	660
	CTAGCTTTGA	GAGGGCTCTA	TTTAAAGGCG	TTGTTCTCTG	GATATCTCTT	CATCATCTCT	720
	CTGACCAATG	ATAGTACTCT	GGCTGTCTCT	CATGCTGTGT	TTGCTTTAAA	AGCCAGGAGC	780
	GTCACTTTTG	GGGTGTGTC	AAGTGTGATC	ACTTGGGTGG	TGGCTGTGTT	TGGTCTCTCT	840
	COGAGATACA	TCTTTACGAG	ATCTCAAAAA	GAGGCTGCTC	ATTACAGCTG	CAGCTTCTAT	900
55	TTTCCAACA	CTGAGATTAT	CTGTGTGAGG	AATTTCCGCA	CATTAAGAGT	ATCATCTGTT	960
	GGGCTGTCTC	TGGGCTCTCT	TCTCATGCTG	ATCTGCTACT	CGGAAATCTT	AAAATCTCTG	1020
	CTTCGGTGTG	GAATGAGAAA	GAGAGGGCAC	AGGGCTGTGA	GGCTTATCTT	CACATCATG	1080
	ATTGTTTATT	TCTCTCTCTG	GGCTGCCATC	ACATTTGTCG	TTCTCTGTAA	CAGCTTCCAG	1140
	GATTTCTTTG	GCTTGATATA	TTGAGCTPAG	CTTACAGAGT	TGGACGACAG	TATGAGAGTG	1200
60	ACAGAGTCT	TGTGATGAC	GGCTGTCTCT	ATCAACCCCA	TCATCTATG	CTTTGTGSGG	1260
	GAGAGTTTCA	GAATCACTCT	CTTATCTCT	TTCCAAAGAC	ACATTGCGAA	AGGCTTCTGC	1320
	AAATGCTGTT	CTATTTTCCA	GGAAGAGGCT	CCGAGCGGAG	CAGGCTCAGT	TTACACCCGA	1380
	TCCACTGGGG	AGCAGCAAT	ATCTGTGGGC	TTGTGACAGC	GACTCAAGTG	GCTCTGGTGC	1440
	CCATTCAGAG	TTGTGCAAT	GCTTATGTTT	TTATACAGAG	CTCGGCTGGG	GGGTGGGGTG	1500
65	GGAAGAGTCT	TTTTTAAAG	GAGGTACTG	TTATAGAGGCT	CTTAGGATCT	ATCCATTTAT	1560
	TTGGCATCTG	TTTAAAGTAG	ATTGATGCTT	TTAAGCGGCT	CAATATAGAA	AGCCCAATCT	1620
	AAATATGTTT	GATGAAATAT	AGCAACCTTT	TTATCTCCCT	TTCACATGGA	TCAGATTTAT	1680
	GAGCAACTCT	CTCTGAGCTA	GGTATGATTT	CTTATGATCT	TTTAAAGAAA	GCTTCAGAGA	1740
	ATTGCTGATT	CTTGAAGTTA	GTAATCTGAA	CAGAAATACC	AAAATTTATT	CAGAAATGTA	1800
70	CACTCTTTTA	CTGATAGCAA	GGCAATATAT	AGGTTGTAAA	TGTGTTTAAA	ACAGGTCTTT	1860
	GTCTTCTATT	GSGGAGAAAA	GACATGATAA	TGATTAGTAA	AGAAATGACA	CTTTTCTATT	1920
	TGATATTCTC	CTCTGAGCTA	TGTTTATATA	CTTTTACTCT	GATACAGAGA	GGGAGAGAGC	1980
	TTTGTGCTTG	GGAGAGCTGG	GGAGACTTCT	TAAATGAGAA	GAAATTGAG	TTGGATCATCT	2040
	TATTGCTGGC	AAAGACAGAA	GCTCTACTGC	AGACACTGCA	TGGGCGAGCT	TGGCTGTAGA	2100
75	AGGAGACAGA	GCTGTTTGGG	AGAGACTGGG	GAGGAGAGAC	AGGCTGATAT	CATGAGAGAC	2160
	CTTACAGCCCA	TGCTTCGGTG	GTGATGATGA	CTGGAGAGCG	GGATCTCTGG	TTGTTGTTCT	2220
	AGAGAGTAT	CTCTGTGGC	GAAAGAGGCT	CAAGAGAGCT	GAGCATTTAG	GGCCAAGAGC	2280
	CCACCAACAG	GCTTCAGCTG	AGGCTGAGGA	TGGCTCTCTG	TAAAGCTCAAG	GCGTGAAGAT	2340
	GGGAAAGAGG	GAGGATTGCG	TAAAGTAGGG	AAGAGAGGAG	GTATTCGTCG	AGCATATAGT	2400
80	GATCCAGAGT	CAGCAAGAACT	GGGGTGGTCT	TGGTTTGGAG	TGGTGTGAGA	GAGAGAGATG	2460
	AGAGAGAGCT	CTTACTGCTC	AGAGCAATTC	GAGAAACCTT	TGAAAGAGCA	TCAGCACGAG	2520
	AAGAGAGAGG	AGGAGAGTTA	GATCAAGAAG	AAGATGAGAT	GGTGTAAAG	GATGGTGTCT	2580
	GTGTCGAGAG	CTTGAAACCA	GCTCAACCCA	GACTCCAGCG	TGTTCTTAC	TGATGCTCTC	2640
	TGACTTCTATA	GATTTCTCTT	CCATCCGACG	TGAATATCTG	AGGGGTTCTC	AGGGGAGAGC	2700

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2769 TAGATTATG AATACACGAG GTATGAGGTC TAGAACATA CTTCAGCTCA CACATGAGAT
 2820 CTAGGTGAG ATTGATTACC TAGTAGTCAT TGCATGGGTT GTTGCGGAGCA TTCTATGAGG
 2880 CAACCAAGG CAGCATTTAG CACATATCTC ACATTCAATA AGCATCAAC TCTTAGTTAC
 2940 TCATTCAAGG ATAGACCTGA GCANACATAT GAGCAAGAGG GTCCCATAGA GTGAGGGAAA
 2940 GCGTAAAJA CTAGAAGTCT GCGTGGGAG TGACACAGAG TGTAGGTATC ATTTCTGGA
 3000 TTTCACCTCT ATAGAGCAA GGGGGAGAG GACATATCCA TTGGAATAA AGCTGCCTTG
 3060 AGCTTANAA CCACAAAGAG TACAAATTAC CAGCTCCCTT ATTCAGACT GANTGGGGGT
 3120 GGGGGGGGG CCTTAGGTAT TTATTTCAGA TGCTTCCTCC AGACAAACCA GAAGCAACAG
 3180 AAAAATATGT TCGTCCCTCC CTTTGAAATG AATATACCCC TTAGTGTGTT GGTATATCCA
 3240 TTTCAAAGCTT ATAGAGCTAT GTTTTCTTCT GTCTCTCTCT ATATATTTGT GCACATCACT
 3300 TAGTAGTGT TTGATTGGG GATGCTGATA AACATCATCA CTAACAGTAA GTGAGGGAAA
 3360 ACTTTCTCAG CCTCTGATA TGACGGGTGA GATTGTGTGC TTTCAGAGAG AGGCTACTG
 3420 GGGAAATGTT TTTGAGAGTG CTCTTAGGTT GTGAGAGTG CAACGATCA ATGACACCTC
 3480 ACCCTCTGGG CCAAGTCAA GACATCTGTA CATCTTAGTA TTTCGATATT CTTAGTATG
 3540 TGAAAGTTAC AAATGCTCTG AAGAAGATA TGACCTTAAT AAAAACAACC TTCTA
 3600
 3655

Seq ID NO: 80 DNA Sequence
Nucleic Acid Accession #: Eos sequence

20 1 11 21 31 41 51
 600CTTAGG TTAGCGGAG GGAACGGCA TTTTGTGAA AGCGCGCGCG GGAATTCCT 60
 CAGAACACG GGAAGCTCC CTGCTGGGCC AGCGCGCGCT GGTGTGCTG AGAGAGATGG 120
 GAGCGCGGCC TCGGTTGTT ATCTCAATTA ATGGGAAAT TAAGAAATA ATAGANTAGC 180
 GTAGATCTA ATAGTAAAT TATAGTAGAA GAAATAAACA TAGCTAGAT GGAATGAT 240
 GCTGTATTAA CAAAGCTCTG AAGAATTTC AGCGCTCCGA AGTTTAAAG GAGGAGAG 300
 AGAGACCTC TCAATGTTT TTATCTACG TACCTTTT TTGTTTTT TTGTAATAA 360
 AGGAAGTGA ATCAAGAGCA GCGACGCCAG CGCCAGGCCC AAACTGGAC CTGGGCTGCG 420
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 GCTTGAGTA GCAATTCGA AGAGCGCTCC CGGTTAGGAA ATCGCGCGCG TGAATGCTC 900
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 CACATCGAT GAGCTGCTG GAGAGCTG GCTGAGCGG TTGCTCTGTA TGTGAGTCT 1080
 TTGCTCTGT TGAATCTGT TTGTCAGTGT AGACTAGTC TTGGAAGTCT GCCCACTCC 1140
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 45 CTGGAGTTT GAAATTGATG ATTTTGTTT GTATATAAG GTAAAGTGT GTGTGCCCT 1440
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Seq ID NO: 81 DNA Sequence
Nucleic Acid Accession #: Eos sequence

50 1 11 21 31 41 51
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 55 ATGATGAAGA GAGGTGCCAC TGAGGTTCTT GCTGTGACA TCTTGAACA GTTCAACTC 180
 AGCGAGCA GAGTGTGAG GTGAGGAC GTCTGAGAG AATTCGCG GAGAGTGA 240
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 AGGTTGAGCA TCGTAATCT GAAATCTGAA ATGCTCAGA ATCTGAACCT TCTTGAGCA 360
 60 CACCTGACA CTTAAGGAGA GTGCTCATG GAGGATCTGT GACAATTACT AAAAATCTC 420
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 ACCCGAGCA GCGCCAGCTC CAGACCTTAA GCAATCTGA GCACTGACT TTTTCACT 960
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WO 03/025138

PCT/US02/29560

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WO 03/025138

PCT/US02/29560

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5	GTCCAGAGGA	GCTCTCTCCG	CATCAAACT	GCCGACAAAC	CGTGGCTCAC	AGGAGAGGAA	900
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	AGCCACAGAG	GATCGTAGAG	AGGGACCTCA	GAAGCCGAGAA	TTTCTCTGG	GAGAGCCCC	1020
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Coding sequence: ..1854

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	CTACAGGCCA	GCCCCACTTG	GCAACAGGCG	CGACCGAGAG	CTGTGTPTCC	AGTGGCCGAA	300
	CTGTGAGGCG	GTTGAGAGG	AGCTCTCTCT	CGCTCAAGC	CTGAGAGAGA	CGGCTGTGCA	360
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	TGGAAGAGGG	GGAGAGGGGA	TTCCGCGCAA	TGGGCTGTCA	CTTCTCCGAG	CTTCTCCGAG	1080
	TGCGACCCAG	TTCTTCTTCC	CGAGAGCCCT	AGTCAGAGGA	AGAGAGCTGT	CGAGAGCTGT	1140
	AACTGCAACC	CCACAGATCA	CACAGTGAAG	AGGACACGAG	AGAGCTGTT	TGCTGCTCTG	1200
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	CAGCTCTCTC	CTCATCCAGC	AGCAGCCAGT	GGAGCTGGA	TTTTTGGAGT	CTGTGGGGA	1320

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 60 GTGTGCACTG AAGAGAGTGT CCGCTGTGCA TCCCATGAAA AGGTTTCCCA ATTTCTCTCT 1440
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 65 GTTCTCTGCA GTAAATCCCC TCTCAAGGTT GATAACCTGT CTGGAGATA GAGCCAGACT 1620
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 70 CTGTGCTGTG CTGAAACTCG TGGGGAAGTA GAGACTCAG CTGAGACAA CTTTCACTCT 1920
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 75 AGCCAACCGA CAGCTCTGGA GTCACTCGGT GACCTGTGAT ATGAAAAGA GTTATCTCTC 2340
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Seq ID NO: 95 DNA Sequence
Nucleic Acid Accession #: NM_134421.1
Coding sequence: 527..1108

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ACAGGGCAT GTGTATGCG CAGTACAGA CCGGAAACA CTCTCTGGG GTTCTGACC 300
ACTCCCTCTC AGCTCCCGCG TGCTCTGCG GTTGGCTGT CTAGCTCCA AGAGAGCAG 360
CAGACTTTTC CTTCCTGAG CCGTCCCGAC CAGCTCCAT CTCTAGCTGG GTGAGACAT 420
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CTCTCTTTTG TGTGCTGAG AGCTGAGGCT TCGAGAGAA AGCTGAGGCT TGTATCTCT 1800
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GCAATTCG GTATTAAAT GATAAAATA ATGGCATTT CTGAAAAA AAAAAAAA 1920

Seq ID NO: 96 DNA Sequence
Nucleic Acid Accession #: NM_002149.2
Coding sequence: 375..956

1 11 21 31 41 51

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	CGGCGCGCAG	GGGCGCGCGG	CTCTGATCTA	CTCTCCCGCG	CTCGGGGCGG	CTTGTCGGCG	180
5	CGAGCGCCCT	CGGCGCGCTG	CGGCGCGCGG	CGGCGCGCGG	CTTGCGCTCG	GGAGGCGCGG	240
	CGGCGCGCAG	CTGCGCGCGG	CGGCGGGGACT	GCTCTGATGG	CCGAGTCAAG	ACCGGGAAC	300
	ACTCCCTGGA	GTTTCTGACC	CACTCCCTCT	CAGCTCCCGG	CTGGTCTCTG	GTGTATCGCG	360
	CGCGCGCAG	CGGCGCGCGG	AAACAGACAA	CGAGCTCGCG	CGCCGAGGTG	CTCCAGGACG	420
	TGCGCGAAG	CAGCGCGCTG	CGGCGCGCGG	AGCTCGACGA	GTGTCTCAAG	GCTCTCTCTA	480
10	AGGACTGCC	CAGCGCGCAC	CTGACGCTGG	ACGAGTCTCA	GAGATCTAC	CGGACCTCTT	540
	TCCTCTAAG	CGACCTTCTC	AAGTTGCGCG	AGCAAGTCTT	CGGCACTCTC	GACACCAAGG	600
	CGGCGCGCAG	CATGCTATTC	CGGAGGTTCA	TCATTGCGCT	GAGGTGACCC	TGCGCGGGCA	660
	ACCTCGGAG	GAGGCTCAG	TGGGCTCTCA	CGATGTATGA	CTGCGGCGG	AGCGCTCTCA	720
	TCAGCGCGAG	CGAGCTGAG	CGGCGCGCGG	AGGCGCGCGG	CGGCGCGCGG	TGCTGTGGA	780
15	TGAAGATGC	GAGGAGTGG	TCCACCCCGG	AGAGCGCGAC	AGACGAGATC	TTCAAGGAGA	840
	TGAGACACAA	CAATGACCGG	AAACTGTCTC	TGGAAGAATT	CATCAGAGGT	CGCCAGAGCG	900
	ACCTCTCAT	GTTGCGCTTG	CTGAGGTGCG	ACCCGACGAG	TGCGAGTGG	TCTCTAGAGA	960
	CGGCGCGCTG	GAGCTTGA	AGGACACGA	GCTCTGTGT	CGGCTTTAAG	CTTCTCTCTG	1020
	AAGAGTGGAT	CGCCGCAAT	GTTTCTGTCT	CTCCGCGGCG	CGCGCGCTGG	GCGATGGTGT	1080
20	GCACTGCGC	GGCGCGGTGG	CTGCGGCTCC	CTCTCCGACC	TGACCAAGCG	GACATTCTCT	1140
	CCCTCAAGCT	TGGCGCGCTG	CTTCTCGGCG	GAACTCCGAG	GATGTGGTG	ACATGACGCG	1200
	TTCAAGTGT	CTTGTGTCA	GGCGCTCTCG	CGGCGCGCGG	GATGTGAGG	TATGTGTGAT	1260
	AGGAGACAG	CGAGGACCTC	CGAGGCTGCG	CGCCCGGCGG	CGGCAATGGT	TTTGTGATCC	1320
	CAGTGTACT	TGTGGGAGG	GTTGGGAGCA	GGGCTCGGGA	GGTATACAG	GAGCGCCCTC	1380
25	CGTGTGATG	CGCGCGCCCG	GTTGATTTC	TGACGACAG	CGCTTGCAC	GTATATGATC	1440
	CGTGTGATG	TTTCTTTTAA	TATATAAAT	ATATATGGTG	GATGTGAGG	TATGTGTGAT	1500
	CTCCGCTATT	TAACTGCTCT	GACTGCTTTT	GAGCGCGAGC	CGCTCTTGGC	CGCGCGCCCG	1560
	CTGAGCGCTG	CTGTGTGTGT	GTATTATATG	CTCTTTTGTG	GTGCTTTTTC	TAAAGGAAAT	1620
	CATGTGTGCG	CGGCGCGCTG	ATGATCTCTC	CATCGTGTGT	GTGAGCACAG	GCATTGTGTG	1680
30	GCTGTCTGT	CTGCTGTGTG	ATGTGTGTGG	GATTTCGCGT	ATTAAATAGA	TAAATTAAT	1740
	GCAATTTCT	GAAGAAAAAA	AAAAAAA				1769

Seq ID NO: 97 DNA Sequence

Nucleic Acid Accession #: Bos sequence

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	GTCACACTG	GAATATGCT	ATATATATG	CTACAGGTT	GAATATGAA	TATGCTATG	180
40	ATTATTAAG	CAGTAATTA	AAGTAAAT	TTAGCTTTT	TGGTATAAA	GTATACAGG	240
	AAGCATATG	AATATAAAA	TAGGCTTAT	CTTCTTTTG	TCATAAACT	AATAAAAT	300
	GTTGCTAAG	GAGGCTTCA	TTTTCTAGA	CGCTCAAAA	AGTTAAAGG	TTAAACAAA	360
	TTCTTGAGT	TAGAGACAT	CTAGAGATG	CAATGTGCT	GTTGAGGCT	ATCAATATG	420
	CAATCTGAG	GTTAAACAA	AGCAATAGC	ATGCTGTGG	CAATGCGAG	CGAGGACCC	480
45	TGATGTGCC	CTTCCACTA	AGGTGTCTC	CGAGTGACC	AGGATGGG	TGCTGTGAT	540
	CTCTTTTCA	GATTTCTCA	GCTGTAGTA	ATAGTCTAG	CGAGGCTCT	TCTGTATAT	600
	CTGATGATC	CTGCGGTGA	CGCCCGAGG	GCACTACAG	TGCTGTCTC	CAACATAG	660
	TTGATCTCT	GCTCTCTAG	CGAGGAGGA	GACTTAGAT	TCTTGGAGA	CTGAGGGA	720
	TGCACTGAG	TTAGATATT	TCAAGGCTT	ATCAATGAT	CAGCTCTGT	TCATCCCGA	780
50	CGCATGTGT	GTTGATATT	TGTTGACCT	TTATTTGGCA	CTTGCAGAA	TAATAGATG	840
	CGACCTGTG	CTTATGCTA	TTTGCTATC	CGTTTCAACC	TGGCATTTA	TCAGCAGAG	900
	GAGGAGAAA	AAATATAA	AGCATGTT	AAAGAGAGA	AGCCCTTAT	GCGTCTTCA	960
	ACTCTCAGT	CTATTAGAT	GCAATCGAG	CGCCGAGG	AACACAGAT	CAATTAAAG	1020
	TCGGAATCA	AATGACTCA	GATTTAAGT	CAATATTGT	GTATAGTCA	GTCAATAAA	1080
55	ATGAGATTA	GTAAATCTG	ATCTATTAG	CCCAACAGA	ATAGCTTTT	CATGTTTGA	1140
	AAJAAAGAA	AACTATGAT	CGCCGAGC	CTGAGGCTA	CTGACCTGC	AAAGCTTT	1200
	CACTCTATG	TGTCAAGAG	AGAAJAAAT	CGAGTGTAG	TTTTAACCA	GACTGTAGG	1260
	CGCTGTAGC	GGCGAGTGG	CTATCTCTA	AAACACTAG	ACCGGTTTT	CAAGGCTGG	1320
	CGCCCATGTC	CAAGGCGCT	CGGCAATTA	CGCTCTGAT	CAAGAGAGC	AGTAAAGCTA	1380
60	ACTCTTAGC	AAAGCTCTA	CTTAAGGCT	CGCCGCTGT	TGGTAACTT	ATATATACC	1440
	AAAGGACAT	ATTAGCTAT	GATGCTAGA	CTGACTGAT	AGATACAGA	GCTTGTCTCT	1500
	TGAATATCC	TGCTAAGCG	TGGAAGCTT	CAACACCTA	AACCGAGCA	CGTTATCTCT	1560
	GATATCAG	AGCCGAGTG	AGCATACTG	TGTATAGTA	TGTGACTAG	TTTATCTAG	1620
	GTATCTCA	TCGACAGCA	TCTTAAGCA	CTGTATGAT	CTGTATGAT	CTGTATGAT	1680
65	AGCATGTGG	CGACCCCTG	CAATGATTT	CTGAGAGA	CGACAGGCG	TGCTCGATC	1740
	ACACCGGAA	GCTGCTGTG	CGACTCAAG	CGAGCATGA	GGAACCTAT	CGGCGGACT	1800
	ATTCTCTTA	AAATTGGAC	TGCGAGTA	AGGACTCTCA	CTGACCTTC	TGCACTAGC	1860
	GACTGTCC	AGGCTGAT	AGCTTAAGG	CTGTATGAT	AAAGAGGTC	CTAGCTGCT	1920
	ATTATTATT	AGTTATATG	AATCGTAGG	AACTCCAAA	GGAATCTGT	TGTACATTA	1980
70	CATCTAGTC	AAAGTATGA	ATCCGAGAG	TGACCGGCT	GAGCGTGT	ATGACTCACT	2040
	GTAAGCTCC	CATGATTAG	GACTGATCT	TTTCTAAGT	ACAGAGATG	AGTAAATAGT	2100
	AAAAAAA	AAAAAAGT	CGGC				2125

Seq ID NO: 98 DNA Sequence

Nucleic Acid Accession #: NM_001946.2

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	CTGACGAGCT	ATGCGGCTCG	AGCGGAAACG	CTGTGTGAGC	AGCTCTGAGG	CGGACTCGGG	180
	ACTCTGTGTT	GAGCGCTCG	TGCGCGGGGG	GTGCTCAAC	CGGCAAGATG	ACGAGGCGAT	240
	GGATGCACTC	CTGTATGCGC	AGCGCAGGCT	CGCGCCCTCA	CTGCTGCTCG	TGCAAGGCAAA	300
	GGGCGAGGCG	GCTGCGGAG	AGCTGCTAG	CTGTGCGAG	CGTACCGCG	CGCGCGCGGA	360

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 GCGCGAGCCA GAGCCAGAGC TGGAACTCCA GCTCTAGAGA GAGCAGAGG GCGAACGGA 660
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Seq ID NO: 99 DNA Sequence
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 GGGGCTGGC GTTACTCTTC GCTCTCTTCT TCACTCACTG CTCTCTCTAC CTTCTCTCTC 180
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Seq ID NO: 100 DNA Sequence
 Nucleic Acid Accession #: NM_018325.1
 Coding sequence: 163..1590

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WO 03/025138

PCT/US02/29560

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Seq ID NO: 101 DNA Sequence
Nucleic Acid Accession #: AF258592
Coding sequence: 93..1268

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Seq ID NO: 102 DNA Sequence
Nucleic Acid Accession #: F08 sequence

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TAAGTAGCTT GCAATTCAGT TAGGTGTCCA CCAATG 516

Seq ID NO: 103 DNA Sequence
Nucleic Acid Accession #: NM_018401.1
Coding sequence: 65..1309

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10	CTTTGACCAT	TTTCAGATTC	TGCGGGCGCAT	TGGTAAAGGG	AGTTTGGGAA	AGGTATGCAAT	180
	CCGCGAGGAG	CCGACACATC	AGAAATATGA	TGCATTAAG	TACATGAACA	AGCAAGANGT	240
	CATCGAGAGG	GATCAGGTTC	GGAAATGTTT	CCCGAGGCTG	CAGATCATGC	AGGGCTGGGA	300
	GCACCCCTTC	CTGGCATCTC	CTGCACAGAT	GAGGAGAGCA	TGGTCAATGA		360
	GCTGGACCTG	CTCTCGGAG	CCGACATCGG	CTACCATCTG	CACAGAGATC	TGCAATTCAC	420
15	AGAGGGGACT	GTGAAGACTC	ACATCTGTGA	GCTGGCACTG	GCCTCGGAGT	ATCTTCAGAG	480
	GTACCAATC	ATCCACAGAG	ACATCAAGCC	AGACATATTC	CTGCTGGATC	AAACAGGACA	540
	TGTTTACATT	ACGAGTCTCA	ACATACAGC	GTGTTTGAAA	CGACGAGAAA	GGCTCTCTCT	600
	CATGCTGGC	ACGAGGCCCT	ACATGGCTCC	AGACATATTC	CAGGTGTGCA	TGACACAGGG	660
	CCCCGGATAC	TGTTAACCCT	TGCACTTGTG	GTCCCTGGGC	ATCACAGCCT	ATGAGCTGCT	720
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	CTTCAGATGT	GGGCTGTGTC	ACTACTCTCT	CACGCTGTTC	AGGCGGATG	TGGCCCTCT	840
	GAGGAGCTC	CTACCCAGG	ATCTCTGAG	CCCGCTGTCC	AGCTCTCATG	ACATACAGAG	900
	CCGTGGCTAC	TTCGCGGACA	TGAATCGGGA	CCCGGCTTTC	AAGAAGGCAC	TGATGCCCGG	960
	CTTTGTGCC	AATAAAGGGA	GTTTGAATCT	CGATCCCCA	TTTGAAGCTG	AGAGATGAT	1020
	TCTGAATCC	AGGACCATTC	ACAAAAGAA	GAGCGGATTC	GCAAGAGACA	GATCCAGGGA	1080
	TGCGACAGAG	CGACAGTGGC	CCCTGAATTC	ACACTCTGCG	GACTGTGTTG	AGATCTGCG	1140
	GGAGGAAATC	ATCATATTTCA	ACAGAGAGAA	GCTCAGGAGG	CAGCAGGGAC	AGGGCAGCGA	1200
	GCTCTTGGAC	ACCGACAGCC	GAGGGGGAGG	CCAGGCCCAA	AGCAAGCTCC	AGAGCGGGTG	1260
	CACACAGAC	CTGCTCACCC	ACAGCTGACG	CCGTTGGCTG	AGCAGCTGAG	CCGACATCTG	1320
30	TTCCTCTCT	ACAGAGCTGC	ACTGCTCTCT	CCGCTGCCCA	CCGAGGAGCT	CTCTTTTGTC	1380
	CCCTGATGTC	CCCTGCTCAC	CCCTGAAATC	ATCAGATGCA	GAAAGAGGCC	TGGACTTGA	1440
	GCTGGGAAGC	CTGGGTTCTG	TGCCCATCTC	CATGACTGAT	TCAAGTTGTA	CCTCAGACAA	1500
	GTCAGCGGCT	CTCTGTGCTT	CCGTTTCTTC	CATCTGCGAA	AGGGGTTAAA	CAGCTTCTCC	1560
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35	TGATATTAT	AAACATATT	TTACGCTGAA	AAATTAACCT	TAATATTGGA	AGTGACCCCC	1680
	ATCCCCAGAA	GATCATTAAC	CTGTGACTAT	TTGCATTTTG	GCACATCTCA	GCTTGTGAGA	1740
	GGGCGACTCC	GAATAACACA	GCCTTGACAG	CAAAATAAG	GTCTGATATG	TGGGCGCCTT	1800
	CTATGAGAAC	ACAGCGAGAA	AGGATCTGAA	GTCTGATCTG	CTCTGATCTG		1860
	CTGACGAGCC	ACAGTCTCTG	CCCTGTGAAG	TGGTGACACA	TGACAGACAG	ACTGTGCCCC	1920
40	AAAGTCTCAG	CCGCTGGGTC	TCACTCTCTC	CCCTCATTTA	GAGAGCATC	CTTACCTTTT	1980
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	TGATCATGAG	AATTTGGGTG	CTGAGCATTC	GTATCTCATC	AGGATGTATA	TACAGAGCCT	2100
	ATCCATCTG	CCGAGAGGCT	CAGACCTTCA	GCACACTCTT	CCACTCTCTT	ATCAGCTTTC	2160
	AGGGTTTCTT	CTCTCGGGAA	GGGTGTAAAA	TCACTGTGTC	AGATTCTCTT	TACAGAGAGT	2220
45	ATCCAAATCG	TATTTGGTGA	CGGCTCCCTT	ATTATACAA	TAGGAAGCAT	GGTGCTTTTG	2280
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	CAGGAGAGAG	CTTCTGTTCT	AATCGGAGTA	TGTTTGGATG	AGCAGGAGAA	GCTTACAGT	2400
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	GATGACTCT	AGATATGCT	TTTTTGTGAG	CABAAATGTC	ATCATATTAT	AGTAACTTTC	2640
	TTCTCTCACT	CACCCAGCAG	GTCACTTTTC	TGTCGAAACA	AACTGTTTGA	GGATTCTTCC	2700
	AAATGTTCTT	CCGTGGGCTT	TGTATATTGT	TTTGTACAT	CCCTCGAAG	TTCGACTGTG	2760
	TTTTTATTTT	TTCATCCAGC	TTCCATTTT	CAGTTTTCAC	ATGATTAATC	AATCCTTGGG	2820
55	CGCTCTGAT	TCAATCTCTA	GAATCTCTTA	AGACATATCT	ATGATTAAT	TAGATTATTT	2880
	ATTTTATTTT	TTTTAAAGAG	AAATAGTCAG	TGTTTCTCT	CTTCAAGCC	AGACTTATTC	2940
	TGATTTGTGT	GCTCTCTGTC	AGGTGACTCT	TTTTGACAGC	TTTTCTTAC	TTCATGTGCC	3000
	CATCAACAC	GCTCTCTGTC	CCACACTCTC	CAGCAAAATA	AGGGGCTGTC	TGCTCTCTCT	3060
	ACTCTCAACC	TGGAGGCTCT	TAGATGATCT	ATGTTGTTCT	AGGCTGGGCT	GAGTACAGGA	3120
60	ATTAGGGGCA	GGAGCTGGAA	GTGCCCTTAG	GAACACACGA	TTTCTGGGTT	CTGTGTAAGT	3180
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Seq ID NO: 104 DNA Sequence
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Coding sequence: 63..1460

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	CGGCTCGGAG	TGTTCTCTCT	AGGAGGCTCA	TACAGAGATT	TGGATGCGC	TACAGCGACA	240
	CGGCTCGAT	CTCTCTGACA	CTCTCTTACG	TGCTCTTACG	AGGAGCTGCG	CTCTCTAGG	300
	TGTTGTGAAA	CCGCTTTGCG	TGCGCGCGCC	TCACTCTGTT	GGGCGGCTCT	TTTGGGTGGC	360
	TGGGCTATGT	GGCTGTGTC	TTTTGCCGGA	GCATCATCCA	GGTCTACTC	ACCACTGGGG	420
75	TCAATCGAG	GTGAGGTTG	GCACCTAACT	TGCGGCCCTC	GCTCATGATC	CTGAAACCGT	480
	ACTTCCAGCA	GGGCGGGGCT	ATGCGCGAGC	GGGCGGCGCG	AGCGAGGCTC	CTCTCTCTTC	540
	TGTTGTGCTT	GAGCGGCTTG	GGGCGAGCTC	TGCGAGAGCC	CATCGCCGCT	CGGCGCGCGT	600
	TCTCATCTCT	GGGCGGCGCT	CTGCTCAACT	GGTGGGTGTT	TGCGGCCACT	ATGAGGCGCC	660
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80	TGAGCGGCTG	CCGCGAGAGC	GGCTCTGTGTC	TTTACAGGCT	TTTACAGGCT	GGTCTGTGTC	780
	TGGGCTCTTT	CGTCCCGGCC	GTGTTGTGTT	TGAGCTAAGC	CAGGAGACTG	GGGCTGTGCG	840
	ACACCAAGGC	CGGCTCTGTC	CTACCATCTC	TGGGCTTCAT	TGACATCTTC	CGGCGCGCGC	900
	CCGCGGCTTT	GTGCGCGGCT	TGTGGGAGAG	TGCGGCCCTA	CTCGGCTTAC	CTTCTCAGCT	960
	TCTCATGTTT	CTTCAAGGCT	CTCGCGGAGC	TGGCGGGCTC	TACGCGGCGC	GAATCAAGCG	1020

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GCTCTGTGGT CTCTTCATCC TTCTTTGGCA TCTCTACGG CATGTGGGG GCCCTGAGT 1080
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Seq ID NO: 105 DNA Sequence
Nucleic Acid Accession #: NM_006598.1
Coding sequence: 5..2256

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CAATATGCA GTCTGTCCA AAAACGGCA GGGAGAGGCC AACTACATG AGTTTCTGA 3180
AGTGTGAGC GAGTGTCTG ACAGAGTCT GAGTGTCTG AGTGTGTG GCGGAGTCT 3240
CACTCATAC TCTATATCC CAGACATCT ACAGGCTCT GCGACAGGA CCGAGAGCG 3300
GTGGGAGC GTGGGCTGG GCTTGGGCCA GGGAGACAGA GCGCAGAC ACCGTGCC 3360
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AGGCTCTCT GAGTGTCTG TGAATCTTGA TGTGTGTG AGTGTGTG GAGTGTCT 3480
TGTCTTCTG TGTCTAGGA TGTCTAGGA GTGACCTGA GTGGCCAGA CTGTCTGCA 3540
GTCTACAGA AGCCAGTAG CCGTGTCTT GTTCTTGA AGTCTTCT CTGGCTGA 3600
TTTACCATG GTTATGTTT CATTTTACC CCATCCAGAA CATTTCTGA AGAGCAGCG 3660

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PCT/US02/29560

GAGCTGAGGCT TGTCTCTGAT GATGAAGGTG AAAGCTGACG CCTTGGCATTG GCTCCGCTCA 3720
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Seq ID NO: 106 DNA Sequence

Nucleic Acid Accession #: NM_004585

Coding sequence: 62..511

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 TGGATACCCC GGGGCTGGCT CTTCAAGTGT CTCTCAAGTC CTGAGACACA GTGCAGAGGT 240
 GAAAGGGGGG CGCCGTGAGG ATGTGTGTGG AGGCTGTTCG TATCGGGTCA ACACAGAGTT 300
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 AAGAACACA GCGCAAGTCA AGCTGTGGAT CTTGTGTGTA AGGCGTGTG GGGGGTCCA 600
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Seq ID NO: 107 DNA Sequence

Nucleic Acid Accession #: NM_004696.1

Coding sequence: 183..1646

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 TCAATCTGTA GAGAGTGGG TGGTGTGAAA CTTTCTGCTA AATCCCTGAT GGGAGATGG 240
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 TACCGGTTT GGGTCTGCT TTCTATACCT AAGTGGCTGC TGTGGTAGCT ACCAAATACT 600
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 ATAAGGTAT TTGCTGGAGC TGAACAAC TGTTTGACAT TTCTCTCTTT AGAATCTCT 1080
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 TTGACTGTGT AGCCAGGCC AAAACATGCG GAAATGACAT CATGAGAGCC TCTACTGTT 1200
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 CTGAGCCACC TATAGCAGCG TGGTATTATG ATTATACCA GACATACAT GCTCTTTCT 1560
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 CTCITTTGCC CAGGCTGGAG TGCATGTGGC CAATCTGGC TCACTGTAA TCTCGGCTCC 1860
 TGGTCTAAG GATTTCTCT GCTTCAGCTT CCGAATGAGC TGGGACATA GGCACAGCC 1920

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TTAACCAAT AGCTTAATAT TTTATTCAGG TACTCTATGT ATTAAATGAC ACTGGGATG 2220
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TGATTCTG 2529

Seq ID NO: 108 DNA Sequence
Nucleic Acid Accession #: NM_000358.1
Coding sequence: 48..2099

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GCCCAAACT GTGTCTGTGT CAGAAGGTTA TTGGCACTAA TGGAGGTAC TTCAACAAT 240
CGAGCAGTGT GTACCAAGG AAAATCTGTG GCAATCAAC AGTCAACAG TACGATGCT 300
GTCTCTGATA TGAAGAAGTC CCTGCGGAGA AGGCTGTGCC AGCAGCCCTA CCACTCTCAA 360
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CGAGAGACT GAGGCGCTGAG ATGAGAGGAGC CGCGCAGCT CACATCTTC GGGCTTAGCA 480
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CCACGGGGGT GGTGCACTCT ATCAATAAGG TCATCTCCAC CATATCAAGC AACTGACAG 780
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TCGAGAGAT CCGTGTGAG ACTTTGAACC GTATCTTGGG GAACCCAGAA GCCCTGAGAG 960
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TTGCGAATCT CCAATAATAC CAGCATGTGT ATGAACTGT GGTATGACA GCAATCGGG 1800
CCTCTGTGGC GCTAAAGTCT CTGCAAGTGT ACAGAGTGA ATGCAAGCTG AAAGAGATG 1860
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Seq ID NO: 109 DNA Sequence
Nucleic Acid Accession #: NM_145648
Coding sequence: 59..1792

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CGCGCGCGGC GCCATCTCTG CCGAGCGCTG GCTCTACTGT CTGGCGATCG TGCGCTTCCC 420
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TGAAGGCATT GGAATCTTTC AGCAATCTTC TAACAAGAT CTGTTGATT CATGTAAAT 960

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Seq ID NO: 110 DNA Sequence
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 Coding sequence: 48..881

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Seq ID NO: 111 DNA Sequence
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Seq ID NO: 116 DNA Sequence

Nucleic Acid Accession #: NM 016551.1

Coding sequence: 38..1750

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 AATKACTCA CAGTACATCA ATACCAATCT TTCTTTCTT CCGACTCTCT TTTCNAATC 300
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 CACTGTGAT TGTGGGACT CAGGACATA GCGCTCCGAC AATATGGTGA TCTTACTTTC 420

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PCT/US02/29560

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Seq ID NO: 117 DNA Sequence
 Nucleic Acid Accession #: HM_003820.1
 Coding sequence: 294..1145

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 GCGCTGGGCG CAGCCACAGC GCGCCTTCAG ACCCGAGCTG TCTGCGGTTC TGACTTGTG 1500
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 70 GCTCTGCTGT TCTATTCTTC ATGAACAGT GTATTGTGGG AGATGCTGTG GAGAGATGTA 1680
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Seq ID NO: 118 DNA Sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 42..1070

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 80 TCTGTGGGT CATTCCTAAT GGTCACTGCG TGTGGGTTCT TGCCGCGCTG TACCTCTTGA 180
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 AATTCTGTGT CAGCTGTGCT GGTGCTCTTT TTCTCATCAA CAGCTACTGC TCTGTGGGCT 360
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60	Seq ID NO: 119 DNA Sequence								
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	Ordering sequence: 137..853								
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	CTTCAACTGT	CTCTCTTGCG	TGGGAGGAGT	TGGCGTGCTG	TGCTTGCGCA	TCGTGCTGGC		240	
70	CGCCACAGAC	GGGAGCTGCT	CCAGCGCTGC	CTCTCTCTTC	CGGCTGCTGC	CGGCTGCCAC		300	
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	CTCTGCTCATC	AGCATACGCG	CTCTTTGATC	TTCTTGCTCT	CTCTGCTGCT	TGGTGTCTCT		420	
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	CCGACGAGAC	CTGAGGAAGG	CTCTCTTCTT	GTAACGCGCT	CGGCGCAAG	TGGGCTCTAC		540	
75	CACGCTGCTG	AGCATATCTC	AGACGCGTCT	CGGCTGCTGC	CTGCTCTTCA	ACTTACAGCA		600	
	CTGCTGTGAG	GTCATACAGC	CCAGCGGCTG	ACTCTGATCT	TGCTGTTCTG	ATTACATGTA		660	
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	CGAGATGCTT	GCGCTGAGCT	TGCTGCTGCT	GGCATCATTT	CGGCTGCTGC	CGGCTGCTGC		780	
	CGAGATGCTT	GCGCTGAGCT	TGCTGCTGCT	GTATATGCTC	CAGGCTGGTA	CGGCTGCTGC		840	
80	CTACTGCGCG	TAGGCGTCCC	ACGCGCGGCT	TCCTCTGCGT	AMGAGCGGCT	ATGCGGAGAG		900	
	TGGCGGCAACC	AGAGCTGCTC	TTGCCACAC	CAGCGTCTGA	CTCTGCGCCC	ATGCTGGGAA		960	
	CAGGAGGAGG	CGGACGAGTG	CTGCGAGGCG	CGGACCAACT	CTTTTGCTGCA	GCTCTGCTGC		1020	
	CGGAGTGCTT	CAGGAGGAGG	CGGAGGAGG	CGGAGGAGG	CGGAGGAGG	TGCTGCTGCA		1080	
	CGGAGTGCTT	CGGAGGAGG	CGGAGGAGG	CGGAGGAGG	CTTTTATGAT	GGCTCTGAGG		1140	

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PCT/US02/29560

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Seq ID NO: 120 DNA Sequence
 Nucleic Acid Accession #: NM_005629.1
 Coding sequence: 639..2546

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Seq ID NO: 121 DNA Sequence
 Nucleic Acid Accession #: NM_013332.1
 Coding sequence: 206..397

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PCT/US02/29560

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CATCTCAAAA AAAAAGAGAA AAGAAAGAGC GTGTTTAATG CAGAGGTGTC AGATGATTCG 900
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TGATATTTTC AACCTACTT CTTAAACATC TGTCTGGGT TCTTTAGTC TTGAATGTC 1080
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Seq ID NO: 122 DNA Sequence
Nucleic Acid Accession #: NM_020142.2
Coding sequence: 274..537

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GCTAAGTGTG GGTGGGCTGA GTCCAAAGAA GCAAGCGCTG GGCAGAGCTA AGCTGCTCTG 180
GGCTGGGCTC ATCCAGGAGC GAGTGGGAGC CAGTCCGAGC AGCTGCTGCTC 240
CGATCCGAGC GACCCAGCTG GGAAGAACAC GATATGTGCG GAGCCAGCTC TGCGGCCG 300
TTCTACCGCG AGCTCAAAAG ATACTCCGGG ATCATCCCGA TGATCGGCTT AAATCGGCTG 360
GGCATGGGCA GGTCCGCTCT TCTGTTGCT GCACTGCGCC TTGCGAGCCC GAGAGTCTCG 420
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GGGTTTCCCA CCGAGAGGGG AGGCTGTCTC ACCCTCACT TCTCTGCTG CTCGACAGAG 720
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CAGCGAGGGT CACACAGAG CCGACAGCAG CCGCTCTGCC CTCTCAACCG GGCCTGAGAG 840
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CTGAGTGGCA AGGAGGTTG CCGGCTCCAC GTTAGCCAG CCTCTGAGAG CAGCCGCGAG 960
GGCGGCTGCT CTGAGGATGG GTGTGTGCG GAGCTGCGCA GCTCGGGGCA CTTTGGCTC 1020
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Seq ID NO: 123 DNA Sequence
Nucleic Acid Accession #: Eos sequence

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CGACTCCGAG AAGAGAACCG GGTTTTGTGT CACATAGCAG GAGTGACTC CCGTGGGTGT 180
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GTGGTGGCAT GTCCATTAAT TTGGATAGAG CTTCCTCAAT CTTCCTCAA ATGATAGTGT 300
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ACGTTGAGA GCTGAGAAAT GTTCTACTGA CACAGCAGAG CAGAGTATC CCGCATGAGA 420
GGGACAGTA ACATCACTCT ATGTACACT CTTTGACAT AAATATAGTA TTTCTCAAT 480
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Seq ID NO: 124 DNA Sequence
Nucleic Acid Accession #: NM_02204.1
Coding sequence: 74..3229

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PCT/US02/29560

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Seq ID NO: 125 DNA Sequence
 Nucleic Acid Accession #: NM_005501.1
 Coding sequence: 74..3274

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 TACCCCATTC GTGTGTGTTA AGGAGAGCCG GAAACCGGCG AGCCTCTTGG GGTACTGTGG 240
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 GGAGCTCGCT GTGCGCGATG GCTGACACCA GAGCTGCTGT GCTGTGTTCA GTTGTGCCACT 360
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PCT/US02/29560

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5	GACAAATAG	GGGTGCGCAG	ACCTCTGTGT	GGGCGCCCCC	TACTACTTGG	AGAGGAAAGA	1080
	GGAGATGAG	GGTGGCATCT	ATGTTCTCAT	GGACGAGGCG	GGACACTGCT	TGCTCTGTCA	1140
	CCCTCACTC	CTTCTTCACT	GGCCAGATGG	CTCTGGCTTT	GGTTTATCTG	TGCCACGAT	1200
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	GGGCAAGTG	TACATCTATC	ACAGTAGCTC	TAGGGGGCTC	CTTAGACAGC	CCGACGAGGT	1320
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10	GGAGATGAG	GTGGATGAGT	ACTCTTACAC	AGACCTGTCA	GTGGGAAGCC	TGTCAAGACA	1440
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	CTTTCTTAC	AACCAAGATG	CGGGGAACCC	CAGCTACAGG	GGAAACATGA	CTGCTGGCTA	1620
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15	CGCTGTCTC	CAGCGCTTCT	TCTCCATGCC	CGAGTAGGCC	TGGCAGAGGC	TGAGCTGTCT	1740
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	ACCTTTGGGG	ATCGCCGATC	GGCCCCGGCT	GGGGCTGGGG	TGCTTGGAGC	CGTACCGGAT	1860
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	CGTACGAGAC	ACCGCGACCT	CGAGCGGCTC	CGGGGAGGAG	GGCCACGAGG	CGCTGCTCAC	2100
	CGTGTGGTG	CGTCCCGCCC	TGCATGTGTC	CTCAGTGGCC	CGCCCGGGGG	CGTGGCAAGC	2160
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	GGCTACGCC	TTTGAAGTCA	TGGGGGTGAC	CGTGCACACA	AGGAGCCCTC	AGGTGCAGCT	2280
25	GGAGCTCTCC	ACGTGAGTCT	ACGAGGACAA	CGTGTGGCCC	ATGATCTCCA	CTCTGCTGGT	2340
	GGACATATCA	CTCCAGACCT	CGCTTNGCAT	GTAAATCATC	CGGTCATCAA	CGTTCTTTGG	2400
	GGGGCAATG	ATGTGGATG	CTGACATGAA	AACTGTGGAG	GATGTATGAA	CGCCCTCTAA	2460
	GTATGAATTC	CAGCTGGGCG	CAATGGGGGA	GGGCGTGGTG	GGCTGTGGGA	CGCTGTCCT	2520
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30	CAAGCTGCAT	GGCAATGTGT	CTGTGGGCTG	CGAGCACCTT	GGAGAGCTTA	TCAACCTCTT	2640
	GAACATCACT	CTCTTCTGAC	CTGGGGAGCA	CGCTCATATC	CGACAGGCGA	CTGCTTCACT	2700
	CGTGGTCACT	GGGGGAGGCC	AGGGCGCCCC	ACCTGTCACT	CTGGCTGCTG	CGAAMAAAGC	2760
	CAAGTGTGAG	CGTGTGCTGA	CGTGTGGGAC	AGGGCGTGCC	CACCTGTGAT	GGCTACAGTG	2820
35	CGGCTGTCT	GAGATATPAC	AGTCTCTTGT	CGCTGCTGAT	GGCTGCTGAT	GGCTGCTGAT	2880
	CGGCTGTCT	GAGATATPAC	AGTCTCTTGT	CGCTGCTGAT	GGCTGCTGAT	GGCTGCTGAT	2940
	ATTCCTCCGA	ACCGACATCC	CGACCATCAA	CATGAGAGAC	AGACACAGCT	GGTCTCTGT	3000
	GGACATTCAG	TGGAGCTGG	TGGAGGAGCT	GGCGGCGGAA	ATCGAGCTGT	GGCTGCTGCT	3060
	GGTGGCGGT	CGTGGAGGGG	TGCTGTGTCT	GGAGCTGATC	ATCTCTCTGC	TGGTGAAGTG	3120
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	CGCGAGGAG	GGAGCTGACC	CACTCTCCAG	GGAGCCGCTG	GGACACAGAA	AGCACTGGST	3240
	GAGGAGCTGG	CAGACTCGGG	ACCAATCTCT	CTGAGCTGCT	CGCTGATCCC	ACCCCTCTCT	3300
	CGCCGAGTGT	CGCCTTTCTT	CTATTATATC	AGTAAATATG	CGTCTGACAG	TCCAGAGGGG	3360
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55	GGATGCGACC	TTCTCACTCA	CACTATCAGC	CGAGCTTCCA	GAGAGCCCCA	GAGAGAGCCT	4140
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	CATTTGGAAA	CGTGAAGCTA	GTTCGAAAAA	CGCTCTGCTA	CGCCTGCGCT	TGGGAGGCCC	4380
60	ACTCCGACAG	CGGCGGCTCT	TCCATGGTAC	TGTAGAGAGG	GAATCTGCTC	CGCTGCTCTT	4440
	TGCTCTCTTT	GTATATGAGG	TTCTCACGCC	GACCAATAAA	CAGCTCCGAG	TTTGT	4495

Seq ID NO: 126 DNA Sequence

Nucleic Acid Accession #: NM_003786

Coding sequence: 71..4654

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70	CAACTGTGCT	GTGGACACAG	AAAGACCGGA	CGCTCACTCC	TGCTTCCGGA	ACTCCCTGCT	180
	GGCTCTGGGT	CGCTGATCTT	ACCTGTGGGT	GGCCCTGGCC	TGCTACTTGC	TCTACTGGG	240
	GACACATGTT	GGGTGCTACA	TGATCTCTCT	CGACCTTCTC	AGGCTCAGGA	TGGTCTTGGG	300
	TGCTCTGCTG	TATGGGAGAG	CGTGGGGGGA	CGCTTTTATC	TGCTCTCAGT	CGCTCTCTCT	360
75	TGGCGGCG	CGCTCGGCTG	TCCTTTTGTG	CAGCCGCTTG	GTGGTGGGGG	TGCATCATCT	420
	GGTCCGCAAC	CTGCTGATAC	AGTATGAGCG	CGTCCAGGCG	GTACAGCTCT	GGGGGTCTCT	480
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	CTTGTGGCTG	GTACTCTCTG	CGCTCATCTC	GGCTCTCTTC	AGGGAAGAAC	CTCATTTTCT	660
	CTTCGGAAG	AATGTGAACT	CTAACCCCTA	CGCTGAGAGC	AGCGCTGGCT	TTCTCTCCGG	720
80	CGCTTTTCTT	TGTTGGTTCA	CAAGAGTGGC	CATCTATGSC	TACCGGATCT	CGCTGGAGGA	780
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	GGAGGCTGG	AGGAGAGGAG	AAAGAGAGAG	GGCATGACAC	AGGCTCTGAG	GGAGCGCTGG	900
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	CTCCTCTCTG	AAAGGCGCTC	TGGCCACTCT	GGGCTCGAGC	TGCTCTATCA	GTGCTCTGCT	1020

WO 03/025138

PCT/US02/29560

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Seq ID NO: 127 DNA Sequence
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 Coding sequence: 102..899

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WO 03/025138

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Seq ID NO: 128 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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Seq ID NO: 129 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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Seq ID NO: 130 DNA Sequence

Nucleic Acid Accession #: NM_005458.1

Coding sequence: 461..3286

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Seq ID NO: 131 DNA Sequence
Nucleic Acid Accession #: NM_014817
Coding sequence: 247..2682

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Seq ID NO: 132 DNA Sequence
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Coding sequence: 206..2926

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AGTGGAGCT GGAATGAGT TATGAGATTA GACAGATAT ACCTTATTA TTCACTGATC 1260
AGACATGAA GGCATCCCA CATATGGCT TCCAAACCA GCCACGCGC TATCAGACT 1320
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TACACAGCC TGGAGAGC TATGAGAAAT CATCTGCGA GATCTACTAC AGAGTTTCC 1500
CATCAAGCC GGCACAAACA GCAAGACGG GTGTACAC OTGTGCAAC CAATGACCT 1560
TGAACAAAT AGAATTTGT TCTTACTGT TCGTCCAGAA AATCAAGTGT CATTAGCCCA 1620
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TGAAACCCCT TATTTTGGC CCAATCTTA GATCATTC CAGAGAGAGT GCGTCAATC 1740
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TAGATACACT AATATTCTG ATCTGCCAA TTGGCTAAA ATAGACTCTG TGAATGACA 1860
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TGGAGACT ATTAATGCT CCGTAAAGC AGCCAGCAT ACACCCAGC CTCCACATTA 2760
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TGTGTTTT TTAAGAAA AATGGAAA AAAAGGCT TTAACCTGA GAGCTTCTG 4020

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ACGACAGCCTT TGCCTCTGTG TTGTGTACCA GAATATAAAT GATACACCTC TGACCCGAGC 4080
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Seq ID NO: 133 DNA Sequence

Nucleic Acid Accession #: NM_016941.1

Coding sequence: 8..1864

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10	CATTTCCTC	CCCCAGAC	GGCCCGCTGG	CCCTCTCGAG	CTCGACATCC	ACTCTTTGCG	120
	CGCGGTTCCA	GGCCCTGGGG	CCCCCGAGTC	CCCTCGACAG	CGCCCGCTCC	CCTTCGCGCT	180
	CTCTCTCAGA	GTCTGCTCTA	AGCCGTGGCT	CTCGAGAGAG	GGCCCGGAGT	CCCCGTGCGC	240
	CGCGGGGCG	GGCGTGGAGC	CGCGTGGAGC	GTCTCTACAC	GAGCGACCG	GAGCCCTCCG	300
	CGCTGATCTC	CCACTGCGCG	AGCGGCTCTT	GAGGTGCCC	TTCCGGGAGC	CTCGGCTGG	360
15	CACCTCTCTC	TTCACTATG	AAACCTGGAG	AGAGGAGTTA	GGAGACGAGA	TTGAGGGGCC	420
	CGCTGTGAGC	CTGCTGGGCC	CGTGTGCTGG	CAGCGCGCGC	TTTGACACCG	GAGGCCCTGT	480
	GGCGCGGAC	ATTCAGGGCG	CAGGGGCGCT	GAGCTGTGCG	TTCTGTGTAC	GGCGCGGTG	540
	CGAGCGCGCT	GGCGTGGGGA	CGGGTGTGAC	GGCGCTCTGC	CGTCCGCGCA	GGCGCCCTTC	600
	GGGTGTGGGT	CGGGAGCTGC	GGCCCTGGGC	ACCGCTCGAG	GAGCAATGTG	AGGCGCGCGT	660
20	GGTGTGGGCA	GGAGGCTGCA	CGCCGTGAGC	TGGCTTCTGT	GAAGACCGCG	GTGAATGCGC	720
	ATCTGTAGAG	GGTGTGAGTC	GACCCCTCTG	CAGGGTCTCT	GTCTCTACCA	CGAGTGTGCT	780
	CAAGCCCAAG	GGCCCGCTCT	CTGTACCAAC	CGAGTGCCTT	GTCCCTGGGC	CTGGGCCCTG	840
	TGACGGGGAAC	CGGTGTGCCA	TGAGGGGAGC	CTGTATGGAG	ACACCGAGGT	CCTTTGAATG	900
	CACCTGTGCG	GTTGGGTTCT	AGGGGCTGGG	GTGTGAGGTG	ACCGGGGTGA	CATGTGACAG	960
25	TGGACCTTGA	GGTGTGAGTC	GACCCCTCTG	CAGGGTCTCT	GTCTCTACCA	CGAGTGTGCT	1020
	CTGCACTCTG	CCACTGTGTT	TCCAGGCTCT	CAACTGTGAG	AGAGGGGTGG	ACCGGTGCGG	1080
	CCTGACGCCA	TGCGGGAATG	GCGGACTCTG	CTGTGAGCTG	GGGCAAGCGC	TGGCGTGGCG	1140
	CTCCCGGCGC	GGTCTGGGCG	GTCTGTGCTG	CGAGACGACG	CTGAGACCGT	GGCGGGCGCG	1200
	CGCTGTGCTG	AGAGGAGCTA	CGTGTGTGGA	GGGCGCGGCG	CGGCAAGCGC	CTCTCTGGCG	1260
30	CGCGGCTCT	GGCGGCTGCT	ACTGCGCGGA	CGCGCGGACG	CGGTGCGGCT	CGCGCGCGCT	1320
	TGCTCAAGCG	GGCCGCTGCT	AGCGCCACTT	CTCCGCGCTC	GTCTGGCGTT	GGGCTTCCGG	1380
	CTACATGGGA	GGCGGGTGTG	AGTTCCCGAG	GGACCCCGAG	GGCGCAAGCG	CCTTGGCCCG	1440
	AGCCCGGCGC	GGCTCAGCG	CGGGGGAGCC	CGCGGAGCTAC	CTTTGGCTCT	CGGCTCTGGG	1500
	ACTGCTCTGC	GGCGGGGCTG	TGGCGCGGCG	CTGTGTCCAG	TGGCGCGGCG	1560	
35	TGGGCACTCC	CAGAGTATCG	GGTCTGCGCT	GGTGTCTGGG	ACCCCGAGCG	GGTCACTGCA	1620
	CGGACTCCCG	GATGCACTCA	ACAACTTAAG	GAGCAGGAGG	GGTTCCGGGG	ATGATCCGAG	1680
	CTGTGTGCTA	GATTGGAGAT	GGCTGTGAGA	TGTAGACCTC	CAGGGGATTT	ATGTCAATAT	1740
	TCGCTCTTTC	ATGGCGGGAG	GGGAGGCTAC	GGCTCTCTTC	TTCCCTCTCTA	CGAGAGCTG	1800
	GGCGCGTGGG	CAGAGCGGAC	ACCTGCTTTT	TCCCTACCTC	TCTGTGATTA	TGTCCGTGAA	1860
40	ATGAATTGGG	TAGAGTCTCT	GGAAGGTTTT	AGGCCCATTT	TCAGTTCTAA	CTTACTTTCA	1920

Seq ID NO: 134 DNA Sequence

Nucleic Acid Accession #: FGENESH prediction

Coding sequence: 1..411

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	CTCGACCATC	ACCCACTGGA	ACATGCCCAA	TCTTGCCTGA	TCTCAGAGAC	TAAGCAGGCT	120
	CAGCGCCAGT	TACCACTTGG	ATGGGTGAAG	TGGCGCTTGC	ACTTTGGGAG	CTCACTGTCC	180
50	AAAGAGTTGG	AAAGAGAGTA	CCCGGCTCTA	TGTATGGGCG	AAATGTGAGC	ACAGATATGT	240
	AAAGACTCTT	CTCTAGATTT	ACCGCACTGT	GATCTGGTGA	CAGCTGTATG	TTCCACTGTA	300
	GTAATATCTC	CGGAAATCTC	CCCTGTGTTT	GGATTCCATA	TCGTCAACA	CGAGACTCTG	360
	CATGTAGAAG	CGATGGTTAA	CATCTCCAAA	GGCTCTCTGT	GCGAAATGTA	G	411

Seq ID NO: 135 DNA Sequence

Nucleic Acid Accession #: NM_024812.1

Coding sequence: 184..621

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60	CGGAGAGGGG	GAGCGATGTG	GGCGGCGGCC	GGCTCTCTGC	GGGCGGGGCG	TGGCGCTCCG	120
	GGGTGTGGCG	GGCGGACGAG	CGGACAGGGG	AGCAGCGCGT	GGGCGCTCCG	GGGCGGGGCG	180
	AGGATGGGCT	GGGCGGGGAG	CGGAGGGGAG	GCACTGAGAG	TGGCGGGGCG	CGGCGGGGCG	240
	ACCGGGAGCA	CAGAGTCCAC	CTGGCTCAAC	TACACGCACT	CGGCGGGGCG	GGCGAGGGCG	300
65	CGCGCGCGCG	ACAGGGGCCC	GGGAGCGGGC	GGCTGTGACT	CGGCGATGCT	GGGAGATGGA	360
	CTGCTCTGCA	ATGGTGTGCC	CGGATCTACA	GGCCGAGGTG	GAATACCCAA	CCGACGAGAG	420
	AGGAGGAGCT	GGGCGGGGAG	CGGCGGAAAT	CCGCGAGGCC	TGGCTGAGG	CGCTCTGACC	480
	CAGAAACAGA	ATGGCTCTCA	GACCCAGAGG	GCTAAAGAG	ATGCTAAGG	AATGCTCCCA	540
	AAAGAGTCCA	CCATTAAATG	AACAGATAGC	ATCCACAGA	TGGCAGAG	TGGAGAGATC	600
	ACAGAGCACT	GTTCTCACTA	CAGAGAGTCT	CAGCAGAGAG	GGCGAGATGA	CTTCTTCAGT	660
	GTCTCTTACG	GGACTGAGAT	CATCAAGAGA	ACCTGAGAGA	AGTGGCTGCC	CTCTTACGAG	720
	CGTGAATCTT	ACTGAGTCCC	TGGCAAGAGC	GTTCTTACCT	GGGCAAACT	CGTCTCTGAG	780
	TGTTTGGGAC	CTCTTGAGGC	TTCCTTCTAT	CATGTAAATG	TATTTGGACA	GTGCTTACAT	840
	ATGTTAATAA	ACTGCAGATG	TGCAGTTCAG	TTTGTCTCTT	TGCACCTCT	GTAATACGGT	900
75	CTGTGTGAAA	AGTATGAGAT	TAAAGCTTGA	GGTCAAGTTA	TGAAACAGAA	AGTATGAGAT	960
	GCATTTTGTG	GGTATGAGAT	CTGCTGAGAT	CTGCTGAGAT	CTGCTGAGAT	ATGATGAGAT	1020
	ATCTGTGTTT	GGTATGAGAT	ATCTCTTCTC	TCTCTCATTT	TAAATATGTG	CATTACAATG	1080
	CTTACCAAGT	TCACTTAAAA	GCTGCTTTTC	ATCCAACTCT	AAACCCCAAT	ATGAAAAAAA	1140
80	TCAAGGTAGA	GAAAACATCC	TGTATATCTT	TGTTTCTCTT	GCTTGTGATG	AGAGAGATCT	1200
	GATCTGATCT	CCGATGAGCT	AGGCTGAGCT	CGATGAGTCT	GCTGCTGAGT	GTGCTGAGT	1260
	AGCAGTCAAT	CTGTGCTCTC	ATCTGCTTGG	AAAGTCTCTC	TATTCGAGTG	TCCATGTGGG	1320
	CCCTCAGTGC	TTAATGTGAC	CATGCTGTGG	GCGAATGATC	CCAAATAGG	ATACCCCTCA	1380
	GGGCTCAGCT	AGACATGACA	ATTTTGATCA	GCTTTCAGGT	TCCCTTTGCT	TGCTTCTCTG	1440
	ACTGTCTTTC	CTTCTTACAG	GGGCTCACTG	CAATGTGTTA	TCAAGAGTTG	AAAGCTGCGT	1500

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AGGAGAGGGA GATGATCCAG AGACATGTGG CAGCAGGCAT GGCCTCCCTT TGGCCTCTCT
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 TAGCTGTACG AGAAAAGGGA TGTTTGTGTA GAATTAATTT TCTAGTATGT CTTGGAACAT 1740
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 AGGCTGTGGA TTGGTAAAGA TAGACTATAA GTTGTGCCAA ACTATATACA TAAATTCCTA 1860
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 ACATGGAGGT CAAGAGTCAG ATAGGCAACC TCTTATCTGT CTAACTCTGT TATCTTCTAA 1980
 GACAGAGTGG GTAGTGTGAT TTTTCTCTCT TCTCTTCCAT TGGCAGATGT TATTATATAT 2040
 CACAAAACAT TAATATGCGA TCTGTGTGCA GTTACTATGC AGATGTTCAG GATTTTGGGG 2100
 TCTGGTTAGT CTGACTATAT TATCTCTGAT CTAAACATGA CTTCATAACT AGGAGACTGA 2160
 ATTAGACCTT TAAGGTATAG TGTGTGTTCG AAATCACTCT GCAATGAGAA CTCTTATATAT 2220
 CAGGGTAGGT TGTGTCTTTA AACTAGTGTG TCTAATCAAT GTACAGAACT TTACATATAT 2280
 GCAACTATTA GTTGAAGTGA TTTTCTGATG TTTTGGAT TTATCACTT AGAATAGTGT 2340
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 CATATGTGCC CACTGGCATT ACTCAGCAGG AGCCCCAGC TGCCAAAGGT TGGCAGTGAT 2460
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 TTTTCTCTGC ATACCTTCAC TGTGCAATGT TGTTGGAT TTATCACTT AGAATAGTGT 2580
 CTCTCTTTTA TATAGAAAAA CTTTCTCACT TACAGGGGAG AAGAAAGTCT AGGGCAGATG 2640
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 GTGACTAAAA ATGCATCTGG CTACTTTTTC ATGTATGTAT GAGACAGAAA CTAACTCTTA 2760
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 AAGAT

Seq ID NO: 136 DNA Sequence
 Nucleic Acid Accession #: XM_040550.1
 Coding sequence: 62...415

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CTTGTGTTTC GGTTCGAGAT TCCACAACT CCACTGCTGT TCTTCGAGCG TGGTCTGAA 60
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 GGGAGATGTG CCAGAGGTCAT CTGTTTATGC GAGGAGGGCT AGTGTGTGTA GSACTGCGGC 960
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Seq ID NO: 137 DNA Sequence
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15	TTTTTATTCG	ATGTGAGCCA	GAAAAATTTC	GTATGCCCCA	AGATAGCTTT	GTCTCGGATC	900
	ATAGTGAATG	TGCTGTCTCG	AGATCATCTT	ATTCTCGATC	CTCAGCTGTT	ANGTATCTTG	960
	GATCCAAAGG	CCCTGGGCCG	TCTCGACCGA	GGAATACAG	AGCTTCAAGT	AATGGAACAT	1020
	CGACGACCA	ACTTTCTACT	CTTAATATCA	CGAATCTCT	CAGTTCTCTC	CGAATAGTC	1080
20	CAGGAAGTTT	CNAGAGATTA	AAAGTATCTG	CTCATGGCAG	ATTCTCTTCC	AATGATAAGG	1140
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	AGTACACTGA	GAGAAATGCG	AGTGAACATG	TGTATACAGT	AGGCATAGCC	CTGAGATATC	1560
	TGCTATGGCT	CAGCATGGAT	CACAGAGACN	TGCAACACAG	GAATCTCTTG	GGTGTGATAT	1620
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35	CAGGTAAACT	AAAGATGAGC	TTTATATATC	AGTGAAGTCT	ACGACACAGC	ACTACAGGAC	2100
	GGGTCTCTCG	CATCATGTTT	GATTTGACAG	TTTGAAGAGC	ACCTCAGAGT	TTCTCTCTTT	2160
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55	GCACCAAACT	CGTGTGCTCC	TGAGAGCGAG	GAGCTGTGCG	AGCAAGATGA	CTGTGCTCTC	3300
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	TGAACCTTCT	GGAGGCTGCG	TGGCAGTTTT	TGCTTTTFTT	CCACACCCCT	CGCTCTTTTA	3480
60	ATATTTGTAC	ATATATCCGTG	TATTTGTTTT	ACCTGCTCAT	CTTTCAACTT	GGGAGGCCCT	3540
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Seq ID NO: 140 DNA Sequence:
Nucleic Acid Accession #: NM_015163.2

Coding sequence: 1801..3933

65	Coding sequence: 1801..3933						
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	CCAGACNAGA	AAGCAGNAGA	GAAGAAARCA	AAGAAAGAGA	AGAAAGAAAG	AAGAAAGAAAG 180	
	AAAGACAGGAA	AGCAGAGNAG	CAGCAAGACG	AGCAAGCAGG	CAGAGAGACA	AGGCATGAAG 240	
	AAGACARAGA	AAGAGAGAGAA	GGAGAGAAAG	GGAGAGAGCA	GAAGACAGAA	AAGACAGAGAA 300	
75	CGACAGGACG	GAGAGAGAGA	GGAGAGAGGA	GAGAGAGAGCA	GGAGAGAGGA	GGAGAGAGG 360	
	CTGGGCGCGG	TGGCTCTACCG	CTTGCACTCC	AGCACTTGGG	GAGGCTAAGG	CAGGCGGACC 420	
	ACCTGAGGTT	GGGATTTGGGA	GACCCAGCTG	ACCAACATGG	AAAAACCCG	TGCTCATGCG 480	
	AGTGAACAACT	ATTACGACAGG	CCAGGCTGGC	CATGCTGTGA	ATGCCAGCTA	ATCAGAGGAG 540	
	TGAGGAGAGA	GATAGCTGCT	AACTGTGGGG	CTGTGGAGGT	GGTGGAGGCT	GGTGGAGGCT 600	
80	ATTGCGCTCT	AGCCTGGGCA	ACAAAGGTGA	AACCTGTGCT	CAAAAAGAAA	AAAGAGAGAA 660	
	AGAGAGAGAA	GAGAGAGAGG	AGAAGAGAGA	AGAGAGAGAA	GAGAGAGAGG	AGAAGAGAGAA 720	
	AGTAAATAGG	AAGAAAGAGCA	AGAAAGAGCA	AGGCTAGGCA	AGTCAAGGCA	AGGCCAATCT 780	
	ACCTGCTTCT	ACTACATGCT	AGAGAGATCA	GGAAATGAGT	CAACACACAC	AGGCTATTA 840	
	GGCGGCTTCC	CATCTGTCTCA	ACCCGAGCGG	AAAGATCCAC	GGCGGCTTCC	GACACAGCA 900	
	AAGACAGGGA	AACCCCTGAC	CAAGAGGAGG	AACATATGAG	CCGAGCCAGG	GTCTGTCTCC 960	
	CGGGTGTGTC	TGGGCAACCA	GGGAGGCGGG	GCCCTCGAGA	CTCCGTCTGG	AAACATCAAT 1020	

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PCT/US02/29560

Seq ID NO: 141 DNA Sequence
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10	GTGAGAGGGA	AGACATAGCA	GTGTTTGGTA	TCCAGAGAGA	ACCTCTTCTGGA	CGGAGCTCTCT	240
	CCGACCGGAG	TGACATAAAT	GGAGGTGGAG	CTGCCGCCGA	GGGTGTGGAG	CTGAGGTGAG	300
	GCCTCCCTCAG	TCCAGAGAGA	CTTGGAGAGA	TCTTGGATGA	GGCCAACTCG	CTGGGCCCTCT	360
	AGCTGGAGCA	GTGTGCGCTG	CAGATATGGG	AGAGCGCAGG	CGAGGCGCTG	GGGCTGTGCCC	420
	GAGTGAAGCC	CAGTCTTGCG	CGGAGAGACT	TTGTGCTGAA	GGATAGTCTT	GTCCDAGAGC	480
	TGCTTCCGAC	TGTGAGCTCT	TTGAGCGGGA	CGACCTCCCT	CCGAGAGAGC	GTGAGGCTTC	540
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Seq ID NO: GAD8 DNA Sequence
Nucleic Acid Accession #: NM_022123.1
Coding sequence: 76...2781

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	AAAGAAACT	TGAATTTCTA	TGAATTTGGC	AGGTTGTTTC	CTTCTTCCCG	AGCCATTACC	240
45	AGCCAGCTCG	ACAGAGGATC	CATCATTTGA	CTTACAATTA	GCTATCTGAA	AAGAGGGAGC	300
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	TCTAATGACA	CTTCACTAGT	TACAGGAGCA	AAAGGAGACT	CCCAATCCGA	CGAGAGGGG	1440
65	AGCCGCTCCG	AGAACGGGGA	AGACCCGGAG	CCCGACCGGA	AGAGGTGGGG	CAACCGGTGT	1500
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	CGGTGTGAGA	ACTGCGAGCT	ACTGAGCTTC	GAGACGCGCA	AGGACTCTGA	CAGACGAGCG	1740
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 Nucleic Acid Accession #: XM_166946.2
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 Nucleic Acid Accession #: XM_022123.1
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	GGCGGGGCG	CGCGCGCGG	GGGGGGGGG	GGAGCGCGGT	CGACTCTCT	CGCTTACACT	2340
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	ACTCGCGCG	CGGCTTCTG	GGGACAGGG	AGCGAGGGG	CGGGGGAGG	CGAGGACTG	1140
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Coding sequence: 63..75		
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20	TGCGCCCTCG AGGCCACCC TTGAGAGC CTGGCACCTT GCACATCTG AACCTGCTCT 780	
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	ACCGATAGT TCTCTCAGAA TACTCTAGA GCTTCAAGGT CTCCGAGTCC AGAAACGTTC 1200	
	TGTTGAGCTC ATGCCCTCTT CATGTGGACA GCTTCTGAGT GGTGACACAG CAGGCGCTTC 1260	
30	TTCTGTTCTT GATTGTGACA GCCCGAGTCT CAGCTAAGTG ACTGTGGGT TGTGTGAATC 1320	
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50	CAGTGTGACC AACAATATT AGTAGTAAAT CCGTCTTTTC TGCATTAATG TAATGGCAC 2580	
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	ACACTTTAAG ATCTGGCAGA GTTTGTCCT CGCATTTCTC TTCTTTTTTC AGACTTTTT 2760	
55	TGATTTCCCT TGATGATCT TTGGAATCAG CTTGTCAAG TCCAAAAATA TCCGTGTGGT 2820	
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65	CTTCGGGCCA CCGGTCACTT CATGGGCAAG AAGAGTCTGG AGGCTTCCAG CCCATCCCAT 240	
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	TCGTGAATCC TCTGTCTAAA GAGGCTCTTG GCGCTGAGCC TCGAGCGCCC CGCACCCCAA 360	
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70	ACACACAGCG GTGGCTTAGA TTGTCCAC ACAGGGAGG TGCTGAATGG GAGCCGTGTG 480	
	ATGCGCCCAT CTGGATGTAA ATCTTGAGCT CAATCTCTGT TTACTGCATT ACTGTGATT 540	
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	GGGCACTACA TCGTCTCTTC AGAGAGACCC GGGCAGTGA GCGGGGAGAT AGTATGGAG 240	
	TGATGACCCO CTTTCCGCC TACATGAGA AGGTTCCCTT CTGCGAACAG CAAAACAGG 300	
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	ACCAAGCTGA	GCTCGAGAG	CTGCGGCTG	GGCTCGATCA	ACTCAACGCC	AACAGGCCCC	420
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	AGGATGAAC	CNACTGTGAG	CTGGAGGCC	AGAACAACTT	GCTGCCCTAT	AGACAGGAAG	540
5	CAGATGAGC	CACCTCGGCT	GCTCTGGATC	TGGAGAGBBA	GATTGAGTGT	CTGTAGAGGAG	600
	AGATGCTGTT	CTTGACGAG	ATCCAGAGAG	AGAGAGTCTG	GGAACTCTAC	GAGCACTGCG	660
	CCGCAAGCA	GCTCAAGTGT	GAGCTTGAOS	TGGCCAGGCC	AGACCTCAAC	CGACGCCCTGA	720
	ANAGATCCG	CAGCACTGAT	GAGGCAATGG	GCTCGACBAA	CATGATCATGA	GCCGANAAGAT	780
	GGTACGCCCT	CAAGTTTGTCA	GACTCTGACG	AGCCTGCTGC	CGGCAACGCG	GAGCTGCTCT	840
	GCACAGCTCA	GCAGAGAGCT	AACTCACTAC	GGGCACTGCT	ACTCTGACAG		900
10	TGGAGTCTCT	CTGCGCGCAO	AGCAATCTCC	TGGAGAGSCA	GATGGCGGAG	CAGSAGAGAGC	960
	GGCACTGTGG	GGAGGCGGCC	AGTTATCAAG	AGGCGCTGOC	CGCGCTGGAG	GAAGAAGGGCG	1020
	AGAGCCTTCA	GGAGGAGATG	GCCCCGCCAT	TGGAGAGAGT	CGAGGAGCTG	CTCAATTGTCA	1080
	AGCTGGCCCT	GGACATCGAG	ATGTCGACCT	AGCTGAGAGT	GCTTAGAGGGC	GAGGAGAACG	1140
	GGATGACAT	TCTGCTGAG	ACTCTCTCCA	GCTCGAGAT	TGGAGAAAC	AGCCTGGATCA	1200
15	CCAAGTCTGT	GTCAAGAGGC	CACCTCAAGA	GGACATCGT	GGTGAAGACC	GTGGAGATCG	1260
	GGGATGGAGA	GCTCATTAAG	GAGTCCMAGC	AGSAGACARA	GAGTGTGATG	TGAGGCCAGA	1320
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	CGGCTCTGTG	TGGACGATTT	CCGCGAGCT	GAGTCTCCCA	CGACCCGAGC	TGCTCTCTCT	1440
	CGCTCTCTGT	CGCTTAGTCA	GCTTGTCTGC	CTAGGCTCCG	TCAGTATCAG	GCTCTGCCAGA	1500
20	CGGCACTCCG	CGACGACCCA	CGAACTCCAA	CTAACAGAGA	ACTCAACCCC	AAAGGCCAGT	1560
	TGGAGGGGCA	TGGCCMAGC	CTTGCTGTAG	ATGAGAGAGG	AAGSAGAGAA	GGGCAAGAGG	1620
	CGGGGGGCA	CTCTACAGAT	CGGCTCTCA	ATCTCTGATT	CGTGTCTTTA	TGGAAACTGT	1680
	TGGCAAGAT	GGAGGTTCTC	TGCGAGTATC	TGGGAAGTGT	CGCTTTGAGT	TTCTCTCAGC	1740
	TGCTGGAGGA	AAACTGAGAC	TCAGACAGGA	AGGGGAAGGC	CCCAACAGCA	AGTATAGCCCT	1800
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	ATTATAGAT	TGAGCCACCA	TGCCAGCTCT	AGAGGGTTGT	TCTCTAGAC	TGACCCGTAG	1980
	CGCTCTAGA	TGGGTTGGGA	CGTCTGCCA	CTTGGGCGAG	TCACCTGCCC	AGATCCGAGA	2040
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	TGTGGGTACA	GAGAGGCTCA	GCCCCAGGAG	ACTGCCCTGT	CGAGACTGGA	GGGAGCGCTG	2280
	GTAGAGAGTC	AGGAGGAGGC	AAATGGGATG	GGACTAGGCA	TACAGATAGG	GGTGTGTGGT	2340
	CGACAGTTC	ACTGGGCTCT	TGAGATTTGG	GAATTAGGA	AGTACTGAG	CGCTTGTAG	2400
35	ATTCTGAAC	AGSAGAGAA	GGGATGTTAT	CGATGGGGC	AGGCTCAGAC	TTTGTCCACT	2460
	TTCTAAAGCG	CTCTTCTGTT	CTGTGTCATA	CGAGGCCGCG	CGAGCCTCTG	AGCCCTGGG	2520
	ACTGCTGCTT	CTTAAACCCA	GTAAAGCCAT	GGCAACACTC	TGACCTCTCT	CAGCCGATAG	2580
	TGA CGCGCTG	CTTTTCCCTA	AGCCAAAGGC	CGTCTCGGCT	CTCTTCTACT	CGAGAGGCA	2640
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40	ACTGAAAGCA	CTGGCTCAAT	TTCTCTCAGC	CTGGAGGCGG	GGTCTCAGG	CGTGTACAGT	2760
	CGACCCGAGT	GCACCCACTC	TGCTTTGACT	GAGCAGATGT	GTGCGCAGAC	TGGTGGGATC	2820
	TGTCGCCAGA	GATGGGAGT	GGAGGGGCCA	CTTACGGGTT	CCTGCTCTCC	CTTAGAGGCC	2880
	GAAGAGAGGT	CTCTCTGAGT	CTCGAGAGCT	TGGTCTGACT	TCTCTCTACT	TCTCTCTCT	2940
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Seq ID NO: 149 DNA Sequence
Nucleic Acid Accession #: L29126.1
Coding sequence: 445..1845

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	CGCTCCGAC	CTTGTGGGC	TGCTTGCCCT	GGAGCTGGTT	AGGCTCAGC	AGGCGAGGCC	180
55	TTGTTTGTGT	TGTCGAGGA	GGCAACTCTC	TGGAATTAGC	TGGCAAGGCG	GTATGTAGCT	240
	CCACATCTCT	TGTCGAGT	CTGCGCGGCT	TCTCTCTTGA	GGCAAGACTG	AGTCTCCGAC	300
	CCAGGGAGAA	ATCCACCGGG	GTGCGAGTGG	AGGGGGCAT	CGAGCGAGGG	AGAGCGGGGT	360
	CGAGAGCCCA	GAGCGCGGCC	AGGAGCCAGG	CCCCCACTA	TCATCTCCCC	TGAGGAGAGC	420
	TAGGAGCGGC	GAGCAGGCGA	GGTATGGGT	CTCTCTTCCA	CGCTCTCGGG	CTGTGTGTGT	480
60	TGCTCCGATG	CTGAGAGAT	CGAGGCTCTC	ATATGGAGAT	CATACTATTA	TCAGTTACAG	540
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	GCTCTGAGT	TGGAGAGT	CTTCCAGCA	CGCTCTGAGC	GTATCTGAGC	GAAACACTG	780
65	GTGGGTGAGA	AGAGGTTTGA	GTGAGTTTCA	GATCTGTGTA	CAGATGGCTT	GATAACACTG	840
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70	CGCACTTTA	AGGTCACAC	GTTCGAGGCG	CGACACTGGT	GTGAATTATG	TGCAAAATTC	1140
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80	ATGATGAAGA	AGAGAAATTT	CATGATGATCA	GAAGATCTGG	GGATCTGTGT	TGGTCCCACT	1740
	CTGATGAGCG	CCCTGAGAGA	CAGCACTCTC	ACCAAGCTGC	ATGATATGG	GTACCAJAAAG	1800
	CTGATTGTCT	AGAAATTTAT	TCAGAAAGGA	GACGTTTTAT	TCTATTCACT	CAGGGAAGTG	1860
	AGCTGAATGC	CCGACACCA	CTAGATGAGT	ACAGCTAAGG	ATAAACACTT	TCTTACCCT	1920
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5
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 AGCGCGGTGG CGGTGTTTGG GAAGATTAC GTGTGCTAAC TGAGACCTCA CATCTCCCA 2160
 GCAAAAGGAG AAAATCAAGG CCGACATCTC ACCTGCGGCT CTGCTCTCTG TCGAATATGA 2220
 GACTTCAACA TGTATGCTGT TCGTCTTTTC GAGAGTAICT TGCGCTCTCA TGCACTGATC 2280
 AACACAGCAT ACCAGATGAC CAGGTGAGCC CATCGCTCTT CCGCTGCTGA AGAACAGAG 2340
 TTCTGTATCA TTCACTCCAC TCGGACAGAA AAAATCTATT TCCGACACAC AGCAGAACTC 2400
 ATTACACAC TAAATAGGGG AAGGAGCTAT TACAGCTTAC AGATTATCCG CGAGCAAGAC 2460
 CATTAATCTA CAGCTCTCTG CTCTAAACAG CATCTGATCC CAGCGACAGA AACCTCTCTC 2520
 GTGATATGCT TCGAGCTCTA GGCACATCTG CCGACATCTA CAGCGACAGA GAGCGAGAG 2580
 GAGGACTRAG CTCAGGTGCG TCTAAGACCA AAGTGGCTCT TTCTTCAAC CAGATGCAAC 2640
 CGAGGATTTT CCCTGCTCTC CTCTCTCTCT CGAGAGGGGG GGGCGGGGGG GGGCGGGTGG 2700
 TTCTATAGCA TGTGTGTCTT GGAATCGGAA GCAATTTTGT CTGTGAGAAC AAGCTCTCTC 2760
 CGCGGGGTCT TCACTGAGTG CATTGAGGCG AGGCTGTAGA GCGCATTTGT TTGAGAGTGT 2820
 CCTCTCTCCG GCGCGCGAGA GACCGGACCG CCAAGCGCCC TCCCGCCAGG AACAGAGCAA 2880
 AGGATGTGGT CCGCAGCGCC CACCGGAGCC CACAGGACAC CGCGCCCTAG ATTCCAGCCA 2940
 CCAAGCGGGA CAGTAGAGCC GCGCGACACT AGCTCTGTGT TTCCCTGTAG CGACATATCA 3000
 CCTGTGTCT CGTGTGAGTG CATTGAGGCG AGGCTGTAGA GCGCATTTGT TTGAGAGTGT 3060
 CGTGTTCATA TATGGCGTTG CTACTCTCTG TAATGAGGAC GTTCCACATG GTGAGGGGCT 3120
 ACAAGAAUAC GCTTTTCTGT ACAGAGTCTA ACTGTAGCTA GCTTAATGAT TAACCTGTAT 3180
 GAATTAAGTC GTATTTTCTT ATGGTGTTAA CTTGATCTTC CACTGTCTCT GTCATGGGTT 3240
 TGTATTGCTT TTTGATGCTT TGTGATGCTT CAGGAGGAGAG AGCTGTGAGC AGCTGTGAGC 3300
 TTGCGCTGTG ATGAGAGAGC AGATCGGAGG TAACGTCTCC CTCTCAAGG TTGCTTTCAG 3360
 AGCTCTGGG GAGCTTCTTA AACACTGAGC GGGAGAGACG CCAATAGCAC CATTAAAG 3420
 AAATACCTAA ATAAAACTTC TCTCCACTC AGCTATGCTA GCGCTTGGCT GTATGTGTGC 3480
 ACTGTCTATT TACATGAGCT CTTACAGCCA TCTGTGTCT CTCTGTGACC GTATCAGCT 3540
 CTTCCTCATG ACAATTTGTT

Seq ID NO: 152 DNA Sequence
 Nucleic Acid Accession #: XM_087461.1
 Coding sequence: 236..118

1 11 21 31 41 51
 | | | | |
 CGCGCGCGCG GCGCGCGCG GAGCCACCAA CGAACCGGG TCTTGAGGGA TCCCGCGGCC 60
 GAGCCACCAA CTTTCAGCG CTGCGCGCGC CCGCTCGCGG TCTTGACAGC GCGCGCGGCC 120
 CCGCAGCTCG GCGCGCGCGC GCGCTCCGCG GGTCCGACCG TGAGCTCGCG GCGCGCGGCC 180
 CGCGTGCGCA TGCACACCGC GCGCGCGCTG CGCGCGTAGG GCGCGCGCGC AGGCGCATGCT 240
 GCGCGCTCTG GCGCGCGCTC TGCGCGCGCG CTGCGCGCTG CCGCGCTCTG CGCGCGCGCG 300
 CGCGAGGCGG CCGCGCGCTC TCGCGGTGCG CTCANATGCT TCGCTGACAG GCTCTCTCGC 360
 GCGGACGCCA TGCGCGCGCG CGTCTGTGCG TCGCGCGGCC CGCGCGCTCC AGCGGCGCGC 420
 GCGCGCGAGG AGGCGCGCGC GCGCGCGCGC CCGTGTGAC ATCAGCGTGC AGCGCGAGAT 480
 CGTGTAGCTG CTGCTGTGCG GTGCGCGCGC CCGCGCGCGG TTCGAGTGC ACTACTGCT 540
 CTCTCGAC AAQCGCGAG GCGCGCGCTT CTTCGCGCGC GCTCTGAC GCGTGTGCGC 600
 GCGCTGTCTC ATCGAGACAG TGCGCGTGGC GCGCGCGCGC GCGCGCAGG ACTGTGCTCT 660
 CTGCGTGGCG TCGCGCTGAG TGCGCGTGGC CGCACCGCG GCGCTCGCG CCGCGCGCGC 720
 CCGCAGCGCG GCGCGCGCGC CCGCGCGCGC GCGCACCGCG CTGCGACCTT CCGCGCGCGC 780
 CAGCGCGCGC CCGCGCGCGT GCGCGCGCGC CTGCGCGCGC CAATCTGCT GCGTACGCT 840
 CAGCTCTGAG GAGCTGTGAG GCGCGCGCGC CTGCGCGCGC AACCTGAGC CATTTGCGCT 900
 GAGCTGTGCT GCGCTGTGCT TCGCGCTGCT CATCTGTGTT TGAGGCGTGG CCGCGCTCAT 960
 CTGCGCGTGT CCGCATATCG CCGGCTCTCT GCGCACCGCG ATGACACAG CCGCGACAC 1020
 GCGCAGCAGC ACCGCGCGCA CCGCGCGCGC AGCTTGTGCG TGCGCTCTCA GTTGTGAGAA 1080
 CCGCGCGCGC GCTGCGCGCG CCGCGCGCGC GGTCACTTGT GCGGTGTGCG CAGATGACG 1140
 GCGTCTGCTC CTCTCTGTGT GCGTCTGTGT TCGCGCGCGC GCGGTGTGCT TCCCGCGGGA 1200
 GACTGTGCGG GTGTGCTTGT TCGTGTATGT ATGTTTAGTT CCGTCTCCCG AGTGTGCGCG 1260
 GCGGAGAGAC CCGCAGCGCT TCGAAGAGCA AGGTTTGTGC TGCGCTCTCA GTTGTGAGAA 1320
 GCGAATATTT AAGCTCTGCT TGTATGTGGA GCGGTGTGCG CCGGAGAGCG GAGGCGCGCG 1380
 AAATGTGCGC CTCTCTGCTC TATGTGATCC CCGTGTGCGA CTCTCTCCCG GACCCACGCT 1440
 GCGCTAGATT CATGCGAGAA AATGACCAA TCGTGTGTAT TTGTTTATA TATTATATA 1500
 CTGTTTTAAA TGAAATTTT ATGAAMAAA ATACAAACCA AAAGAGTTAA ATTGCTATTG 1560
 CTGTGTGAT AGATGCTCT TATGTGTGGA TGTGTGTGGA TTTGTAAATT GTGGTTT 1620
 AATTATTATA AAATGTGCGG GAGGCGATGG GAAGATTATA ACACGATAT ATGTGTACCG 1680
 CTGAAATGCA ACTTTATGAA CTTTTCCTAA GTTAGCTTAT CAGTGTAGCT GCGCTGTGCG 1740
 GTGTTTCTCT TTGTACTATT GTGTCTTTT GTCTTTTAT ACAGACATT TTCTCC 1796

Seq ID NO: 153 DNA Sequence
 Nucleic Acid Accession #: XM_012261.1
 Coding sequence: 1-843

1 11 21 31 41 51
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 ATGATCTCCC AAGGAGAGG GGTCCCCAGC ATGACAGAGC TTGAGTTCT CCGTATGTTG 60
 TTCCATACAA TGCTCAATAT CATCGACGAA CAGAGAGTG AAAATCTCT AGGCTCTTCC 120
 ACTACACCTG AAAAAGATAT ATTGTGTGTG CCGGAAATGT GCGAGCTGCT TCTGTATGCA 180
 GAGTGTGCGC CGATATCTAT TTACTCTTAT GATGTGTGCG CCGACAGCTA CGTATGACT 240
 ATACAGACAC AGGCGATATT GCAATTAAC CCGGAGAGCT AGGTGAGGCG CCGCTGTGCG 300
 GACCGCAGT CCGAGCTGCA AGTGTCTGCG GTGATGTGCG CATATGACT CAATATGCT 360
 TTGTAAAG AGAGGACCA CATGTCTGAG GAGCCTGAGG GAGCTGTGAG GTGACACAA 420
 GTGCAATTTG TCTAGCACTC CTGAGGAAA ACACACTGT AGAGCGAGT CAGTGTGCT 480
 AAGCACACAG CCACTGTGCA CCACTCTCTC GCGTGTGCTA CCGCCCTGCG GAGTCTCAT 540
 GAGTGTCAAG CTCACACAA CATTTCACTG GCGTCTAGTG ATCCGAGAA GCGGCTCAC 600

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PCT/US02/29560

5
 ATGATCTGT CTGCGTCCA CATCGAAGCT TTGACATTA TCTCAGATT TGTCTTCAGT 660
 GAGAGACATA AATGCCCACT GATGAGCGG GAGCACTGG AGAAACCTT GCCCTTGATT 720
 TTGGGGGCTA TCTTGGGCTT CATTCAATG GTAACACTGG CGATTACCA GTCCACACAC 780
 AAAATGACTG CCAACCAAGT GCAGATCCCT CGGACAGAT CCCAGTATA GACATGGGG 840
 TAG 843

Seq ID NO: 154 DNA Sequence
 Nucleic Acid Accession #: NM_144586
 Coding sequence: 261..686

10
 1 11 21 31 41 51
 | | | | |
 GGCAAGAGGC CGGAGGCGCG GTGCTCGGCC CGGAGGCGCG AGCGGAGGGA GCAGAGAGCCC 60
 CGAGCGCGGA GCCGAGAGCC GGGGATGTGA GGGTCGCTGA GCGGCACCTG GGGTCTCTCT 120
 AAGCTACAG CTCTCTCTCC GGGGAGGCG CGCTCGGCGA AGACCTGCG CGACGACGAG 180
 CCCTCGGAGC GGGGGCAACC TCCGCTGCTG TCGCTCTCTC TGATGGGCTT GCCCTCTCCC 240
 GCGCCCGGGA CTCGSGGAGA ATGTGGGTCC TAGGCAATGG GCGCAACTTT TGCGGATTTG 300
 TCTTCTCTCC AGGCTTTGCG CTGCAATGCG AGTCTCAACA GTGTGAAGAA TTCCAGCTGAT 360
 ACAAGCATCT CTCTCTGCC GAGTTCATG TGATATGCG AGTGGAAGTT CAGACATGAT 420
 GTCAGAAAGA AGTGTATGAG CAAAGTCCCG GGATCATGTA CCCGAGTCC TGTCATCAT 480
 CAGCGCCCTG TCTCATGCC CTGCGCGGGT ACCAGTCTTT CTGCTCCCCA GGGMAACTGA 540
 ACTCATGTTG CATCAGCTGC TGCACACACC CTCCTTTGTA GGGGCGAAGT CCCAAGAAAA 600
 GGGGAAATCT TGCTCTGCC CTGAGGCGAG GCGCTCGCAG CACATCTGTC TTCTCTAAAT 660
 TAGCTCTCTT CTGCGACAC TCGTGAAGCT GAAAGGATG CACCCGCTTC CTGATTTGTT 720
 CTTCGAGCCG TGCGGCCAAA CCCCCACCT CCGTAGTGA GTTTCTCTG GGTGTCTCTT 780
 25
 TATTCGTGGT AGGGAAGCGG AGTCGCTGTT CTCCTTTGTT CCGTGCAAAA TAATGAAGA 840
 TGTGTGAAA GCACTTTGAA TAAATCTCGC CTGACTGAT TTTCATATG TACTTGAAGG 900
 AAGGAGGTGG AGTGAAGTT CACCCGAAA AAAAAAANA AAAAAA 946

Seq ID NO: 155 DNA Sequence
 Nucleic Acid Accession #: NM_004694
 Coding sequence: 166..1737

30
 1 11 21 31 41 51
 | | | | |
 TTGGGGGTTT ATTCTCTTCC CTCTTAACCT GACAGGGTCT TCGCTCTGCA TTGAGCGAG 60
 AGTGCGATG TGTATGATCA TCTTAATGCC GCGCTAAAGT TCCAGGCTCT ACTCAAGCAA 120
 TCTTCCACC TCGAGCCACC AAGTGCGCTG GACTACAGAT TAAGATGAC CAAAATAA 180
 TTAAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGTATGGAG ATGGGGCTGG 240
 CGGGTAGCTG TTTCATTTTT CTCTGTTGAG GTCTTCGACT ACCGGCATAT CAGACATGTT 300
 GGTGTCCTCT TTATGATGCT AATGAGCTCT TTTTCAATG CCGATGATCA TTTTCAATG 360
 40
 ATAACTCGAA TGTGTGTGTT TGCTTAAACA TTTTCAGCTC CCGTGGGAC AGTCTCTGAC 420
 AATGTTCTTG GACACGCTCT GGTATGATGG AGTGGGSGGC TACTTGTGAC CACCGGGATG 480
 GTGGCGGCTC CTTCTCTACA AGAGGTTTCT CATATATGCG TGCCCTATGG CATCATCTCT 540
 GGTCTGGGAT ACTATGTTAG TTCTCTGCGA ACTGTACCA TCGCTATGCA ATATTCTTGG 600
 45
 AAAGAAGCTT CAAATGTCAC TGCGAGTCTC TCCACAAGAG AATGTTGCG TGTGTTTCTC 660
 TTGCGACAG CATCATGGC TCTGAAGGAG CGATTGGCT GAGATACAG CTTCTCTCTC 720
 GTGGGCGTAC TACGTTAAAT CATTTGATC TTGCGAGCAC TGCTCAGACC CATCATATC 780
 AGAGGCGAG GTTATCCGGA AATAGTCATC CAGGAAATC GGAARAGG CAAATATG 840
 CTGAAATG AAAAAACAG AACCTAATTA GACTCATG CTCTAGAGT AGACTAATC 900
 50
 ACCTCACCTA AAAATGTGCG TACTCACACT AACCTGGAA TGAAGCGGAA GCGGACATG 960
 CAGCAGTCCG TGTTGAAGAC CAGCCCCAGC CCAGGCGAAA AGAAGGCCCT GCTATTAGAC 1020
 TTCTCATTTT TGAAGAGAA AAGTTTATTT TGTATGATAT TATTTGGTCT CTTTGACAA 1080
 CTGAGATCT TTGACGCTC CTGTATGTC ATTCTCTG GATTATGCT GGGCATGAC 1140
 CAGGACCGCG CTGCTTTTT ATTATCTACG ATGGCGATTG CAGAAGTTT CGAAAGATCT 1200
 55
 GGAGCTGTTT TTGCTCTCAA CAGGAGGAGC ATTCTTAAGA TTATCATGTA GCTCATCTGC 1260
 CTGATCTTAT GACTGTGTC CTGTTTTGCC TTACTTTTGT CTACTAATG TCGGGTCTGT 1320
 ATTCTACGA GATATGTTT TGCGTTTATG GTTGGAACA TAGAGGACT CACTTCCAC 1380
 TGCTTGCTGA AGATATGCTG GTGCGCATTG CAGAGATGCT CTTCTGACG TGGGTTCTAC 1440
 ATCTTCATTG AAGCATAGC AGACATGGCT GAGCGCGCCC TTGACGTTT GTTGTGGAG 1500
 60
 CAAAGTAA TCTACAGCAG GGCCTCTAC TCTTGCGCAG CTGCGATGC CTCGGCTGCT 1560
 GTGTGCGCT CCGTGCGAG ACCGTTFAGG ATGCGTCACT ACTACGCTA TCGTCAAGT 1620
 GAAACAAAG TATGAGCCA TGTGGGAAG ACTTTACAG ACATACCTGA AGACTTCTGT 1680
 GAAATGGAT TTGCAAAAA TGACACAGA GTTCAGCTGC AAATGAGGCC GGTATGACAC 1740
 ACTTTCTTAC AACACAGACC ACTGTGTGCT CTGAGAGAGG AGTGGGTGGG CCGAACGGGG 1800
 ACACAAAGG GCGATGAGC AAGCCGCTCT TCTGCTGATC AGGCTGCTCA TTTTAAGGG 1860
 65
 AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTGTTT TGTTTGTTT TGTTTAAGC 1920
 TTTTITTTTT TGCTGTGTTT TAAAGCGAAA ACAAANAACA ACCAAGCACT CTTCATATA 1980
 TAAATCTGCG TGTATTCAGT ACGATACAAA GACATATGTA GAAGACTCT TTGTTTACAA 2040
 TTCCGATATT AATGAGTGG CATGACTGCG CAAAGTGGT TTAAAGCTT TCGCTGGTA 2100
 TAAATGTTT TCTTTTTCCT TTTCCTTTCT TTCTGATG TCCTTGAGT AAACACTACT 2160
 70
 CCGTAAATA ACAACATCA ACCGAGTCA TTGAATGAA ATTGGCACT C. 2212

Seq ID NO: 156 DNA Sequence
 Nucleic Acid Accession #: NM_004833.1
 Coding sequence: 246..1277

75
 1 11 21 31 41 51
 | | | | |
 TCAAGCAATT AGAGCTCCAG TTGTCACTCC TACCACACT GGGCTGGGG GTGAGGGGAA 60
 GTGTTTATTA GGGGTACATG TGAAGCGTCC CAGAAAGTGC AGAGCTTTG TAGCTTTGAA 120
 AGTCACCTAG GTTATTTGGG CATGCTCTCC TGAGTCTCTC GCTAGTTAAG CTCTCGAAA 180
 80
 AGAAGTGGC AGACCGGTT TGCTGATGCG CCGAGGAGCT AGGAGCTGTA TCCAAAGTT 240
 GTGCAGAGA GATGAATGTA AAGAGAGGAG AGGCTGCTG AGGCTGCTG AAGCAAGG 300
 ATGAGCAACT GATGAAGTT AGGTTCTTTC TTTCAGAGCA GTTTAATATT CCGACAGAG 360
 AACTACATAC TCAACACAGA ATACAAATAG CTACTCTGAT GATTCAAAT GTGGGGCGG 420
 TGTCTCAGT GATGAAGACC ATTGTATTT TTGCAAGTT GAAATATATG TTCTTGGCA 480

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AGCTGCTTCA GGAAGGAGAG GAGAAAGTTG ATAGCAATTA CAAATCGSTA ACMAAACCAA 540
 AGCCACTAAG TCAACGTCGA ATGAGTCTCT GTCGACTCTC AGCCATCAGA AATGATGTGC 600
 CARAGCAACG TGGTCGACCA AAGTCTCTCT CTCATGTTAA GCGTGAACAG AACAGATGCG 660
 TGCGCCACGA GAAATCTATC AGAGAAGGGT TCGAAGANGC CGTGTTCGCA GTTATGTTGC 720
 TCAAAAGCAA GAAGCCCTCT ACCTTTGAGA CCGAGABAGG CAGGACAGAG ATGTTTCTAT 780
 CTACAGTGCG TACAGAAAGG GANTCTCTCT TTGTAAAGGT TTTTAATACA CTGCTGAAGG 840
 ATAAATTCAT TCCAAAGAGA ATAAATTATA TAGCAAGATA TTATCGGCAC AGTGGTTCCT 900
 TAGAGGTAAI TAGCGCTCCA CGTGTGTGAG ATGCTGATCT TGACCACAAAG GTTAAATGTC 960
 CGCTGGAACAT TATCAAGAAA CTGTGTTGAA CCCCAGAGAT CAACAGCTCT CAACACTGCG 1020
 CCTCTGGAGC AATGTGGAAT GTTGTGTGTT TAGTCGAGAA GGTATACAGA AAGACAGAAA 1080
 ACATATTATT TGACTTAAGT GACCAACTGT GGAATAATGA AGTACTGGGG GTTAGAAAGG 1140
 AGGACACATG GAAATGTGAG GAAGGAGATA AGTTCTGACT TACATTCTCT ACACCTTCGA 1200
 AAAATGEMGA AAAACTACAG CTGACATCTG GAGTTCATAG CACCATAAAG GTTATTAAAG 1260
 CCAAAAGAAA AAGAGTACGA AGTAAAGAAJ AGCATATCAA GCGATCTGCT CTAGACAGAG 1320
 TTTAATTGAA GAATATGTGA TACAGGCTCT TCAATCAGAT TGTATAGTAC CTGAAGCTG 1380
 CAGTTCACAG GCTCTCTCTCT CCACCAATT AGGATAGAAT AATTGCTGGA TAAACAAATT 1440
 CAGATATCAA ACAGATGATC ACAATAAACA TCTGTTCTCT ATTCC 1485

Seq ID NO: 157 DNA Sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94...378

1	11	21	31	41	51	
TTCTTTTCA	GTTCAGGATT	TCTACTCTCT	CCAGAGAGAG	GAGCAAAAGCT	GAGTATGACG	60
CAACAGCAC	ACGACGACCA	GCAAAAACAA	ACATCATGTC	TGAAGGGGAT	CGCTATATGCC	120
TGCTGCTGCA	TATGTGTGTC	TACAATTTGT	CAAGGCTCTC	CCATCTGTCA	AAGAGGAGCC	180
TGCTTTTGA	TAGCGCTGCT	GTTAAAGACA	GTGAAGTGG	CAGATATTGA	GGAAGCTCTC	240
ATATGTACC	CNAGTACCA	CTGTGACAA	ATAGAATGA	TTATTACCT	GAAGAATAAT	300
AAAGGACAC	GATGCTTAA	TCCAAATCT	AAGCAAGCAA	GGCTTATAAT	CAAAAAGTT	360
GAGAGAGAA	ATTTTTAA	ATATCAAAAC	ATATGAGTCT	AAATTAACAG	GCATCTGAA	420
AACCTAGAC	AAGATCTGCT	GTATCATGAG	CTTCTAGGAG	CTTCTAGGAG	TAGGAAAGCT	480
AGACTTTCT	ATGGTTTGT	GACTTCTAAC	TTTGTACAG	TTATGTGAAG	GATGAAGGT	540
GGCTGAAGG	ACCAAAACAA	GAATATCAGT	CTTCTGAT	GAATGACAT	CAGATTCGA	600
CTTCCCAAG	GAGTGCAGCA	ATTAAATGGA	TTTCTAGGAA	AAGCTACTCT	GAAGAAGCT	660
GTTTACACT	GGATCTGCT	AGCTGCTCT	AGCTGCTCT	AGCTGCTCT	ATACATTCAT	720
GCATTTCTAG	GCTGAGAAC	CTTCTAGATT	TGATGCTTAC	AACATTTCTG	TTTGACTAT	780
GAGACATT	CTGTCTCTAG	AAGTATCTGT	TCGTATTTGA	TCTTTATGCT	ATATACTAT	840
CTGTGTTAC	AGTGGAGACA	TGACATTAAT	TACTGAGTCT	AGGCTCTTAT	AGTCAAGG	900
CATCTATGTG	GGGGAAGCCA	TCTCTCTCT	TCCTCTCTCT	GCAATATCAC	ACTCTTCTC	960
CCAAATATCA	ATTCATGATC	CAATATGTAG	GAAACATTC	TTATGATCA	TTTGTGTTG	1020
TTTATAACCA	ATTCATATA	TGTAAATCAT	AAATGATCT	ATGAAAAAA	TTATACGCTA	1080
TGGATATCT	GCACAGCTGC	ACATATTCTA	TAAACAAACT	AGACAGCCG	GTCTTAATTT	1140
GATGTTTTTC	AGCATTTTCA	CAATGAGAG	TTTGTGAGCA	TTTGTGAGCA	GTGTTGTTAC	1200
TCTACTTTT	GTTTTGAATC	GTTTGTATAA	ATGATAGCAA	TATCTTGAC	ACATTTGAAA	1260
TACAAAATGT	TTTTGTCTAC	CAAGAAAAA	TGTTGAAAAA	TAGCAAAATG	TATACCTAGC	1320
AATCACTTTT	ACTTTTTGTA	ATTCGTCTCT	TTAGAAAAAT	ACATATCTCA	ATCAATTTCT	1380
TTTTGTATGC	CTATATACCT	TAAATTATAG	GTATACTGCA	GACTGATTTA	AAGATACAAA	1440
GTCAATTTTT	TCTCTATATA	ATAGACGACA	CTTCTCTTTT	TTAAAAAAA	AAA	1493

Seq ID NO: DNA Sequence 158
 Nucleic Acid Accession #: NM_002562.1
 Coding sequence: 27...1814

1	11	21	31	41	51	
55	AAAAGCCAGG	GAGGAGGAGCT	GTCAACATCG	CGGCGTGCTG	CAAGTGGGAT	GATGTTTTC
	AGTTAGAAC	GACATCAATC	CTCGGATATG	AGAGATATGA	TATGTGAC	ATTAAAGGCT
	TCCTCAAGT	GATCACTCTT	TCCATGATT	GCTTTGCTCT	GGTGAAGTAC	AAAGCTTACC
	AGGGAAGAA	GCGTGTATC	AGTTCTGTGC	ACACCAAGGT	GAAAGGGGATA	GCGAGAGTGA
	AGAGAGAT	CGTGAAGAT	GAGATGAGGA	AGTTGTGTC	CAATGTTCTT	GACACCTGAG
60	ACTACAGATC	CGCTCTGAC	GGGAGACTGT	TCCTGTGAT	AGAGAAATCT	CTGAAACAG
	AAGGCCAAGA	CGAGCGGTTG	TGTCCCGAGT	ATCCCAAGCC	CAAGACGCTCT	TTTCTCTCT
	ACCGAGTTG	TAAAGAGGA	TGGATGAGC	CGCAGACAA	AGGAATTCAG	ACCGAAGGT
	GTGTATGCA	TGAAGGAGC	CAGAGAGACT	GTGAAGTCTC	TCCCTGTGTC	CCGATGAGG
	CAGTGAAGA	GAGGCCGCA	TCCGCTCTCT	TGAAGATGCT	GGAAGACTCT	ACTGTGTCA
65	TACAGACAA	TATCCACTCT	CCCGGCCACA	ACTACACACC	GAGAAACATC	CTCCGAGT
	TAAACATAC	TTTATCTCT	CACAGAGACT	AGAAATCCCA	GTGTCCCAT	TTCCGACTAG
	GAGACATCT	CCGAGAACCA	GGGATTAAT	TTTCAAGTGT	GGCAATTCAG	GGGCGAATTA
	TGGGACTGGA	GATCTATGCT	GAGCGAACCT	TAGACGTTGT	GTTCATCATC	TGCGATCCA
	ATAACATTT	CGTCTGATCT	GACGACAGAG	CCACCAAGCT	CTCTCTGTAC	CTCGCTTACA
70	ACTTCAGATA	CGCAGATAC	TACAGAGGAA	ACAATTTGGA	GAAACGAGCT	CTGATAAAG
	TCTTGGGAT	CGGTTTATC	ATCTGCTGTT	TTGCGACCG	AGGAAATTT	GACATTTATC
	AGCTGTTGT	GTACATGCG	TCAACACTCT	CTACTCTTGG	TTTGGCCGCT	GGTTTATGCT
	ACTTCTCAT	CGACATCTAC	TCCGATGACT	GTGCTGCTCT	CGATATTTCT	CCCTGATGGA
	AGCTGTGTCA	CGCCTGTGTT	GTACAGGAT	ACTACTACAG	GAGAGAGTGC	GAGTCCATRG
75	TGACGCAAAA	GGCGACATTA	AGATATGTGT	CTTTGTGGA	TGAATCCCA	ATTAGGATGT
	TGACGACGCA	GCTACTAGGG	AGAGACTTGC	AGAGATGCAA	GGGCCAGAGA	GTCCCAAGAC
	CTGGATGCA	CTGACAGAT	TTTCTGAGGC	TGCGCTGCGC	CTCTCATGAG	ACATCCGCA
	TTCTTGCGCA	ACCGAGAGAG	ATACACCTCT	TTAGAAAGGA	GGCGACTCTCT	AGATCCAGGG
	ATAGCCCGGT	CTGTTGCGAG	TGTGGAGGCT	GCTTCCCATC	TGAATCCCT	GAGAGCGACA
80	GTGCTGTGGA	GAGACTGTGC	TCCCGGAAAA	ACCGCGGGGC	CTGACTACAC	ACCTCAGAGC
	TGTGTAGGAA	GAGACTGTGC	TCCCGGAAAA	TCCCGGGGGC	CTCTCTCTCT	CCAGAGAGC
	CTTGTCTGAG	GCTGATGCTG	GATTCACGAA	ACAGCGCGCT	GGGCGACTGT	GCTCAGAGCT
	GCTACGCGAC	CTGCGGCTCT	GCTTCCCGAG	ACATGCGTGA	CTTGTCCATC	CTGCCAGCT
	GCTGCGCTG	GAGGATCCGG	AAAGAGTTTC	CCAGAGGTGA	AGGCGAGTAC	AGTGTGCTTA

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PCT/US02/29560

AGAGTCTCTTA CTGAAGCCAG GCACCGTGCC TCACGCTCTGT AATCCACCTT TTT

1853

Seq ID NO: 159 DNA Sequence

Nucleic Acid Accession #: NM_001793.2

Coding sequence: 54-2543

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5	1	11	21	31	41	51	
	AAAGGGCCAA	GAGCTGAGCG	GAACACCGCG	CCGCGCTCGC	GGCAGCTGCT	TCACGCTCTT	60
	CTCTGACGAC	ATGGGGCTCC	CTGTGGAGCC	TCTGCGCTCT	CTCTCTCTCT	TCGACGCTGT	120
10	CTGCTCTCGA	TGTGGGCTCT	CCAGCGCGTG	CCGCGCTCTC	TTCCAGCGAGC	CTGAAGTACG	180
	CTTGGAGCGG	GGAGGGCGGG	AGCAGAGACC	CGCGCGCGCG	CTGGGGGAAG	TATTCATGGG	240
	CTGCCCTGGG	CAAGAGCCAG	CTCTGTTTAG	CAGCTAATAT	GATGACTTCA	CTGTGCGTGA	300
	TGGGCGACGA	GTTCAGAGAA	GAGGCTCACT	GAGGGAAGAG	AATCCATGTA	AGATCTCTCC	360
	ATCGAACCT	ATCTACAGAA	GACACAGAG	AGATTTGGTG	TTATCTGCTC	CTGATGCTG	420
15	TGAAATGCG	AAGGCTCCCT	TCCGCCAAGG	ACTGAATCAG	CTCMACTGTA	ATAAAGTAG	480
	AGACACCAAG	ATTTTCTACA	GCATCACGGG	GCGGGGGGCA	GACAGCCCCC	CTGAGGGTGT	540
	CTTGCGCTGA	GAGAGAGACA	CAGGCTGGTT	GTGTTTGAAAT	AGGCCACTGG	ACCGGAGGGA	600
	GATTCGCAAG	TATGAGCTCT	TTCGCCACCG	TGTGTGAGAG	AATGTGCTCT	CATGAGAGGA	660
20	CCCATGAAC	ATCTCCATCA	TGTTGACCGA	CCAGAAATGAC	CACMAGCCCA	AGTTTACCCA	720
	GGACACCTTC	CGAGGGAGTG	TCTTAGAGGG	AGTCTTACCA	GGTACTCTTG	TGATGCGAGT	780
	GACAGCCAGC	GATGAGATGA	ATGCCATCTA	CACCTACMAT	GGGTTGGTGT	CTTACTCCAT	840
	CCATGACGAA	GACCAAGAG	ACCCACAGGA	CCCTATCTTC	ACCATTCGAC	GGAGCAGAGG	900
	CACCTACGAC	GTCACTTCCA	GTGGCGCTGA	CCGGGAAAAA	GTCTCTGAGT	ACACACTGAC	960
	CATCCGAGCC	ACAGACATGG	ATGGGGAGGG	CTCCACACCC	ACGGCAGTGG	CAGTATGGGA	1020
	GATCCTTGAT	GCCATGACAA	ATGCTCCCAT	GTTTACACCC	CAGAAATAGG	AGGCCATGTG	1080
	CCCTGAGAAT	GAGTGGGCGC	ATGGAGTACG	GAGGCTGAGT	GTCACTGAGT	TGGAGGCCCC	1140
	CACCTACGCA	GCGTGGCTGT	CCACCTACCT	TATCATCTGG	GGTGCAGAGG	GGACCATATT	1200
	TACCATCACCC	AAAAACCCCT	AGAGCAACCA	GGCATCTCTG	ACAACACAGA	AGGGTTTGGG	1260
	TTTTGAGGCC	AAAAACACAG	ACACCCCTGA	GTGTTAAGTG	ACCAACAGAG	CCCTCTTTGT	1320
30	GCTGAGGCTC	CCACCTCTCA	CAGCCACCAT	ATGGTGTCCG	GTGGAGGATG	TGATATAGGG	1380
	ACCTGTTGTT	GCTCTACAGT	CTAAGATGTT	TGAGTGTCCG	GAGGCGCATC	CCACTTGGGA	1440
	GCTCTGTGTG	GTCTACACTG	CAGAGAGACC	TSACAGGAG	AATCAAJAAG	TCAGCTACCG	1500
	CTGCTGAGA	GACCCACAGC	GGTGGCTAGC	CATGAGACCA	GACAGTGGGC	AGGTGACAGC	1560
35	TGTGGGACCC	CTGACCTGCG	AGGATGAGCA	GTTTTGAGAG	AGACACATCT	ATGAGATCAT	1620
	GCTCTGCTG	ATATCTGCG	CACCTCTGAG	ACCGGACAGC	CTTCTGACCA	CTTCTGACCA	1680
	ACTGATGAT	GTCAATGACC	ATGGCCGAGT	CCCTGAGCCC	GCTCAGATCA	CAATCTGCAA	1740
	CCAAAGCCCT	GTGGGCCAGG	TGCTGACAT	CACGAGACCA	GACCTGTCTC	CCACACCTTC	1800
	ACCTTTCCAG	GCCACGCTCA	CGATGACCTC	AGACATCTAC	TGGAGGGGAG	AGGTCAAGGA	1860
	GGAAGTGAAC	ACCTGATGAA	GAACTCTCTG	ATGACAGATCA	CATATGAGCA	CTGATGAGCA	1920
	CCGCTTTCTT	CTGTCTGACC	ATGGCAACAA	AGAGCAGCTG	ACGGTGATCA	GGGCGACGTG	1980
	GTGCGACCTG	CATGGCCATG	TGGAAACCTG	CCCTGGACCC	TGGAGGGGAG	GTTCCTGACT	2040
	CCCTGTGCTG	GGGGTGTCTG	TGGCTCTCTG	GTCTCTCTCT	CTGTGTCTCT	TTTGTGTTGT	2100
	GAGAAAGAG	CGGAGAGAGG	CGCTCTGAGC	CTCTACTCCA	GAGAGTGAAG	CCGCTGAGAA	2160
45	CTCTCTCTAC	TATGGCGAAG	AGGGGGGTGG	GGAAGGAGAC	CAGGACTATG	ACATCACCCA	2220
	GCTCCACCGA	GGTCTGAGGG	CCAGGCCGGA	GGTGGTTCTC	CGCAATGAAC	TGGCACCAAC	2280
	CATCATCCCG	ACACCCATGT	ACGCTCTCTG	CGCCACCGAC	CCAGATGAAA	TGGCGCAACT	2340
	TATATTTGAG	AACTGTAGAG	CGGCTACACG	AGCCGCCACA	GCCCCGCTCT	ACGACACCTT	2400
	CTTGTGTGTC	GACTATGAGG	CGACGGGCTC	CGACCGCGCG	TGCTCTGAGC	CCCTCAGCTT	2460
	CTCCGCTCTC	GACCAAGACC	AGGATACAGA	TATCTGAAC	GAGTGGGGCA	GGCGCTTCAA	2520
50	GAGCTGAGCA	GACATGTAGG	GTGGGGGGGA	GAGAGACTAG	GCGGCGTCCG	TGACGGGCTG	2580
	GGGACCAAGC	GTGAGGCGAC	AGGACATCTC	CAGAGGGTCT	CAGTTCCCCC	TTGACATGAG	2640
	GACTTGGGAG	CTTGTGAGAA	ATGTCGCTTA	CGAATCTGGC	GAGAGCGGCG	TGATAGTCTG	2700
	AGCTTAGAGT	GTTTGTCTTC	TTAGCGTTTC	AGGATGAGAG	AAATGTGGCA	GTTCGAGCTC	2760
	AGCATGAAAC	AGCTCTCCAC	CTGGGCCAGG	GTGGCTCTCT	AGGCCAAGTT	TGCAGAGCTC	2820
55	TTCTACCTGT	CGTAAATATG	CAGGACTTGT	GTCTGTGGGC	TGGGGTCTGT	GTGACTGACC	2880
	TACAGTGGAG	CTGATGAGAG	GATGTAAACC	TTCTTAGGCT	CTGCTGGTGA	ACTTATAGT	2940
	TTTTTTTAAAT	GCTATCTTCA	AAAGCTTAGA	GAAAGTTCTT	CNAAGTGCCA	CGGACAGACT	3000
	GCTGGGCCCA	CTGGCCCTCC	TGCATTTCTG	GTCTTCCAGC	CCGAAATGCT	CCCATCTCGA	3060
	TGATCTCTGT	CGTTTGTATA	CTGATGTGTC	CTAGTTTGCC	CCCTATTTGT	TATTTTCCCT	3120
60	GTTCGCTTGC	TATAGAGAA	GGTGTGGAGC	AATCTGTGAT	ATGTACTAGG	ACTTTTATAT	3205
	TAAAGAACT	TTTCCAGAAA	AAAAA				

Seq ID NO: 160 DNA Sequence

Nucleic Acid Accession #: NM_002571.1

Coding sequence: 99..587

	1	11	21	31	41	51	
65	1	11	21	31	41	51	
	CATCCTCTCT	CTCTCAGAGC	TCAGAGGCAC	CCACAGCGCC	AGCATCTGCT	TGCTCTCTCC	60
	TCACCCCTCGG	CGTGGCCCTG	GTCTGTGGTG	TCCCGGCCAT	GGACATCCCC	CAGACAGACC	120
70	AGGACCTGGA	CTCTCCCAAG	TTGGCAGGCG	CTCGGACTCT	CATGGCATTG	GGAGCAACCA	180
	ACATCTCCCT	CATGCGACGA	CAGAAGGGCC	CTCTGAGGGT	CCACATCAAC	TCACCTGGTC	240
	CGACCCCGCA	GGACACCTGT	GAGATGTGTC	TGCA CAGATG	GGAGAGAACAC	AGCTGTGTGT	300
	AGAGAGACT	CTTGTGGAGC	AGACTGCGGA	ATTCGAGGAG	CTGTGAGACT	AACTATACAG	360
	TGGCGAAGCA	GCCGACCGTG	CTGTACTATC	ACTACGAGCA	TTTCTTGTTT	CTCTGCTACG	420
75	AGGACACCA	CACCCCATCT	CAGAGCATGA	TGTGCCAATG	CTCTGGCCAG	GCTCTGGTGG	480
	AGGACATGTA	GATCATGCG	GGATTTATGA	GGGCTTTTCG	GGCCCTGGCC	AGGACCATAT	540
	GCTACTTCTG	CTGATGAAA	CAGATGAGAG	AGGCTGCGG	TTTCTGAGCT	AGCTCTGGCC	600
	CGAGGAGAGC	CAGACTCCCA	CCCTTCCACA	CTCCACAGAC	AGTGGAGACT	CTCTCTGGCC	660
	TTTCAAGAAA	TAACACACAG	TGGAAGAGAG	ATGACGTGGT	CATCTGTGTC	GCAATCCCTC	720
80	TCTCTGCTCA	CACCTGCAAC	ATTGCGCATG	GGAGGCTGCT	CCCTGGGGGG	AGAGTCTCTG	780
	CGAGAGTTTA	TTAATAAACG	CTTGGAGCAT	G			811

Seq ID NO: 161 DNA Sequence

Nucleic Acid Accession #: NM_001327.1

WO 03/025138

PCT/US02/29560

Coding sequence: 89..611
 1 11 21 31 41 51
 5 AGCAGGGGCG GCTGTGTGTA CCGAGAATAC GAGAATACCT GGTGGGCCCT GACCTTCCTCT 60
 CTGAGAGCCG GCGACAGGCT CCGAGACCAT CGAGGCCGAA GCGCGGGGCA CAGCGGGGTC 120
 GACGGGCGAT GCTGATGGCC CAGGGGGCCCT TGACATCTCT GATGCCCTCA GGGGCAATCC 180
 TGGCGGCGCA GAGAGAGCGG GTGCCACGGG CGGACGAGGT CCCCAGGGGCG CAGGGGCAAC 240
 AAGGGGCTCG GGGCGGGGAG GAGGGGCCCC CGGGGGTCCG CATGGCGGCG CGGCTTCAGG 300
 10 TCGGAATGGA TGCTGAGAGT CGGGGGCGAG GGGCGGGGAG AGCCGCGCTC TTGATGCTCA 360
 CCTCCCATCG GCTGATGGCA CAGCAATGGA AGCAAGAGCT GCGCGGAGG GCTTGCGTCA 420
 GGAATGCGCA CCGCTTCCCG TGCCAGGGGT GCTCTGAG GAGTTCACCT TGTCGGGAA 480
 CATACTGACT ATCCAGCTGA CTGCTGAGA CCACCGCGCA CTGCGAGCTC CATCAAGCTC 540
 CTGTCTCCAG CAGCTTCTCC TTGTGATTGG GATCAAGGAG CTGCTTCTCC CGATGTTTTC 600
 GCGCTACCTC CCGTATGGTA AGGAGAGGCT AGGAGGCTCT GCGGCGGAT CTGAGTGAT 660
 15 CGCTCTCCG CTAGGGAAAT GTCCAGCAC GAGTGGCGCG TTGATTGG GGGCTGATT 720
 GTTTCGTGCT GGAGAGAGAC GGCTTACAT TTGTTTCTG TAGAAATAA AACTGAGCTA 780

Seq ID NO: 162 DNA Sequence
 Nucleic Acid Accession #: NM_020994
 Coding sequence: 53..459

1 11 21 31 41 51
 25 CCGTGTGGCG CCTGACCTTC TCTCTGAGAG CGGGGCGAGG GCTCCGAGC CATCGAGGCC 60
 GAGGGCGAGG GACAGCGGGG TTGCGAGGGC GATGCTGATG GCGCAGGAGG CCTTGCAATT 120
 CCTGATGGCG CACGGGGGCA TGCTGGCGCG CAGAGAGAGG CGGTTCCAC GGGCGGACGA 180
 GGTCCCGGCG GTCGCGCTCG AGCAGAGGCG CTGAGGCGCA GAGAGAGGCC CCGCGGGGTT 240
 CCGGATGAGG GCTGCGCTCG TGCGGAGAGT GAGAGGTCCC CCGTGGGGC CAGAGAGGCC 300
 GACAGCGGCC TGCTTCAGTT CGAGCTGACT CTGCGAGACC ACCCGCACT CGAGCTCTCC 360
 ATCACTCTCT GTCTCCAGCA GCTTTCCTCT TTGATGTGGA TCAGCGAGTG CTTTCTGCCC 420
 30 GTGTTTTCG CTGAGGCTCG CTCAGGGACAG AGGCGCTGAG CCAGAGCTGG GCGCTCTTCC 480
 TAGGTGATCG CTGAGGCTCG ACAGATAGGT CTGAGGACGA GTGGCGACT CATTTGTGGG 540
 GCGCTGATTG TTTTCCCTGG AGGAGGACGG CTTCATGTT TTGTTCTGTA GAAATAAAG 600
 CTGAGCTA 608

Seq ID NO: 163 DNA Sequence
 Nucleic Acid Accession #: NM_006928.2
 Coding sequence: 1..1986

1 11 21 31 41 51
 40 ATGATCTGGG TGCTAAAAG ATGCTTCTT CATTGGCTG TGATAGGTG TTTGCTGGCT 60
 GTGGGGGCTA CAAGAATACC GAGAAACCG CAGTGCTCTG GTGCTCAAG GCAACTCAGA 120
 ACCAAAGCCT GGAACAGCGA CGTGTATCCA GATGTGACAG AAGCCGACAG ACTTGTACTG 180
 TGAAGAGGTG GTCAAGTGTG CTTCAAGGTC AATGATGATG GCGCTACACT GATTGTGTCA 240
 45 AATGCTCTCT TCTCATTTCT CTGAGCTTC CTGAGAGGCC AAAAGTATT CCGAGATGGG 300
 CGATTATTCT GGCTCAACCA TACCATCATC AATGGAGGCC AGGTGTGGG AGGACAGCCA 360
 GTGTATCCCC AGAAACCTGA CGATGCTCTC ATCTTCCCTG ATGGTGGACC TTGCCCATCT 420
 GGCTCTTGCT CTGAGAGAG AGCTTGTGTT TATGTCTGGA AGACTGGGG CCAATACTGG 480
 CAGTGTCTAG GGGGCGCAAT GTCTGGACTG AGCTATGGA CAGGCGAGC AATCTGGG 540
 50 ACACACACCA TGGAGTGAC TTCTCAACAT CCGCGGGGAT CCGAGACTA TGTGCTCTTT 600
 GCTCATTTCA GCTGAGCCTT CACCAATTAT GACACAGTGC CTTTCTCCGT GAGGTGTGTC 660
 CAGTGTGGGG CTTTGTGATG AGGAAAGCAG CAGTCTCTGA GAACTAGCC TCTGACCTTT 720
 GCGCTCGAC TCGATGACG CAGTGGCTAT CTGCTGAGAG CTGACTCTCT CTACACTGG 780
 GACTTTGAG ACAGTAGTGG AACCTGATC TCTCGGCCAC TTGTGTGCAC TCATCTTAC 840
 55 CTGAGCGCTG CCGCAGTCTC TGCCGAGGTG GTCCGACAG CTGCACTTCC TCTCACTCTC 900
 GCTGTGCTCT CCGCGATTCC AGACACACA GATGGGACGA GGCACACTGC AGAGGCCCTC 960
 AACACACAG CTGAGCTCAT TGTGTGCTCT TCTGGACCCA CAGCTGACA GTGTGAGG 1020
 CCAACTGAG AGCCCTCTGG AACCAATCT GTCCAGGTGC CACACACTGA AGTCAATAGC 1080
 ACTGCACTG TGCAGATGCC AACTGCAGAG AGCACAGGTA TGACACTGGA GAAAGTGCCA 1140
 GTTTGACAG TCATAGGTAC CACACTGGCA GAGATGTCAA CTCGAGAGCG TACAGGTATG 1200
 60 ACACCTGAG AGGTATCAT TGTGTGCTCT TCTGGACCCA CAGCTGACA GTGTGAGG 1260
 ACAGATGGG TGGAGACAC ACTGAGNGAG CTACATATCC CTGAGCTGCA AGCTCCAGAT 1320
 CCGAGCTAA TATGTGTAC GAAAGTATT ACAAGTTCCT TGGGCGCCCT GCTGATGGT 1380
 ACACGACCTC CAAGCTGGT GAAGAGACAA GTCCGCCCTG ATTGTGTTCT GTATGATAT 1440
 65 GTTGTCTTT CCGTCACTCT GACATGTTC CAGGATATG AAGTGCGGA GATCTGCGAG 1500
 CTTGTGCTCT CCGTCAAGG GATGATATT GAGCTGACT GTGCTGCGA AGGCGAGCT 1560
 OCCAGGAG CCGTCACTGA GATCTCATG CCGAGGTGCC AGCCCTCTG CCGAGCGCTG 1620
 TGCCAGCCTG TGCTACCGAG CCGAGCCTCG CAGCTGTGTC TGACACCAT ACTGAGGAT 1680
 70 TCGTGGGGA CATACTGCT CATGTGTCT CTGCGTATA CCAACAGCT GCGAGTGCTC 1740
 AGCTCCACG TTTATGAG TGTATGAGTA GAGAGCTCTG TGTGCTGCT CTGATGCTG 1800
 GGCATCTCG TGTTGTGAT GCTGTGCTG CTTCGATCT TGATATATAG GCGGACACT 1860
 ATGAGCAAG ACTTCTCCGT ACCCGAGTTC CCACATAGA GAGTCACTG GCTGCTCTTA 1920
 CCCGATCT TCTGCTCTG TCCATGTGT GAGATAGCC CCGCTCTCAG TGGGAGAG 1980
 GTCTCA 1986

Seq ID NO: 164 DNA Sequence
 Nucleic Acid Accession #: NM_001922.2
 Coding sequence: 415..1974

1 11 21 31 41 51
 80 GCATTAAG TCAGAGCTA AGCAGGGAGG GAGGGGTTT AGAATACCA GCATATAAG 60
 TAGATATCT GGGATGCTCT GATGATGCT CAATTAGCA AGCTGCTCT TACGGGGT 120
 AGATGTGAG AAGCGCTACC CTCATTAAT TTGTTGTTA GAGGCGCTCT TAGAGAAAT 180
 AAGCTGTGA GTTGTGGA TCACATAAA TTGTGTGTC AGCTTCATG ACACATGTC 240
 ACATGTGAA CCTCTGTGAT TCTGTGGGT ATTTTATTA GAGAAAGGA ATAGAAAGA 300

WO 03/025138

PCT/US02/29560

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AAGAAATAA AAAATCTCTG AAAGAAGAG ACTGAAGAG TAGAAGATA GCGAAAGCT
 ACTGACAGG CAAGGAAGT AAGAGAGAG GAGAGCTCT CCAATTATAA ACCCATGAC
 CCCCTTTGGT GGGGGTTTCT GCTCAGTTC TTGGGCTGCA AAATCTGCC AGAGGCCAG
 GCTCAGTTC CCCAGCTCTG CATGACGGT GACGCTCAG TGACCAAGGA GTCTCTGCCA
 GCTCTGGGT CAGAGTCGG CAATCTCTGT GACCTCAGC AAGGCCGGG CAGTGGTGA
 GAGGTGAG CCGACACAG GCTCTGGAGT GGTCTCTACA TCTTACGAA CAGAGTAC
 GTGAGCTGT GCGCAAGAAA ATTCTTCCAC CGACCTCGCA AGTGCACAGC AATCTTCCC
 GGTCTAAT GTGAGACTG CAGTCTTGGC TGGACCGGTC CCAACTGCC GCGAAGAA
 CCACCTTAT TTGGCGGAA CATCATCTC TTGAGCTCTC AGGAAAGGA GCAGTCTTGT
 GGCGCTTAG ATCTCCGAA GAGAGAGT CACCCGACAT ACTGTATAC CAGCAAGAC
 TCTCTGGGC TCTCTGGGCC CAATGAAAC AGCCCGAGT TTGCCAACTG CAGTGTATT
 GATTTTTTT TTGGGCTCCA TATTATTCT GTTAGAGATA CATATTAGC ACAGGAGCC
 CCTCAAGGG CATTAGATT CTTCACATCA GBACTGCGAT TTGTACTCT GACGCGTAC
 CATTTTGT GTGACAG AGATCTCGA GACTCATGT GCAATGAGT TTTCCTTGT
 CCTCATGGA ACTTTCGAC TGGAGGAGC GAGTGTGAT TGTGTACGA CAGCTGTCT
 GGGGACGGA GACCAAGCA TCGCATCTG ATTAGTGGG ACTCAAGAT CTCACGTGG
 GAACGTCTCT GTATAGCTCT GATGACTAC AACCACTGT TCACCTTGT CAGTGAAC
 TATGAGGTT TCTGAGAGT AATCAATG GAGAGAAC GATGAAAT GCAACTCTA
 AAGACATAC GAGTCTCT GTCTCTCG AGTTTUAAT ACTCTCTCT CTTCAGAC
 TCTACTCCA GTTTCAGAA TCTTTGGA GGGTTTGATA AAGCAGATG GACTCTGAT
 TCTCAAGTA TGAGCTCTCA TAATTTGGT ATTCTCTCC TGACAGGAC AAACCTTTG
 CCAATCTAG CCGCATGTA TCCATTTT GTGGTCTCT ATCTCTTAG TATTCATC
 TTGATGAT GATCAAGAG ATTATCTC CTGGAGATG CTGCGTCCA GAGCTGGCC
 CCTATTGGT AGAATGGAT GTACACATG GTTCTTTCT TCCCTCCAGT GACTAATGA
 GACTCTTT TAACCTGAG CCACTTGGC TACAGCTATG CCACTGATCT GCGAGTTCA
 GTTGAAGAA CTCAGGTTG GCGCAACT CTCTTAGT TATGGGAGC ACTGTGGT
 TTGTTGCT TTCTGCTGT GTTCTCTT CTTCATATA GAGTCTTG AAAGAGT
 ACACCCCTAA TGGAGACACA TTAAAGCAGC AAGAGATACA CAGAGAGAC CTAGGGTCT
 CATGCTTAC CTAAAGAG AGGCTGGCCA ACCCAGTT CTGACCTGA CAATAAGGA
 ACTATCTCT ACTGTCTCT TTGAGTTGA AGATCTTTGA CATAGCTCT TCTATAGTA
 TATGATGA ATTATGCT GTTCTAGT GTTCTCTCT TTTCTCTCT TGTATACGA
 ACCCACTAA TGGTCTTGG GCTACTCTA CTCTCAATA AAGTAGACC TACCAATTG
 TGATATCAA TAATAACCC CCCCCATA TTGATTAGC CTCTCTCTT TCTGAAGCA
 TTTAAAAAA A

Seq ID NO: 165 DNA Sequence
 Nucleic Acid Accession #: XM_059422.3
 Coding sequence: 207..1400

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 45
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1 11 21 31 41 51
 TGTGGGGCTG CCCGGGCTCG GGGGCTCTG CAGGGCGCAC CCGTGCCTCT TTCGGCTGT
 GAGCCCTCT GCGCGCGCG CTGGGGCTG TCGCTCGACT CCGCGCGCG CCGAGACCG 60
 TCTCCGCTCT CGGTTTGGG GCGACGCC TCCTGGGCG CCCCTCGAC ACTCGAGG 120
 AAGGCTGTC CTGTGTGGA GAGACATCA ACTGCACT CCGCTCTTC CTCTGGCT 180
 CTGTGAGCT GCGTCTCAT TCGTCCCAT TCAATCTCT GTCTCTGAG GAATAGCT 240
 CCAACAGGG GATCCAGTT TTCAATCAG TTGTGAATG GAGGCTCAT GACCAATCG 300
 TGATCTCTC CCAATGATT GCGTGGCTC TGAGATATCT TCACTGGGG CGGAGCGA 360
 GAGCAGGA GCGGCTGCC ATTGTGTA GATAGGGCT AATGGTAT GGTAAATAT 420
 TAAAGAGAT CAACAAGGC ATGTCTCCA AGAGAATAA AGACATTGT ACAGTGGCTA 480
 AGCGCTGTT TGTTAAGAT GCGCTCGAA TTGAAGTGC TTTTGTACA AGGAACAAG 540
 ATGTGTCCA GTGTGAGTG GGAATGTA ACTTTAGGA TCGAGCTCT GCGTGTAT 600
 CCACTATC ATGGTTTAA ATGCAACA GGAATATAT TGCATCTGT CTCTCCAG 660
 ATCTTATGA TGTGTGCTC ACCAGCTGG TCGCTGCAA CCGAGTAT TTCAAGGCTC 720
 TTGGAATC AGGTTTCCA CCGGAGACA CAAGAAGAC CACTTTCTG CGACCGAC 780
 GGAATCTTA TCAATGCGA ATGTGGCC AGCTCTCGT GTTGGGTGT GGGTGCAG 840
 TGTCCCGTA TGTCTGCT TACACTCTG GATGAGTCT GATCTGGG GAGAGCTA 900
 GATCTGAT TGCATCGCC ACTGAGACT CCACTCCGT GTCTCCATC ATCCACACA 960
 TCAGAACAA GACCATAGC AGCTGATGA GATCATGT GCCCAAGAG GTGCGATGA 1020
 TCGTCCCA GTTCAAGCT GTAGACA CAATTTGGA GAGGCCGCT AAGTCTGT 1080
 GATCTCTA CATTTTAT TCTCAAGG CAAATTTGC AATAATGA AGCTGAGAA 1140
 AACTCATG TTCTCATC TTGCAAAAG CAATATTGA AGTCAGTGA GATGAGCA 1200
 AAGCTCAGC AGCAACACT GCAATCTCA TTGCAAGT ATGCGTCCC TGGTTATAG 1260
 TAGACAGC TTCTCTTT TCACTCGC ATATCTAGC AGTGTGTG TATTTATG 1320
 GAGCATAA CAAAGCTG AGATGATGA AGATGATCA ACTACTGAT GATCTCTT 1380
 GCTAGAGA AAGCTCTCT TCTGCTAT TCAATGTC TGTAAATAT TTTGTGAT 1440
 GCTCTTTT TCAAACTAG TTCTTAGGA CAGACTGAT GCAAGTGT CTCTTGG 1500
 AGGTATGGA GGGAAAGAC AAGCAGATG GCTGAGAC TGTACTGAG AATCATGA 1560
 AAGCTTCCA GATCTTAA AGATCTCTA AACTACTGA TGTACTCTA GGTACATG 1620
 CTCTTGTG ATTTCTCTC TGTGTTTA TATATAGT GTTCTCTT TCTCTATGT 1680
 CGGCTTTT AGAGAAAT TAATCAGTG GACAGAAAA AAATGTTT ATGTAGCT 1740
 TTACTTTTA TGAAAAAA ATATTTCCT TTTAAATC TTTTCCCA TCCCTCCA 1800
 AAGTCTGAT AGCAAGCT ATTTTGGTG TAGAAGGCT GAATCTCTA GCTCTTGT 1860
 GTTGTGTG TGTCTTCT TGTGTTTA TATATAGT GTTCTCTA AATTAATG 1920
 TAAAGACT CTTCTCTCT AGACAAGTT GCTGTGTGC AGTGTGCTG TCACTACT 2040
 TCTGACTCC TTGATTTC ATTTTGTAT TTGTACAA ATGAATAA ACTGTATGA 2100
 GTACT

Seq ID NO: 166 DNA Sequence
 Nucleic Acid Accession #: XM_040512.3
 Coding sequence: 382..1302

80
 1 11 21 31 41 51
 GGGCGCGCG GCGACAGGAG TTGGAAGAG GACGATGCT TTATCAGCT CGAGGTGCC 60
 GCGCGCGCT TTTTGGGCTC CCGGACCCC GGGAGTGGGA CCGGACATG GGGAGGCTC 120

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	AACTCGTTCA	CTCAGGGAAAT	CGTGGCCATC	GCTCTCTCCA	GGCGGACCTC	GGAGAACTAC	180
	TGCTCCCTGG	ACAGCGCAGG	CGAGGCGCGC	AGCACCAGCG	CGTTCGAGCA	GCTGCGAGGG	240
	TCGCGAGGCG	GCTCATCTC	CCAGAGATCT	TCTCTGGAGA	CCGTGGAGAA	TATTGGAGAG	300
	AAAGCCCTCT	TCGAGGAGAT	TCGAACTCTC	TCAGCTTCAC	CCGAGCCAAA	GAATTTTGG	360
5	AAAGTTCAAT	TTATCAAGAA	CAAGGCGGCA	CAGCATACCA	GGATGCGCAG	AATATGCTTT	420
	ATCAAGTGGCA	GAAGATCCTT	CTGTAGTATA	TTTTCAGTGC	TGCGCTATGC	GCACAGTACC	480
	CAAGTCGGGG	ACTTGAAGTT	GGAGGAGGGA	AGAACAATCA	CTGTGTCAGT	GATTTTGAAA	540
	GAGATCAATT	GTCCTGGAAG	TGTGGAGCTG	GCTGCTGATG	GGAGAGCTGT	TTCCTATACC	600
	CAATTTCTGT	TACAGCAAAA	CTGTTTGGGA	GGCGGAGAAA	ATATCATAGA	CTCCACTCTC	660
10	TCTTTCTCTC	AGTTCCTGTA	CGTGAAGCAC	CGAGGCTCTT	CCATAGGCTC	GGCAACCGCG	720
	ACCCGAGGGA	GCTCTGAGAC	AGGTAGTGAC	CTGGGAGACT	TTATGAGCTA	TGAACCAAAAT	780
	CTCTTGGAAT	ACCCGCAATG	GCTCTTGAGC	AAACCAAAAC	GCTTTCTGAT	CTTCCCTTCC	840
	TACATACACA	CAAGTATTGA	CTAGGTGAAG	CCTCTGGATC	TCAGAGAGAA	CATGACAGAG	900
	ACCTTCAAGG	AGAGATCTCC	TCGATTTTAA	CGACAAATTA	GAGCTTGAAA	AGCTCTGAAA	960
15	CGAGAGATCG	GGAGGCTTGC	CGAGGAGGAC	TGTGGCCTTG	AGGAGCCGAC	GTTGGCCATG	1020
	GCTCTGCTCT	ACTTTGAAAA	GCTCGGCTTC	AGGCGGAAC	TCACAAACAA	GAACCGGAAG	1080
	CTGTGTGCTG	GGGCAATGTT	GCTGTATGCA	GGCAAAATTT	GAGTGTACCT	GAAGAAACAC	1140
	GAAGTGAAGC	ATTATATTGA	CAACTGGGAA	GAGAGATCTC	GCTCGAGAC	GGGACACTGT	1200
20	ATTGCTCTTG	AATTCGCGGT	GTTAGTGCCG	TGGGAATTCG	CGCTCCACTT	CGCCGAGGAC	1260
	GAAGTCATCG	CCCACTACAG	ACGGCTGCTC	CGAGATTCCT	AGACCTGGCC	CGAGAGGAGC	1320
	CCAAAGGCGCA	TTTCTTCTCA	CGTTGGTGG	GAGAGCTACT	CTTACTACTG	GAATGAGAAA	1380
	AAAGTGAAGC	TGCAATATCC	AGACTTTTCT	TCTCTCGAC	ATATTTTGGG	GGAGAGCAGT	1440
	ACTAGAACT	TTCCAGGAG	TCTTGGTGTG	GTAGCCAAAG	GGAGCCATGA	GCTATGGACT	1500
	CGCTCAAGAC	GGGAGGAGGA	GGTGTGTGCT	GAGAACAGAG	AGGCTGCTGC	CTCTGTCCAC	1560
	TAGGAGCAAG	CCCTAGCTGC	CCGACGCCAG	TCTTTCTCCC	CGGACTTCAC	AAACTGTAGA	1620
	AGCTGTGATC	AGGCTCTCTT	CCAGATCTGT	TCCGACTTGG	AGGTGTAGAG	GCTGTGAGCT	1680
25	CGCGGGGAG	AGAGTCTCGA	AGATTTGGGG	GAAGAACTTT	AAAGATATCC	CTCATGTGTG	1740
	CAAGAGATGT	GCAATCTATT	TTTTGTGATG	GCAATGGAAG	TGCATCTTCC	CTCTGGGCGT	1800
	GTTGGTGTGT	GAATGTGGAA	GTTGTCAAGA	GATACCTGAG	CAGCGCTAGA	CCCCCGAGAG	1860
30	CAATCGGCTG	CTTGAAGGAG	CAAGCTCTTG	TCGATTCGAG	TGAGTCTGAC	TGACATCTGA	1920
	CAATATTATC	TAGATGATTT	CTGGATAAGA	ATTCTCTCTC	CGGTACAGAA	CAGTTTGAACA	1980
	TCTCTCACCC	TTAGAAAATG	ACTGACATTT	TTTTGTACT	GCTCTCACCC	ACCAAGGGGA	2040
	TAAAGAGGCG	GAGTTCTGAG	TTTTGGATGA	GTCAGTCGCG	TGGAGAGGCG	TGGAGCGCTG	2100
	CGCTCTGTAA	CTTCTGCTGG	CTGCGCACCC	GGCAAGTGTT	ATTTAAGCTT	CGAGCTTCTT	2160
35	CGACTGTGGA	GATGAGAGGG	AGAGGCGGCA	GCTGCTCTCT	GATTTTGTGA	CTGTTTGTGA	2220
	GTCGATCAGA	AGCACAATTA	CTGTGCTATC	TATATCGCTA	TATAAAGGTT	TTTTATAAAA	2280
	ACCCAGGATA	GGAGCAAGAC	GCATGATTGG	TGTTTGAGGC	GTTTCCGACG	TGGAGCAAAC	2340
	TGCGTTTGGG	GCTGTGGTTA	AGCTAGTAAA	GGAGGCGGTG	GCTCTTCTCT	AGATTTGCCA	2400
40	GTTGCGGCTG	TACGTTCTCA	CAAGTATTGA	CGCTGCTCTC	ACTGGAGGAG	CGAGGAGGAG	2460
	TCTGTATAGG	CGATGTCCAC	ACACTGTGCT	CTCATAGTGC	CGAGAGAGAG	CGACGAGCTG	2520
	AAGTTCCCTC	GACTGAGAGG	AGCCTGTGCG	CATGTAAAAA	GAGAAATAAA	CTCTTGTGCT	2580
	TTTTTTGT						2587
45	Seq ID NO: 167 DNA Sequence Nucleic Acid Accession #: BC008826 Coding sequence: 188..2695						
	1	11	21	31	41	51	
	1	1	1	1	1	1	
50	GGCAGAGGC	TCGCGCTCT	GGACTAGGAA	CGGACGCGCC	CGCTCCGCGC	GTCCTCTCCT	60
	CTCTCTCAG	CGGTTTGGG	GAGGGCTCTC	CCAGCTCTCG	GATAGTTCCC	GAGGGTCATC	120
	GGCGCGGAG	TGCGCTCTCC	CTTTGCTCTT	CAGCTGATTA	TAAATTTGGA	GGAGAGCTGT	180
	CGCGAGGTG	ACCAAGCTGG	CGGCGGCTGT	CGCCAGGATG	ATGGCGCGCG	GGCCGGGAGA	240
	GAATCAACCG	CGTAGCGGGT	TCCGCGTGA	AGTGTCCACT	CGCTCCGGCC	AGGGCGCGGT	300
	CAACGACCTC	GGCGGCTTT	TTATCAACCG	CAGCGCGCTG	CGACCACTCA	TCGCCCAAAA	360
55	GATCGGGAG	ATGGCGCAC	AGGACAATCG	CGCTCGCTCT	ATCTGACGCG	AGCTGGGCTG	420
	GTTCCGCGG	CGGCTCTTGG	AGATCTTGTG	CAGCTGAGCA	CAGCTGAGCT	CGATAGCTGT	480
	TGGTGCATC	GGCGGACGA	AGGCCAAGT	GACAAAGCTC	GAGCTGGAGA	AGAAAATTGA	540
	GGATACAAA	AGAGAGAAC	CGGCAATGTT	CAGCTGGGAA	ATCCGAGACA	AATTAATCAA	600
	GGAGCGGCTC	TGTGTGGA	AGACGCTGCC	GTCAGTATGT	TCCATCAGCC	GCATCTCGAG	660
	AGTAAATT	GGGAGAGGGA	AGAGGAGGGA	CGGCACTCTG	GAGGAGAGCT	AGGCGAGAGA	720
	AGGCAAGAG	AGGCGACAC	AGNCACTGGA	CGAGCTCTCT	GAGAGAGAGC	CTCAGACGCT	780
	CCATCGAGAT	GAAGCGCTG	ATATTGACTC	TACACAGAT	TTACACTTAA	AGAGAGAAA	840
	GGCGAGAGC	CGAACCACTC	TACAGACAGA	AGGCGCTGAG	GAATCGAGGC	GTCGTTTGA	900
60	AGAGTCACT	TACGTTCTCA	TTTATATTGA	GGAGAGAGCT	CGGCGAGGCG	CGAGCTCTCA	960
65	CGAGGCGCGA	GTACAGCTCT	GTTTATGAAA	CGCGCTGCGA	AGATGGAGGA	AGCAAGCTGG	1020
	GGCCATCAA	CTGATGGCTT	TCAACCATCT	CATTCCGCGG	GGGTTCCCTC	CGACTGCCAT	1080
	CGGCACTTGT	CGAAGTACC	AGCTTTCGGA	GACCTCTTAC	CAGGCGCAAT	GTATTTCACA	1140
	AGCTGTGGA	GATCGACGA	GACGATTTCA	CGAGGCTCTA	CGGCTCTCTC	CGAGGCTGT	1200
	ACACCAAGAC	ACCATCTCTT	CGAACCCAGA	CAGCAAGCTC	GCTCTACTGC	TCCCGACGCT	1260
70	CAGGATGGA	TTTTCAAGT	ATACAGACAG	CTTTGTGCTC	CGTTCGGGCG	CCTCCAAACC	1320
	CAAGAACGCC	ACCATATGCA	ATGGCGCTCT	ACCTCGAATT	TCAATTGGTC	ATAATCTGTC	1380
	CTCAACAGGC	AGATTCTATC	GTTGTCGAAA	TCAGAGAACT	GGAAGAAAGT	CTGTCTGAGT	1440
	GTCATATGCA	GAGGTGGA	AGACCGGAAA	ATCTCTTAGG	AGAGAGCTGT	CATCCATGGA	1500
	CAACCAAGT	AAATTTGCTA	AGACCGGAG	CGAGCTGCGC	AGAGAGAAAG	CATCTCTCCA	1560
75	GCTCTGCCAG	GAGGCTGCTC	GGNCAAGGCC	TGGATACAG	TTTTCCAAAT	GGCTCCGAAG	1620
	CGCTGGCTCT	CTCAAGATTA	ATGACTTTGA	TAACTGAGCT	ACATTTGGCC	CTCAAGCTAG	1680
	TCTAATGCT	AGTCAATATA	GTTGAGGACT	CTCAAGCTCT	ATGACGAGC	AGATGAGCT	1740
	TGGAGAGGG	GATGTGCAAT	CTATGTGTTA	CGCCGCACTC	GGCCCAAGGA	TGGCTCTTAC	1800
	TTTACCGAGT	CTGTCTGAGA	TNAGCAATCC	GGAAAACATG	GAATATCTTT	TGGATTAATCT	1860
80	CAACCTCTCT	TACATACACA	CATCATATAC	TGTTTGGAGC	CAGTCTCAGC	CTGAGCAACT	1920
	GATCGGAGAG	AGGCTGCTCT	ACTGCGGAGC	CGGACCAAGC	ACCAATTTGA	ATTCTCTGAC	1980
	CCCAAACTAC	CAAAAATCAA	CAATATGCGA	ATCCAGATG	AGGCTCTTGC	CCGAGATGCC	2040
	TATACAAACA	CTTCAGGACA	ATAAGTCGAG	TTATGGAGGT	ATGAGTCAGT	ATAACTGTGC	2100
	GCTCTGAGCT	TGAGAGAGT	TGCTGACTTC	TGACTTCTCT	CGCCATAATG	ACATTATGAC	2160

WO 03/025138

PCT/US02/29560

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ACCAGCTGAT CCTGGGATG CCCAGCCAA GACCCGGTT CTGGGCGAG ACTCATGAT 2220
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 TCGAATGAC CTATGGATG GAGATACATT GGAATTTAAC TGTGACAATG TGTGCCCCAA 2640
 CCAAGCTTC CCACAGATG TCAGACACAC GACACATAG TGGGTGTGAG CTGAGGGTT 2700
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 AAAAAA

Seq ID NO: 168 DNA Sequence
 Nucleic Acid Accession #: NM_005761.1
 Coding sequence: 250..4956

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 AGCTGATGGG AGGCTCGTGA GTCTTGCGGG GAGTGTCTTA GCGCGGGCGC TGGAGAGGGC 1200
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 GATATTTGT CTGGAGAGCA AAGTGGCCCT AAATATCGA TAATTTGAG CAGTAAGAGA 1800
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 AATGTGACT CTAGACGGGA GCTCTGCCAG AATAAAGTCC AGGCCAACCG GACCTGGACC 1920
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 CCGTTCACAG CTTCGAGCCC TTCTGATTAT GAGAGAAACC AGGACAGTGT TCGATGGCT 2160
 GTGAGAGAGA CATCAAGAGG AAGAGAACCC AAGGAGACAG AGGGGACAGC AACCAACAGC 2220
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 AAGAGAACCA GTACCTGTGA TAAGATATGT ATACAGGTTA GCGATGTGCT AATGATCAC 2400
 CACATGAAT CTCTCTCTCC ATCAAGCCGG AAGAGAAATG AGATGTGTGT TATTCAGTTT 2460
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 CTATATTTCT CTGATCACG CTGATCATGT GGTGTGCTGA ATATACCAT GATGGTCCGA 2580
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 AGTCAACAC TAAATATCT GAAAGGAGG CTCGCGAAG ACATGCTGTA CGGCTTTGCT 3240
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 ACTGTGCAAT TAAAGCTGCT CTTTGAAAA ATCCCGGAAA ACAGAGTGC AGATGTTGT 3900
 CGGATATTT CAGTCAATGT TCTGCACTGT GACACCATGT GCGAGGCCAA AAGAAAGAT 3960

WO 03/025138

PCT/US02/29560

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TTCACGACAT TCTTAAGCAA AATGGCTCT CTTATGGAC TCGACGTAA TGAATTGGT 4620
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ATTCTTGAAG ATGGGATCAC CAGCTAAAC ACCATTGGCC ACTATGAGAT ATCAAAATGA 4740
TCCACTATAA AAGTCTTTAA GAAATAGCAA AATTTTACTT CAGATGTGGA GTACTCGGAT 4200
GCACCACTGC ATTGTATTTT ACCAGATTGC GAACATCTCC AAGATGTGCA AGCAAAAGAA 4260
CATCGAGGGA ACACAGATTT CAAGATGAAA GAATGTATTC TGCAGAAAGT CTTCTCGGAC 4320
AAGGTGGCAA TTCTATCTGT GCTTGAAAAA CTTTITAGAA GCATTGGAG TTACCAACAC 4380
ACGACAGCTC CATTGCTATT AAAATACTTT TTGACTTTT TGGAGGCCA GGCTGAAAC 4440
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TCTCGGTGAT ACCTCTGAAA GAACTCTGAG TTTGTCTTTC ACATTAGAA GACACAGCT 4560
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GAGTGGCTCT TGACAGATAT TTAACAATAT ATCTGAAAT ATTTTATGTA GATTCTAAT 4860
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GGCAAGTTC TTAGACAGAC TTGGAGACAA AATGGCTCTC TGGCTATCTC TTGTGCTTGA 5040
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Seq ID NO: 169 DNA Sequence

Nucleic Acid Accession #: XM_063670.1

Coding sequence: 1..708

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ACCGTGAAGT AATTTATAAT GTGCGTCGAG GGTACTGTTT ATCCCCAGAC TGAAGATGG 120
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CTGTGCTCTCA CTTCTGGGCA TTATCTGTCT AATTTGGAT TCTTCAATGT GTCTAGTGCT 240
TTTCTCAAGT CATGTGCTCTT CACTCTGGAT CTGACACGAC CAACTCTCTA 300
CCTTCAAGCT TTGACAGTCA CACTGCTCTC TTCTCATATG AATAGAGGG AGATGGGTTA 360
GTATCCATGT TTCAAAGACT GGTCCTAAGG ATCTAGAGGG TTTTGTGGAT GTCCAAGTG 420
GAGATGCTAT ACCACACTAA TGAATGTTAT ACTGCTGGAG AGGGGGTGGG AAATGTATAC 480
AGCTAAAGCT GAGGAGAGCT GAGTGAAGAG GAGTGTGCT CCGCGAGTAT GGAAGAGCT 540
ACCGCGAGCT CCGTCTATGT CGACATAGAC AAGGGCTCTG ACTTGGCTGT CTTGCTCTCT 600
CTCTGCCCTT TCCCTTGTGT GATGATCATC CGCTGTGCCA GGTTCATCAT GGAACCTCTAC 660
AGCCCATCTC CCACATCCAC CTGGGAGGAG CAGACACTGG AGCACTGA 708
  
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Seq ID NO: 170 DNA Sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..936

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GCTCTGCCCT TAAATAGCCA GGAAGCGCGC GCTCTCGCTC AGAGCCGCCCT CTCGGCTGCT 120
GGCGCGGCGT GCGCGCGGCC GCTGGGGGCT CTGACTCTGT CGAGGCCGCG CTTGGGCAAG 180
CGCCCGCGCG CCGCGCGAGC CGCGCGGCCG CTGACCGGGA AAGCGGTATC CGGCGATCTC 240
CGGCTCGCCC TGGCTGGGCG CGCGCGCCAG CAGAGACCCC GGAAGGCGAC GGAACGGGCG 300
TCCGACGCC TAGAATAATTA CTCTGACCTC TTGTCCAAGG CATCTGCTAT AGCTACTGGG 360
ACACACACCT GTGAAGACTC TACATTTGCA AGGTTCTACG TCCGCCACCC TCTCACCACT 420
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ATGTTTGAAT TCTTCTATCT GTCCATATGG TTCTCTCAGC CATTGGGACG GACTCTTTTC 540
CACTTGGATC TGCTCAACAC CAACCTATCA CTTTCAAGCT TTGACAAGTA CACTGGCCAG 600
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GGCGAGAGG GAGCAGCCCA CAGTCTGTGC CCGAGATAGG AGAGGCCACG GCCCGAGGCC 780
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Seq ID NO: 171 DNA Sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..2094

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ACAGCAAC TCACATGATG TGAAGAAAT TTGCAATCTT ACTCATCTGA CGAGGCTCA 180
ATATCCAGAA TCTACATGCA ACCCAACAA ATTTACAGA AAAAACAA CAACCTATC 240
AACAAGTGGG CGAGGATATG GAACGACAC TTCTCAAGG AAGCATTTA TGCAGCCAC 300
AGACACATGA AAAATGTCCT ATCATCACTG GCATCAGAG AATTCAGAT CAAACACCA 360
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TTTGTGATG GACTGGACAT CACACTCATG ATCTGGGTA TACTGGCAT ACTGGTCAAT 540
GGAGCTGGCC TTCTTTAAT GCCACTGGTT TTAGAGAGTA TGAGTGATAA CCTTATATG 600
GGATGTCTAG TCGCAACTTA CACACAACAT TATGACATG GTACTCAGTC TCAAGAGAG 660
TGTAAGAGG ATATGATCT GTGACGCTGT TATTAATGTT GTATAGGTT TGCTGCTGT 720
ATTTTGTGTT ACATACAGAT TTCTTGTGG ATTATACTG CAGCAGACGA CAGCAAGAG 780
ATTGGAAGC AGTTTITTTA TTCAAGTTTG GCACAGGACA TGGCTGTTT TGATAGCTGT 840
GACATCGGTT GCTTTTACAC TCGCATGACA GATGACATG ACMAATCGG TGATGCTGT 900
GGAGATAGA TGTCTCTTCT GTTCAAGAAC ATGTCTACTT TTTCAGATCT CCGTCAAGT 960
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PCT/US02/29560

TATTCCAAAG CTGGGCTGT GGCAGAGAA GTCTTGTCAT CAATCGAAC AGTCATAGCC 1140
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 TTAGTGTCAA ACCCCAGAT TCTGATTTTA GATGAGGCTA GCTCTGCCCT GATTTCAGAA 2040
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Seq ID NO: 172 DNA Sequence
 Nucleic Acid Accession #: XM_166496.1
 Coding sequence: 378..773

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 AATCATAGA AGGATAGCTG GAAATTAATA ATGTTTCTTT CAATATCCA TGAAGCAAT 240
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 ACAATATCAA GTATGACAGA GATGATGTGA CTGATGAAGA GATGAGAGGA CAGCAAGGG 540
 AAGCAATGCT GTATGATTTT ATGATGAGT TTCTTAATA ATTTATATA TTGATAGGG 600
 AAAAAAGAC TGAATGATG AGAGGACGA AACAGAGGAT GCGATTGCT CTGACTCTAG 660
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Seq ID NO: 173 DNA Sequence
 Nucleic Acid Accession #: XM_166305.2
 Coding sequence: 157..1104

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 GACCTGACAG TCAAGACACA CAGCGCCTTG GCGTACGGCT TGGTGAAGCT GCTGACGGG 240
 GCGGGGAGCG GCATCTCTCT CCGCTTGCCA TCCAGTGCC GTGCGAGCC CCGCTGGAAC 300
 CTGCTTACCG GCGTGTCTTT CTGCTGGTGT CCGGCGCTCG GCTTCTCTT CTGGGGCTAC 360
 GTGCTGACAG CAGCATGCTG CCGCTGTCTC ACCGATGCT GCTCAAGGCC CCGCGCGAGT 420
 TGGCATTCGG GCGTGGCGGG CTCTCTGGTG TGCATCAAA TCAAGCGCG CCGCGCGCTC 480
 GCGGCCCTCA CTGGGCTGCC CTTGGGCTGT CTCGGGGGCG CCTTTTACA GTGCGCGGCC 540
 ACCGGGCGCG GCGGCTTGGC GAGCGGCTGT TGCCTGGCG CGAACCGCG CTCTGCGCG 600
 GAGTGTGCT GAGTGTGCT GAGCAGAGCG AAGGCTGCTC CAGTGCAGGA CTTGGTGAAG 660
 GATCTAGAGC CTGATGTGCT GTGTTGGGCT TGGATCTTGA TGTCAATAT TATCATAT 720
 CTCTGTATT TTACATCTGT CAGCCGATGC CTATCTCCAG TTAGTTTCT GAGCTGAATA 780
 TTCTGAAAA TCTATTGGA ACAAGAGGAG CAGATCTCTA AAGTAAAGC CACAGAGAT 840
 GCACTGATAT TGGCAAAAGA GAATATAATA TGTTTCTTGT AGGGCTGCGA TCGCAAAAGA 900
 TATAAAGCT CAGCTGTGCA GTGTTGGGCT TGGATCTTGA TATGTCACA GAAGAAGC GATCAAGT 960
 AAGGCGCACT ACTACAGAT GTTGACANAA TATGTACACA GAAGAAGC GATCAAGT 1020
 ATACGGCTTA CTGAAGAGA TACGGTGATT CCGTGTCTGT GCTTTGTAGA TTCTCTGGT 1080
 ATAAACGCA CTCTGAGTT ATGACCTTTT GAATGATGA AAAAAAAT TGTTTTGAAT 1140
 TATCTCTTTA TTAAAAATA AATATGGTA TTTT 1175

Seq ID NO: 174 DNA Sequence
 Nucleic Acid Accession #: NM_032211.5
 Coding sequence: 152..1428

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	CGAGGAAATC	TGGGGGCTCA	CCGAGCCCAT	GSTGGGCTCG	CCACAGCTCG	GCTGTGGGTT	1560
	TGCTATCAT	CGCTCAAGTG	AAACCTGGTT	TTGTGTGGGG	AGCCCAAGGG	CCAGAGGAGT	1620
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20 GCTTATCTGG TGATCCGAGG ATCCGACAGG CTAGGACCCA TCGTCTGTGA TCACATCATG 540
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Seq ID NO: 161 DNA Sequence
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Seq ID NO: 182 DNA Sequence
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Coding sequence: 174..1016

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WO 03/025138

PCT/US02/29560

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Seq ID NO: 183 DNA Sequence

Nucleic Acid Accession #: U01020.1

Coding sequence: 112..192

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WO 03/025138

PCT/US02/29560

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PCT/US02/29560

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Seq ID NO: 187 DNA Sequence
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 Coding sequence: 194..910

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WO 032138

PCT/US02/29560

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Seq ID NO: 189 DNA Sequence
Nucleic Acid Accession #: NM_014654.1
Coding sequence: 1504..2658

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WO 03/025138

PCT/US02/29560

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WO 03/025138

PCT/US02/29560

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45	AGAACTGGAT	GACTACTCAT	TCTCATGCTA	TAGCAGTTG	GAGTGAATG	GATCGACAGA	180
	TTCACTGACC	TGTCGTTTTG	AGGACCCAGA	TGTCACACAC	ACCAATCTGG	AATTTGGAAT	240
	ATGTGGGCC	CTGTGGAGG	TAAAGTGCT	GAATTCGAG	AACTACAG	AGATATATTT	300
	CATCGAGACA	AAGAAATTTCT	TACTGATTGG	AAGAGCAAT	ATATGTGTGA	AGGTTGAGGA	360
50	AAGAGTCTA	ACCTGCAGAA	AAGTAGACCT	AACCATATA	GTAAACCTG	AGGCTCTTTT	420
	TGACCTGAGT	GTATCTATCT	GGGAGGAGCG	CAATGACTTT	TGGTGACAT	TTAATACATC	480
	ACATTTGCTA	AAAGAGTAT	TAAAGTTTTT	AATGATGAT	GTAGCTTACC	GCACGAGAAA	540
	GAATGAANAC	AAATGGAGGC	ATGTGGATT	ATCCAGACA	AGCTGACAC	TCTCGAGAG	600
	AAAGCTCAA	CCGCGACGAA	TGTATGAGAT	TAAAGTGA	TCCATCTGT	ATCATATTT	660
	TAAAGGCTCT	TGAGATGAT	GGAGTCCAG	TTATTACTTC	AGACTCCAG	AGATCAATAA	720
55	TAACTGAGG	GAGATGAGTG	CTATCTTACT	AACCAACAC	ATTTGAGTT	TTTTCTCTGT	780
	CGCTCTGTGT	GTACTCTTGG	CTTGTGTT	ATGGAATAA	AGGATTAAC	CTTATCTATG	840
	CGCCAGTCTC	CCCGATCTA	AGAGAGCTCT	GGACATCTT	TGTAGAAAC	CAGAAAAAAA	900
	TTTAAATGTG	ACTTTCAATC	CTGAAGTTT	CTCGAGTGC	CAGATTATA	GGGTGATGTA	960
	CATTCAAGCT	ACAGATGAG	TGGAAGTTT	CTGTGAGAT	ACGTTTCTCT	AGCACTAGA	1020
60	TTTATTTGAG	AGGCGAGGC	TGTGAGGGA	CTGTGAGG	CCGACAGCTG	CATCTGAGGA	1080
	TGTATGCTCT	ACTCCAGAAA	GCTTTGGAG	AGATTATCC	CTCACTAGCC	TGGCTGGGAA	1140
	TGCACTGCA	TGTAGGCC	CTATTCTCTC	CTCTTCCAG	TCCCTAGACT	CGAGGAGAGG	1200
	TGGCAAGAT	GGGCTCATG	TGTACAGGA	CGTCTCTCTT	AGCTTGGGA	CTACAAAGAG	1260
	CAGCTTGCC	CCCTGATTT	CTGTATGAC	TGTGACATG	CCGACAGCTG	CAGTCTGAG	1320
65	GGGTGAGCC	ATTCTTACT	CCCTGGATC	AAATCAGGA	GAGCGATG	TCACCATGTC	1380
	CAGCTTCTAC	CAAAACAGT	GAGGTGTAG	AAACCGAGC	TGAATTACC	GTGAGGACA	1440
	AGATATGTT	AAAGCGAAG	TCTAGATTC	CTAGTCTCCC	TACAGACAGA	GAGAGAGACA	1500
	ATTATGAAA	CATGCGACA	TGATGTGTA	AGATCTGGA	CATGCTCTT	GACACTCTT	1560
	CTGATGTTCA	GTGGCACTCA	ACATGATGCA	AGGACATCCT	GCTCTTACCA	TGTGTATTGC	1620
70	GTCAAGGTT	TTAAGGTGAC	CCAATGATC	AGCTATT			1658

Seq ID NO: 192 DNA Sequence
Nucleic Acid Accession #: NM_006272.1
Coding sequence: 73..351

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	ACAAGGAGGA	GGATGTTCTG	CGTGGAGAG	GCCATGGTGG	CGCTCATGGA	GTTTTCAC	120
80	CAATATTCTG	GAGGCGAGGG	AGACAAGCAC	AGGCTGAGA	AATCCGAAC	CAGGAGCTC	180
	ATCAACATGT	AGCTTCTACA	TTTCTTAGAG	GAAATCAAG	AGCGAGGTG	TGTGGACAAA	240
	GTCTATGAGA	CATGCGACA	TGATGTGGAG	GGGATATG	ACTCTCAGA	ATTATGACC	300
	TGTTTGCCA	TGCTTTACTC	TGCTGGCCAC	GAGTTCTTGT	ACATGAGTG	GAGTTAGAAA	360
	GCAGCGAACC	CTTCTCTGTA	ACAGAGAGCG	TCATCGAGA	AGGACAGAC	CAGAGGCTG	420
	CAGCTAGTA	GGAGCTGAGC	TTTCCAGCG	TGTTGTAGCT	AATTAGGAG	CTTGATTGTC	480

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TTTGTGATTG AAAAATGAA AACCTCTTTC CAAAGGCGCTGT TTTAAAGGCC TGCATCATTC 540
TTTCTGCTAT ATTAGGCGCTG TGTGTAAGCT GACTGGCCCC AGGGACTCCT GTTAAACAGTA 600
ACTTAGAGAT CAGGTCTCCAG TGATAAAGCG TGCAACGTGC AGCCGCCCAT GGCCTGTGTAG 660
ACCTTAAACC GAGGAGGAGC CTGACATCAG AATTAACCCG GGGGACACCT TAANACTTCC 720
ACTACTTTA AAAACCAAGC CTTTATCCAG CATATTTTGA AAGACTCCT GTTCTTTAA 780
TGCTCTTCTC ATTCAACGAG ATAAACGAG GTTGGCCGCT GTGGCCCTCC GCGCTGCGAG 840
TGCTCTTGCG CTGCTTCCCG GATGAGGACT GATCAACAGG TGAAACGTCA GCGCTGCGAG 900
CTGCTCTGGA AAGCAACTGC CATCAAGACT GCGAATTCGA GCGCACTCTG GGGCTCTCAG 960
CTGGCGCTTC GTGACGAGCT GATCTGAGCT GCGGCTGCGA GCGACTCTCG CTCGCAACTG 1020
CTCCGACAGC ATGGCGCTTC CGAGGCGACT ACGGGCGGCT CTGAGCCGAC GCGAGGCGCT 1080
CGTTTCAATA AAAG

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Seq ID NO: 193 DNA Sequence
Nucleic Acid Accession #: NM_006157.1
Coding sequence: 103..2535

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GACCTTCAGA TGAATATCT CACCGAGCTT GACCTTGTGA ACCGACCTT TGGAGTTCT 240
CAGGTGTCTG GATGCGCAA TGCGCGAA GCTTTTAT TTGACAGT AGAAGAGAG 300
ATCCATCGAG CTCCTCATGT GAGTGGAAA TTAATTGCG TGTTCCAGAA CAGAGTGAA 360
TTTCAACATT TGCCACTGT ACAGCAGAG CACTCCACT CAGAGTATG ACTGTCAATT 420
CGAGAGCTGG AGCAAGCTTA TTTGAACTG GAGAGCAGTG GCTTGAAGGA TGAATGTCG 480
TATCATCTGA TAGATATGAG GAGCGAGAG ACAGAGGACT TTCTTTAGCG CATGCGAGT 540
GGCAATATGC ACAAGTTTGC ACTGTCAATT AGCGCTCTC ATCTCCTGCT CATGTGTGAC 600
TTGTAACAGT TTTATGAGCG TGTGATAGC CTCCAGATA CCAACCTTCC CCGAGGATCT 660
AATTTATGCG TTGGCGAGCG CAACCAAGG CATGGCTTAT TCAAGAGTAT CATCCAGAT 720
GGTAGAGTA TCTTATAGCG GATCGGTAT GATACAGAGT GATCAATCT AATGTCACT 780
TGCCCAACTG GCGTGTATT CTTAGGCTG GTGCAAGAA TAATGATT TTACAAGCTT 840
TTGGCCAAGA TGACTCGAA ACTAATATT GAGAGACAA GACTTAGTCA ATTGGAATA 900
TGTGATTGTG AGAGACTGTG TCAAGTAGT GAGCTGCTCT ATGAGATCA AGACTCTTGG 960
TATGATGTGG ACATATGAG GAGCTGAGT GAGCTGAGT GATCACTCT TGTCTTACG ATGCCAAG 1020
ATGTGCTATG CCGCTCTCAA TTGCTCCCA GACTCCCTCC CAGTACACAT TGCTGCCAG 1080
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CGAGTTTAA CAGAGACTCG TGCGGAATCG CGAGGTGAG TTTAGTAAA AATTACAGAA 1200
ATGTGCTCTC CTTTGAGCTG GATCAAAAG GATCACTCT TCTCTAGAA TGAATCTCTG 1260
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TGCAAAACT GGAATACAA AGCTACTTGT GAGTGCAGA GTGTGTACAT CTCTGTGAC 1380
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GGAACGTGTG TGCTCCCA CAATGTGTG TGTCTCATG GATTCAAGG AAGCCACTG 1740
GAGAAGATA TTGATGATG TTGAGAGGA ATCATGAGT GCGACACA TTCCCTCTG 1800
GTTAACCTCG CAGGTGTGTA CCACTGTGAG TCGAGAGG GTTCTCATG GATGTGAC 1860
TATTCACTGT CCGGCGAGT CTGTATTGAC GTGACTGAT GTGCTTAAG AACTCAAC 1920
TGTGTGAGAG ATTGTGCTG CATCAAGCT GAGAGGGT TTGACTGTCT CTGCGCTCT 1980
GGCGCTCTCT GCTCTGTGTA GTGCTCTAT GAGGGGGGCG TGAAGACA TGGCGAGT 2040
TGGACTTGA AAGAGACAG GTGTTCTGTC TGCTCTGCGA AGATGTGCA GATATTCTG 2100
CGAGCGACAG CTGTGTATTG CCAAGATCA AGTGTGAC TATTCTGTG CCGAATATG 2160
GAGACGAGAG TCACAGTGA ATGTTTAGAC CAATATGCT ACAAGTGTG TGAATGTGA 2220
GAGATATGGA CCGATATGCT GCGACTGTGG CGGTCTGAG AAGAGAGAT AGATGTGCT 2280
CCCTACTCTT GCGCCACTT GAGCTGTGAG TATACAGCTA TCTTAGAG GAAATGTGT 2340
CCCGCTGTG TCAGTGACCC CTGCTAGCT GATACATCA CCTATGACAT CAGAAAACT 2400
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TCCAAGATGA TTAGAGATG GATGCGTAG TTTGTTT TTTGTTTTT TGTTTTTTA 2640
ACCAAGATA ATTGCAAGG TTCCCACTG AGGACGTTG TTCGAGGTT GCTTTTGA 2700
GATGACMCTT TGCTTATCT TGCTAAGCTA GTCTAGAGTA CTACAGTGC CTGATATTA 2760
ACTCAATGTT TGTATAGGA ATTTGCGCT GTTGTGATC ATGTTTTCT TATCAGATA 2820
TTTGCAATA CATTTAAATG ATCTCACTGT AAATGGTGA TGTATTTTT GGGTTATTT 2880
TGTGTACTAA CCAATATAGA GAGAGACTCA GCTCTTTTA TTATTTGT TGATTTATG 2940
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Seq ID NO: 194 DNA Sequence
Nucleic Acid Accession #: NM_016180.1
Coding sequence: 26..1618

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GCGAGCTATG GTGAGCCGAG TCGTGTGAG CTTAGGCTCG CCGAGCAGCT GTTACAGACT 240
TGTTGTGTTT CTGAGCCCCA TCGTGAGATT CCGTGCCTAG CCGTGTGTTG GATCGCCAG 300
GACCACTGCG GCGTCAAGGT GGGCGCGCGC GAGCACTCAC ATCTCAACC TGGGAGTGTAT 360
GATGCTGTGT GCGATGCTCT TGATACCTCA TGGGCTACT GTTGTGAGC CTTTGATG 420
TACCCGAGG AGAGAGAGCT TTGGGCACT AGTGTGACT ATGTATGTTG TGCTTCTCT 480
TGTTTTTGCT GCGATCTGA TTGATGGGCC CATCAAGGCC TACTATTGT ATGTCTCTC 540
CCATCAGGAC AAGAGAGAG GCGTCCACTA CCGCTGCCCT TTCAAGGTT TGGAGTGTG 600
CCTGGGTTAC TTCTTGGTGT CTATAGACTG GCGCACTG GAGCTGGGA GACTGTGG 660

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TCAATCTGGA  CACACTGTGC  GGGCAATGAC  ATTAAGATCA  CTCCTGAGAG  CACTGTGAAA  960
CATCTCTCTC  CACTGACCTT  ACTTTGTCAT  GAGCAACCTC  ATTGGATAGA  GCGCTTCTCT  1020
GTCCACATAT  CTGTCTCTCA  CAGATTTCAT  GGGCCAGATT  GTGTACCGGG  GGGATCCCTA  1080
TAGTGCACAC  AACTCCACAG  AGTTTCTCAT  CTAAGAAAGA  GAGGTGGAGG  TTGGATTGTT  1140
GGCTCTCTGC  ATGCATCTCG  TGTTTTCTCT  ACTTTATCTT  TACTTTCAGA  AAGTTTGGGT  1200
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GAGAGAAAGA  GAGAGACAG  AGGCCACAG  AGGGACCCA  GACACACAG  GACAGAGGAA  1440
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TGGCTGGAG  TTTCGTGCA  ACACAGCG  GACCGTGTG  GTCTGTGTA  TCACAGCGT  1560
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CAATAAAGAG  ACAATGAC  TAAAAAAA  1650

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Coding sequence: 18...455
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AAATGCGCAT  TGTCTCTTAC  TGGCCCTTGG  GCTGTCACTG  CGAGTCAAGT  GCGACAGGCC  180
AAACCAAGA  TGGCAAGAAC  TGTCTCTCT  AGACCCATGA  CTCTCTCAT  GACACCTGA  240
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TCAACTGCTC  TGACAAGGGA  AGCTGTGTG  AGCAGCAGCT  GTGTGCTCT  TACAAGAGAG  360
GGCTCTGTG  CTCGAGGCG  AACCTGAGCA  CTCACAGAA  GCGACTGCT  TTCTACTGCG  420
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TCAGCATGGA  GCTCTGGCAT  CCCCACCTCA  GTATTAAAC  TGAACACGCC  TGGCTTTTCA  540
AAACTCTGG  GGGAGGATG  TCCCAGCCT  CCGCGAAGC  CTCTACCAT  GCGTTCTGAC  600
CTCTTGAGC  TTTCCGAATC  TCTCCATGT  GGGGAGAGT  TTGTCTCTT  GAGGTTGGAT  660
GGGATCTG  GAGAAAGG  GTGATGTG  GAGCAAGG  GTGTGTGT  GACCACTGA  720
TCCGAGTGG  GAGAGGTTCT  GCGCTGTG  CCGACCTGCT  GCGCCCTCT  TCGTTCTTCA  780
CCCCCTCAA  TATAGTCTG  GAGCTACAC  CGCAGCGCC  ACTATAAGG  GCAATATTGA  840
TCTTTCTGTC  CATGTGGCTG  TATCTTTTAA  AACCTCAAG  CCGTCCAGG  TGTAGATAGA  900
AAOCTCTCA  TAGCTGTG  GCTGCTCTCA  CMTCTGCGC  ATTTGAGG  TTTCTCAAG  960
AAGCTCTGA  GTCTCTGAG  GTGAGGCCA  TCGCTCTTT  AAACCTAGT  GCGATCTGG  1020
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GACAAAGCG  CCAAGTCTG  TGGCTCCAG  CACAGAGGCC  TTGAGTACT  TCTCTTGCT  1140
CCAGCATTT  CTCGAGGTT  AATTACAGG  GCGACTGGA  TGGCTATAC  TTCTCAAG  1200
ACTATCTCC  ACTCTCTAG  GCTCAAGG  TACTCTCTG  GAAGTCTCC  CAGCTGACT  1260
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AGACTGAGC  CCCCAGAGA  TGGAGGCAT  GTCTGTGCA  TCTCTGTTC  CCGTCTTTC  1440
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AGGTTGAC  AGATGGTGT  GGTAACTCA  CCAGATATCA  TCAAGGCCA  AGGCCCTCT  1560
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CTCTCACTA  TGGCAGAG  AGTGAACA  TGGAGGGT  AATTCTGAC  TCCCGCTGT  1740
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CGAGCGCTCT  CTCGGAACCA  CTTCTGTCT  TGGTCTGAC  CTTTGGCTA  TCCAGTTTTC  1860
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CTCTCTCTA  GGTCTGCT  CTAGAGAA  AGACTGAG  GGGCACT  TTCTCTAGA  1980
GAGCTCCAA  TCTGCAATT  GTGTGTGCT  AGCTGTTC  AGCCAGGG  CTGAGCGAC  2040
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TGAGATGTG  TGACTCATGT  GAATGTGTG  CATGAGATC  AAGGACTGT  GCGCTGTGT  2160
TCAATTTCA  GTCTATGCA  CACTCTGAG  TAGGATAC  CATGGGGA  GCTGTGCT  2220
TTTGGGGA  CAGATCTCA  AAATCTCCAT  ACTTCTCAA  TTTTCTGT  AACTTAAGC  2280
TGCCATATA  AGATAAAGT  TAGCCAGG  ATGTTGGCT  ATGCTGTGA  TCCCAACCT  2340
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TCTCAAAAA  TAAAAATAA  TAAAAATAA  TAAAAATAA  TAAAAATAA  TAAAAATAA  2640
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Nucleic Acid Accession #: NM_018833.1
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GTGAGAGCG  GCTTACTGTT  GCGTCTCTCA  GCGCCCTCTG  GCGACTTTTC  TTCTCAAGG  180
GCTCAAGCA  CTAATGCTGT  AGGGACCTCT  GCGGCTGGGA  GCGCTGTGG  GCGCTCTAA  240
GCTAAGAGC  CTTCTGAGT  TTGTGGGAC  ACTCTGCTC  CGCTCTCTTC  TGGCGACCC  300
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ACTCTGGCT  GTTCTGAGC  CTCTCTGAG  CCGAGGAGG  GAGCAGGAC  AGGTGAACA  480
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WO 03/025138

PCT/US02/29560

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    CTTCATGTGC CTCTCTCTCT TTGCGAGCTC ACTGTCTGCA GGGCTGCGAG GAGGCTGCTT 720
    CACCTACACG ATGTCTCGAA TCACTGTGCG GATCCCGGAG CAGCTTTTCT CCTCCCTGCT 780
    GCGCCAGGAC CTGGGTTTCT TCGAGGAGAC TAAGACAGGG GAGCTGAACT GACCTGCTGG 840
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    CCTGGTAAAA GTGGTGGGCG TTATATGGCT CATGCTCAGC ATATGSGCTC GACTCACGCT 960
    CCTTCTCTCG CTGCGATGCG CTTTCAACAT AGCAGCGGAG AAGGTGTACA ACACCGCGCA 1020
    TCGAGAGTGG CTTCCGAGAA TCGAGATGTC AGTGGCCGAG GCGCGGACAG TGTGTGGGGA 1080
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    CTATAAGAG CCGCTGTGAC AATGTGCGCA CTGTATTGTG CGAGAGAGAC TGAAGCGGCG 1200
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    CTACAGGAGG AGCGTGGGGA GTATGTGTGA GACCTGTGTA TACATATATO GGATGTGCT 1380
    CAGCAAGTGG GAGTGTGAGC AGATGGTTTT TCTCTACATG GAGCGACAGC CAAATCTGGC 1440
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    TACTAGTGTG GTTACATGAG TTGCTTTTGG ACACCCCAAA TTCTACATAT TTCTTTTGT 2340
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Seq ID NO: 197 DNA Sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40-417

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    TTGTAAAGCG CTATGATGTT CTTTGTCTCT CTACCAACCA CCAAGTGAAT TTCAATCATG 600
    TTAAGGCCAT GATTTTAGCA ATCAACCAT CTACACAGAT GTTCAACCCA CCAATCCCA 660
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    TGAATTTGAG CTGAGCTCCA CCAAGCTGCT GTGGCCATCA ACCTCTGTAT TGAATCAGC 840
    CTACAGGCTC CACACAAAT GTGTCTGAGA GATGATGCTT GATTGTTATT GGGTATCAC 900
    ACTGAGATCT ACCAGTGTGT GCGTTTGTGA GCTCTCTCTC GATGTTTGA AAGCATGGA 960
    TTCTATCTTG CAGTCTGAG CTACACCTT TATTCTTTT TGTTCCTCTT TGTCTATCT 1020
    AAGTCAGCTC TTCTCATCTC TACCACAATG CAGTGGCTTT CTCTCTCCA CTGACCTGTT 1080
    CATATGCTCT GTTATATCTG AGTCACCTCC TTCTCATCT TGTCCGCAAC ACCCGCAGCA 1140
    AGATGTTCTT TCTCCCAATT CATCTCATCT GAGTCACTCT TAATTCATCT CTTCTCTCTT 1200
    AATATAAATG TCTTGAACAC ACATATATTC TATCAACTCC GTTTCATCT GTTGTAGTAC 1260
    CACATGGGTT AAGACTCAAT GTTAACTAAA TTCTTGGGTT TTATCTCAT CTCTCCAAAC 1320
    AGATTGTGAG CTGCTGTGAG CCAAGAGCCA CAGTATATT CCGTGTCTCT TCCAGAGTGC 1380
    TAAATANTAC TGTGAGACTA GGTGTTAATA ATTTTAAAT TATGTTTGT ATGGGAGGA 1440
    TGGCAACAG ACATGTGCTT CAGAGGAGCT GCTGTGCTCT TCTGHTATC TCTGTTTGT 1500
    CTAGCTGCTG GTACCTCTCT ACTATATTCT TTCAGGACAC TCACTACAGG GACAGGZACT 1560
    GTTCAACAT CTCTGTCTTT TTATGACMG AGTGTGTGTC AGCTCTTCCA ACATATAGAA 1620
    GCGAGTGGTA AAAACATGCG GATATTTCTG GACTGTTTGT AAAAATATA CAGTTTAGCG 1680
    ATAAATCAT ATATGATTA TGAAGAGCAC TCTGAGTCTT GATTATCAAT TACACACAAA 1740
    CCAACCATAC AAAAATTCCT TTCCCGAG AGAAGGCGCT TTCTCAATTA GCTCAGCTT 1800
    TCTAAGATCT AACAAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GCGAAATATG 1860
    AGTTTATTTG TCGGTTTACT TGTTCAGAG TTGTATGAGA GATTATCAAT TACACACAAA 1920
    TCTCCATAGA AGAAGAGCA CCGTGAACATA CAGACGCTCA CCAAGTCTCT 2040
    TMTGTGAGC ATGATTGTGT CCGCATTAGC CTCTCGAGGA TGTGAGAAC TCTTCCAGG 2100
    GAGGTTTCAG TGAATTTGTT AGGAGAGCTT GTCATGTGGC AAGATTTAAA CTTACTACCA 2160
    TTTTCCCAAA TGAATCACT GCTCACAGCT CTGATGATTT AGAGTGTCTT CCGGTGAGGA 2220
    TCCCCACCGA AGCTCTTATC TAATATGAGA ACTCTGCTAT AGTGTCTGT ACTTCTCT 2280
    AAAATTTTAA GTTCTGATA AATTGAGAG TCTGTGAGCC ACTTACTCTG CATCTCAAGC 2340
    GTAGACAGTA TATAACTATC AACCAAGAC TACATATTGT CACTGACACA CAGGTATAAA 2400
    TCAATTTATCA TATATATACA TATAGACATA CACTCTCAAA CCAAAATATT TTCACTTCA 2460
    AAAACAGATT GACTTGATA CTTGTAAATT TGAATATATT TCTTGTATA AATGAGATGG 2520
    TATCATATAA TAGACATTAA ATGAC

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Seq ID NO: 198 DNA Sequence

WO 03/025138

PCT/US02/29560

Nucleic Acid Accession #: NM_006533.1

Coding sequence: 72..467

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1      11      21      31      41      51
5  AAGGAGAGAG GAGGCGGAGG AATATGCGAA CCGGACGACC CCGTTCCTCA CTTCTGCTCT 60
   CACAGTCCAC GATGCGCCCG TCCTCGTGCT GCGTTGCTGT CATCATCTTG CTTCTGCTCT 120
   TCTCCGACCC TGGTGTCCAG GGTGCTCCTA TGCCCAAGCT GCGTCAACGG AAGCTGTGTG 180
   CGGACACAGA GTGCAGCACC CTTATCTCCA TGCGTGTGGC CCGTTCAGAG TACATGCGCC 240
   CCGAGCTGCC ATGCTGACCC ATTCACCGGG CGGAGTGTGT GTATCTCTTC TCCAGAGCTA 300
10 AAGGCGCCCG GCGGCTCTTC TGCGGAGGCA GCGTTGCTGT AGATATTACT GGAATATCT 360
   CTGCTGCTCT GGTGCTATTC CCGCATAGCA TTGTCGCGGA GGACACGACC CTGAAACCTG 420
   GCAAACTCGA TGTGATGACA GACAAATGGG ATTGCTACTG CCGAGTAGCT CAGCTACCG 480
   CTGGCCCTCG CGTTTCCGCT CTTTGGGTTT ATGCAATATC AATCAACCCA GTGCAAAC 538
  
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Seq ID NO: 199 Protein sequence

Protein Accession #: NP_002412.1

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1      11      21      31      41      51
20 MISFPPLLLL LFMGVVSHSF PATLETQEQD VDLVQKYLEK YNNLKDNGRG VEKRRNSGPV 60
   VEKLKMQQSF FGLKVTKGPD AETLKVMKQP RCQVPDVAQF VLTGDNPRME QTHLTIRIEN 120
   YTPDLPRADY DHAIEKAPQL NSMVTPLTPT KVSSEGADIM ISFVRGDRHD NSPFDGPGDN 180
   LAHAFQKQPD LGGADNFGED EKRTNFRRET MLRVPAHEL GHSLSGHSST DIALALMYSY 240
   TFSGQVQLAQ DDIDGIDQIAY GRSONPQPI GQPTPKACDS KLTFDAITTI RGVNMFKDR 300
   FYMRTNFFYP EVELNIVISF WQPLPNGLBA AYEFAADREDF RFKGNKYHA VQQGNVLKGY 360
25 PKDIYSYSPF PRTVKHIDAA LSEENTKQTI FFVANKYMYR DEYKRSMDPG YPKMIANDFF 420
   GIGHKVDVAF NKDGQFFYFH GTRQYKFDPK TKRILTLQKA NSMFMCKKN
  
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Seq ID NO: 200 Protein sequence

Protein Accession #: NP_002412.1

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1      11      21      31      41      51
30 MISFPPLLLL LFMGVVSHSF PATLETQEQD VDLVQKYLEK YNNLKDNGRG VEKRRNSGPV 60
   VEKLKMQQSF FGLKVTKGPD AETLKVMKQP RCQVPDVAQF VLTGDNPRME QTHLTIRIEN 120
   YTPDLPRADY DHAIEKAPQL NSMVTPLTPT KVSSEGADIM ISFVRGDRHD NSPFDGPGDN 180
   LAHAFQKQPD LGGADNFGED EKRTNFRRET MLRVPAHEL GHSLSGHSST DIALALMYSY 240
   TFSGQVQLAQ DDIDGIDQIAY GRSONPQPI GQPTPKACDS KLTFDAITTI RGVNMFKDR 300
   FYMRTNFFYP EVELNIVISF WQPLPNGLBA AYEFAADREDF RFKGNKYHA VQQGNVLKGY 360
25 PKDIYSYSPF PRTVKHIDAA LSEENTKQTI FFVANKYMYR DEYKRSMDPG YPKMIANDFF 420
   GIGHKVDVAF NKDGQFFYFH GTRQYKFDPK TKRILTLQKA NSMFMCKKN
  
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Seq ID NO: 201 Protein sequence

Protein Accession #: NP_002413

```

1      11      21      31      41      51
45 MKSLPILLLL CVAVSAYPL DGAARGEDTS MNLVQKYLEN YYLDEKDVQK FVRRKDSGPV 60
   VKKIREMKQF LGLVETGKLD SDTLEVMKRF RCQVPDVQGF RTFPGIPKMR KTHLTIRIEN 120
   YTPDLPRADY DHAIEKAPQL NSMVTPLTPT KLVSEGADIM ISFVRGDRHD NSPFDGPGDN 180
   LAHAFQKQPD LGGADNFGED EKRTNFRRET MLRVPAHEL GHSLSGHSST DIALALMYSY 240
   NSLTDLIRFR LSQDDINGIQ SLVQPPFDSF ETLVPTVEVF PEPSTPMAC DPALSFDAYS 300
50 TLRGIELIFP DRKFVRKSLR KLEPELHLIS SPWFLPSGV DAAYEVTSKD LVFIKQMGQF 360
   MAIRONEVRA GYPRGINTLG FFPYTKIDAA AISDKERKHT YPFVDEKMYR FDEGRHSNRP 420
   WFKQIAEDFF NKDSDIKAW FEEQGFYFF TSSQLSEFNP NAKKVTHTLK SNHMLAC
  
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Seq ID NO: 202 Protein sequence

Protein Accession #: NP_001845

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1      11      21      31      41      51
55 MEWSSRWKT KRWLMDFTVT TLALTFLPOA REVKGAAPVD VLKALDFHNS PEGISKTTFG 60
   CTNKNSKSGS ITAKYKSVQA QLSAPTKQLF PGCTFPEPDS ILFTVFKPQG IQSFLSLIYN 120
   ENIGQQQGVV VGRSVPFLFE DHTQGPARED YLFTFVFNIA DKKMRHVALS VEKRTKITYN 180
   DCKKTKTKPL DBSERAIYDT NGITVFGTRI LDEEVFEGDI QQFLITGDFK AAYDCEHYS 240
   PDCSSAPKA AQAQEQPIDE YAPEDIIEVD YEAGAEYKE ABSVEGTVT TEETIAQTEA 300
   NIVDPQGVYN YGTMSGYDTE APRVSVIEED PNWVEEI PTE EYLTGDEYGS QRKNSDITLY 360
   BKREIDGRDS DLIWQSGDGL YNFVEYKEYS GDTSPMEEY FGQVPAZEDT ITETSLYNG 420
   AYGEKQKQKE PAVEPQNLV EDPGPAPGFA QINMPQLQGL PTGPGPDGPD RQPGKRPQLP 480
65 GADKLPGGPP TMLMLPFRYV GDSGSKPTIS AQEAQAAIL QQARIALRGP PPGMLTGRP 540
   GPVGQPGSSG AKGESGDGPG QPGVQGVCPF GPTEKPKGRG RPAQDAGRM PPGCAKRDRE 600
   GFDLQPLQGF DGRKGRERG QGPPQPPQDD QMRGDESDIG FROLPLRDEG ROLLPLRQPT 660
   GARQYPMRAG YDGPQPPGN MKRCEGPGP CQCGKPGPQL LKPIQPIQEP PDEKSPQCKP 720
70 LAGLPSGADD PPGHPKQEGQ SGRKALGPP GPQCGIXPGP PRGVGSADGV RGLKSGSKGEK 780
   GEDGFPGFKG DMGLKGDRGE VQIIGPRGKD GPEGPKGRAG PTGDPGPSQO AGEKGLKGPV 840
   GLPVCYGRQG PKGSTGPFPG PAMANGEAR GVAQKPGPRG QRGPTPGRGS RGRAPGTGEP 900
   GPKTSGSGGK PPGKPGVPGP GPKGCGVPGP GPTEKPKGRG GPKGPKRQGD RQETGTPQGL 960
   GPFGQGVGVV PQPQTPEMLV IGKRGVPDPF GPPGKGLGAP AAKCEKARDQ PGPQGISKED 1020
75 GPAGLKGFPF ERGLPQAQGA PGLKAGBSQP GPPGVPGSQP ERGSAGTAPG IGLRGRPCQP 1080
   GPFGPAGKRG APKRGKQGPQ AGRGVQGVFP GPKGAPGAPG SPBEDGRGEI IGEPQKSGK 1140
   GSKGSDPGPG PDLGKSGDGL PGLAGDCEEP GPVQCGQNF GQVQKQKGF PGPVPHILG 1200
   GLPQPKRGKQ ENWDGVGMP PDPGPKRSPQ GPWQADGQPG PPGSVSVSGV VGEKGEFGEA 1260
   GNPGPGEAG VGGPKGERGE KGEAGPGQAA GPPGAKGPP DQGPENGPVP VGFPGDGPFP 1320
80 GELAPAGQGP VGKDGKGLGD PKQKRPDPFS GEAPGPPGPF KRGPQPAAGA EDRQGRKAK 1380
   GEABAGKQGP KTVGPQKQGP ACQKPGRELR GTPGVPQSGQ LPGAQDQGP PGPMPQPLP 1440
   GELKDPQSGK EKGPHIGLIL TQPPRGQGEK GDRGLPTQCG SPQAKDQDGI PGAPGLGPP 1500
   GPQKPPQPGP PKGNKSTGP AQQKDGSLP GTPPGPPGPF EVIQLPLIS SKTKRHRTG 1560
   MQADADNHIL DYSQKMEIF GSLNSLKQDI ENMKFPMGTG TNPAKTKDL QLSHFDPFGD 1620
  
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5 EYWDNRQCC GGDSEFYVCN FTSGQETCIY POKKSEGVRI SSMPEKRPQS WFSEFKRGKL 1680
LSYLVQEDNS IMHYQPTFLK LLTASARQNF TYHCQSAAN YDWSGSYCV ALRPGLSMDE 1740
BMSYDNNPFI KTYLDGCTSR KYEYKTVIEI NTPKIDQVPV DVMISDFDG QNKGKGFVFG 1800
PVCELG

5

Seq ID NO: 203 Protein sequence
Protein Accession #: XP_057014
1 11 21 31 41 51
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10 MHPQCPAASQ QRLRGLLLLL LLQLPAPSSA SEIPEKQKKA QLRQREVVDL YWMLCQGLA 60
GVPRGDCSPG ANGIPGTGPI PGKQGFKEK GECLRESFEE SMTNPYKQCS WSLNYGLDPL 120
GKIAECTFTK MRSNLSRLVL FEGSLRLKCR NACCORMYFT FNGAGCSGPI PIRAIYLYQ 180
GSPENSTIN IHRSTSVEGL CEGIGAGLVD VAIMVGTCSO YPKQGAOSTG NSVSRIIIEE 240
LPK

15

Seq ID NO: 204 Protein sequence
Protein Accession #: Eos sequence
1 11 21 31 41 51
| | | | |
20 MPGKILTRQ APADYRVILK TSQDELDVP DDISVRVMSQ QSVLSVWVDP VLEKQKKVVA 60
SRQITVRYRE KGLAANDWYK QIANRWLIE NLIPOTVYVF AVRIQSEBR GRNSTSVQR 120
TPSANTPTAF EMIAVWUPQG KPTVVAASMD ALPETEDKVK VCLLETOLF3 VSSQPSAKS 180
FQITPTPTTS LSNLKBQPS PIESTLLPMM MWCSLGNAI FSKKAPQTCR AMDLTPKPSL 240
SLCCQCECST QKDFSLCLAY IDIQTKQVHK DPQLGGSVFG PCFLFYFLT MDLIGGSFI 300

25

KCYEDPVSSL TGNLSKSVAA SKADVQNTT DMGKPEKPEP SPSPRAPAS SQHPSVPASP 360
QQRNARDLL DLKRIKLIANG GAKPKPLKRA KRAEELDLQS TEITGEIELS SREDSWSPS 420
ETQDQKTLR PSRIKIGVYV APCPTAVRAK MPALPREECV DKQPSILATO PRPAQPSAS 480
ASPAUJASTQ QTSIRPSELPA SLNDMLDVS DEDERAVGSL HPKGAFAQPR PALSPSRQSP 540
SVLNRDSSV HPGAKPASPA RRTPSGAAE EDSSASAPYS RLSPPHOGSS RLLPTQPHLS 600
SPFSKQKCG EDAPATNSHA PSRSTNSSSV SHLSLSKTVO SEGAAASQCE SHGQDERED 660
QRQAEATATG LQAPASQHF HLHKKPLPA WCRSPSPFI GCPFLQPSG SPQSTVPSRA 720
HFRVPSHDS NPKLSGGIHC DEDEKPLPA TVVNDHVPSS SRQPSIRGWE DLRSPQRGA 780

30

SLHRKEPIE NPKSTQADTH POGKYSLAS KAQDVQGSTO ADTGHSHPKA QPSTDRHAS 840
PARPPAASQZ QHPSVPRMT PGRAPEQDFP PPVATSQBHP GPQSRDAGRS PQPRLSLTO 900
AGRPAPFSGS LSSSESLKPLTA LQKQDEQAGQ STQSDSTVEY AQDVPAPANA 960
ARAKAAASL PHUQVQSPST GAGAGGDHRS QRQHAASPAR PSRPGGQSR ARVPSRAAPC 1020
KSEPPSKRPL SSKSQSVSVA EDEEEDAGF PKQKGEDLLS SSVKMPSSS TPFGKQKADQ 1080
SLAKEKEPA TALAPRGSSL AFVKRPLPPP PGSSPSBASV PSRPPRPSAA TVSPVAGTTP 1140
WRYTTPQRI GHFPAASQV QKQPMHAFR NMLRSQAPRA PGRVPSVPLT QWVKEVLPG 1200
40 SHKSPKQRI INQPGTKHY VDLQRLGVIN AGRVLRQSH QMLRILGLD DQRTIVLESD 1260
TPVVSQDLF LFGQGRHPT LANAQDKPIL SLOCKPLVLQ EVIKKTHRP TTMQPTITT 1320
PLPTTTTTP PTTATMQPTT TTTTLPITT REPTATTIR TTRRPTTIV KTTTTRTIT 1380
TRPTTPIPT CPPTGLEIDD DASHLDHSH GTFCEHABED HPSGLETDY VPTREAYTIV 1440

40

DEVFEETR PPTTTPPTT ATTPRPIEE GAISSEFBEZ FLQAGKRFP APVTYVLMD 1500
45 PSAPCSLTD LDRHQVSLD EIIPNDLKKS DLPQNAHNM ITTVAVEGCH SFVIVDWDKA 1560
TPGSLVTGYL VYSAAYEDI RHFSTQASS VTHLPIDNKL PTRYEYFKVQ AQPHGVGPI 1620
SPSVSVTIES DNPLLVRRPP OGELSGSHLS SHMIPATRTA MDGKM

45

Seq ID NO: 205 Protein Sequence
Protein Accession #: NP_055059
1 11 21 31 41 51
| | | | |
50 MDPFAAAR LCPALLLLLL LLLPPLLP PPFPANARLA AAADPGGPI GHMERILAV 60
PVRTDAQRL VSHVSAATS RAGVARRAA PVRTSPFGG NEEEPGSHLF YNVTVFORDL 120
55 HLRIIRNARK VARGATHQGO GEKQTTVEP LGLCITVGD VAGLAEASV AHCNCDGLAG 180
LIRMEERFF LQSNAPLWQ QCAQGVVYV VYRPPTTFP LGQPALDYS ASLQGLDGL 240
RALGVLEBHA NSSERKARRH AADGVNIEV LLOVDSDVQ FIKGKHVQRY LLTQNIWNE 300
IYHDESLGAL INVVLVRILL LSVQKMSLI EIGNPSQSL NVCNWAYLO KPTQIDIEYI 360
DHAIPLTRD FPGSNQGYA PVTQCHMPV SCTLMEHSDG SAAPVVAET GHVLMDEED 420
60 GRCQSDYVR LGTHAPLWQ ANRPRPWR CQQLSESYL HSYDCLDOP FANQWALPO 480
LPGLYSMWE QCRDFDGLQ MCTARTFD PCKQLMCSHP DMNPFCKTKK GPPLDGTICA 540
PKGCKPKGHC IMLTFDILR DSGHGAASF GSCSTRCTGT VKFTRQTCN PHFPAQGRTC 600
SGLAVPQLC SRQDCPDLA DFRFEDQCRN DLYFENGDAQ WHFLEHND AKERCHLICE 660
SKETGVVSM KRWVLDTRC SCQARSLCY RSKDRWCD QVSSGKQZ KCVQGRN 720

55

80 HCKVYGTTP RSPKQHTT MFEIPAGAH LLIQEVDATS HULAVNHLAT GKILMEHD 780
VDASSKFTIA MGWEYKREDE DURELTQTM FLHGITVLV IPGVDTRVSL TYKVINHEDS 840
LNDNNVLE EDGVYVEVAL KWHSCSKCF QGSGPFTKY CRRRLDHRMV HRQFCAALSK 900
PKAIRACHP QECSPQVMT GEWPCSGTC GRTGMQVRS RCIQPIHET TRSVNARKH 960
DANWSSBAC SRELCQKRM AGHSGCSVT CMCQIERYP PCKTNDQSGP IQGEIRPTA 1020
70 RTCKLQPCPR NISDPKSKST VQVHLSPDP DSPRIKISK GHQCKDSKIF CRNEVLSKYC 1080
SIPQNKLCG KSCNLNNLT NVEGRLEPPP GKINDIVFM PTLFVPTVAM EVRPSSTPL 1140
EVLNASSTN ATEDIPETHA VDEFPYKHOL EDEVPFNMLI PRFSPYEKT RNRQIQELID 1200
EMRKKELMGK F 1211

60

Seq ID NO: 206 Protein sequence
Protein Accession #: NP_076927
1 11 21 31 41 51
| | | | |
75 NGENDPPAVE APTSFSRLFG LDDLKISFVA PDAVAAVQI LSLPLPKRFP ITIVIGIALI 60
LAILGLGHH PDCSKRSLR SPFKCIELIA RCQVSDCKD GEDEYKRVV GQGNVAVLO 120
TAASHKTRH DPKHQRVAT SCAGQGFYV VSDMLKSVS LQGVQVYV SIHMLGLQ 180
VIALHREVV BEGCASCHYV TLQCTACGR RYSSRIVQG NMSLLSQNPM QASLQGVYH 240
LCQGSVITPM WIIITAVICV DYLPLKSTI QVGLVSLLO PAFSHLVEKI VYHSKYKPKR 300
LNDIALAKL AGPLTPNEMI QPVCLPNSSE NPFQKQVMT SGWAGTEGG DASPLNHAH 360

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GKPNHISAVD VKPKDEALY KKKCKYCSKV PGTDSLSQIH LRSHTGERPF VCSVQGRHFT 420
 TSGNKLKVFH RHQVQKAPQ LFAEPQDKVA AGNGIPYALS VPDIDEPLS SLDSKFLVAT 480
 TSVGLPQNLS SGTNPGDLDTG GSLPGDLQPG PSFESEOGPT LQGVQRYNS PRAOQFOQSG 540
 TFEPOSETLK LQULVENIDK ATTDPNECIL CHRVLSGQSS LQMYKTRTGT BRPPQCKICG 600
 RAFTSKRMLK THLDVPHVTI SIKTKQSCPT CQKQFTRAVM LQHLHMMG GQIRNIFLPE 660
 NPDPTQSEB MTVGEHGGTG AICHDVIES LDVEEVSQGE AFSSSSKCVT PLUSTSHASP 720
 TLGFAMMALD DAPKGVQAP NHLRQGSRE NGSVESDGLT NDSSSLMDQI EYQSRSPDIL 780
 ETTSQALSP ANSQAESIKS KSPDAGSKAE SCMSKRTME GRSSLPTSTI KAPPTYKVVE 840
 VPTTFVPSPT LSPQMTFLLA AQPRRAQKQH GCTNRQWQPS SASALQIHER THTGKFPVC 900
 VICGAFATTK GULGVYVTH GANNNSARKQ RKLATIDTMA LIGTGGRVYS ELPFKELIAP 960
 SVNVPQVYNN QYTSMLAGL AVKTHEISVI QSGGVTLFV SLGATSVYNN ATVSKNDGSG 1020
 SGISADVEKP SATQGVFKQG FHFPLEBNKI AVS 1053

Seq ID NO: 212 Protein Sequence

Protein Accession #: NP_005092

1 11 21 31 41 51
 | | | | |
 MNDHDLVFM LAGNEFVSLK SSMEVSELKA QITQKIGVHA PQRLAVHFS QVALQDRVPL 60
 ASQGLPGOST VLLVWQKDE PLSLIVRNKK GRSSITYEVL TQTVAHLQQ VSGLEGVQDD 120
 20 LFMLTFEQKP LEDQLPLGEY GLKPLSTFVM NLRLRGGSTE PGRS 165

Seq ID NO: 213 Protein Sequence

Protein Accession #: E06 sequence

1 11 21 31 41 51
 | | | | |
 MIILIIYFLF LWDSTQWGF KDCGIFNHSI LERAAGVYHR EARSCKYKLT YAAKAVCEF 60
 EGGHLATYQG LSAARKIGFH VCAAGHMAKG RVGYPIVKPG PNOGPKGTI IDYGIRLARS 120
 ERWDAYCYNP HAKCEGVYFT DPKQIFKSPG PNEYEDNQI CTNHRILKYG QRHLISFLDP 180
 30 DLEDDPCLLA DYVEIYSYDV DVHGQVQRVC GDELPDDIIS TQNVTLKFL SDASVTAGGF 240
 QIKYVAMPDV SKSQSQKMTS TTSTGNKNFL AGRFSLH

Seq ID NO: 214 Protein Sequence

Protein Accession #: NP_009046.1

1 11 21 31 41 51
 | | | | |
 MIILIIYFLF LWDSTQWGF KDCGIFNHSI LERAAGVYHR EARSCKYKLT YAAKAVCEF 60
 EGGHLATYQG LSAARKIGFH VCAAGHMAKG RVGYPIVKPG PNOGPKGTI IDYGIRLARS 120
 ERWDAYCYNP HAKCEGVYFT DPKQIFKSPG PNEYEDNQI CTNHRILKYG QRHLISFLDP 180
 40 DLEDDPCLLA DYVEIYSYDV DVHGQVQRVC GDELPDDIIS TQNVTLKFL SDASVTAGGF 240
 QIKYVAMPDV SKSQSQKMTS TTSTGNKNFL AGRFSLH

Seq ID NO: 215 Protein Sequence

Protein Accession #: NP_006389.1

1 11 21 31 41 51
 | | | | |
 MANKASCLCV HVNSEENDLM TPDANPYDSV KKIKEHVRSK TKVPVQDQVL LLOGSKILKPR 60
 RSLSEYIDIK EKHILUTLKV VKPSEDEPL FLVSEDEAK RHLLQVRRSS SVAQVKAMIE 120
 45 TKGTIIFETI IVTCHGSKLE DQGMADYGI RKNRLPLFAS YCIGG 165

Seq ID NO: 216 Protein Sequence

Protein Accession #: NP_002349.1

1 11 21 31 41 51
 | | | | |
 MALQLSREOG ITLRGSAEIV AEFFSPGINS ILVQGIYPS ETFTRVQVYG LTLVLTTDL 60
 LKLYLRNVRE QLMADKYGCS VKLVLVVISN IESGEVLWRH QFDIECKDTA KQDSAPREX 120
 55 QKALQDEIRS VHQITATYV FLPLRLVWSC FDLILYTDKD LVVFEWSES GRQFITNSEE 180
 VRLASFITTI HKVNSMAYK IFVND 205

Seq ID NO: 217 Protein Sequence

Protein Accession #: NP_001889.1

1 11 21 31 41 51
 | | | | |
 MAQYLSTILL LLATLAVALA WSPKSEDRIT PGGIYNACLH DEMVQRALHF AISEYNKATK 60
 DQFIRPLRAY LQARQGTQVD WYFFPDVEVG RYCTCKSQPM LDTCAFHQP ELQNKQLCSF 120
 65 EIYEYPMZHR RSLVSKRQGE S

Seq ID NO: 218 Protein Sequence

Protein Accession #: NP_009162.1

1 11 21 31 41 51
 | | | | |
 MDKLKCPFF KCKEKEVSA SSENPHVGEN DENQDQRNWS KKSVDYLLSMI GVAVGLGNW 60
 RPYLYTSYG GAFLPIYAT MALAGLPLP FLSCSLOQFA SLOPVSVMRI LPLAQGVIT 120
 70 WLLSIFVTI YNYIATYSL YIMFASQGE LPMWCKSSMS DMKCSRPV TRCWSTYWK 180
 GIQEIQWQK SHYDINFTCS IMGSEIYQEG QLPSEQVWVK VALORSSGN ETCGVVNYLA 240
 LCLLAWLIV GAALFKGKIS SKRVYPTAL PFTYVLLILL VRGATLGAS KQISYVIGM 300
 75 SHFTLKKEAE VMDATQIP YSLGVAGGL VALSSYNPKP NMCPSDAIV CLNCLITSVP 360
 ADPLIFSTIG LKWHISQEV SQVSKSGFL AFVATPEALA QLPCEPMSI LFFHMLLIG 420
 LQSPASISTE ITTITQDLFP KWKKNRVPV TLOCCD/LFL LGLVCVYQNG IYVWHLIMF 480
 CAGHGILIAA ILELQGIWI YQGRPIEDT DNGIAGKRI FWMWRACHF VITPILLIAI 540
 80 FIWELVQHIR RYTGATPYD MGVALGCHI VPCTINIPIM AITKIQAQK RIFQRLISCC 600
 RPAHQGPYLL RQNRQERYKD WQDPKKEADH EIPTVSGSRK PE

Seq ID NO: 219 Protein Sequence

Protein Accession #: NP_006389.1

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1      11      21      31      41      51
|      |      |      |      |      |
|      |      |      |      |      |
MAPNASCLCV HVRSEEWDLN TFDANPYDSV KKIEHVRSK TRVPPVQDVL LLGSKILKPR 60
RSLSSYGRPL EKHILHILVR VKPSEELPL FLVGSGDEAK HMLLVQRSS SWAQVKAMIE 120
TKGTIIPETQ IYVTCGRKLE DGMQADYGI RKMGLPLAS YCIGG

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Seq ID NO: 220 Protein Sequence
Protein Accession #: XP_094741.1

```

1      11      21      31      41      51
|      |      |      |      |      |
|      |      |      |      |      |
MKANYSAER FLLGFSQDNP SIQVLFALV LLCYLLTLTG NSALMLLAVR DPRINTPMY 60
FLCHLALVDA GFTTSSVPPPL LANLGPALM LPSSNCTAQL CASLALGSAC CVLLAVMALD 120
RAAAVCRPLA YAGLVSPRLC RTLASASWLS GLTNHVAQTA LMLSLPLCAP RLDRHFICEL 180
PALLALACQD DDDTSTWQV ANNVILLVEV FAVLLASTGA VARACVCRVR SGGRBNVGT 240
CGSHLTAVCL FYCSATITVL QPAQRTHQAR GKFLVSLFTV VTPALNPLIV TLARKKVKGA 300
ARRLLRSIGR GQAQY

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Seq ID NO: 221 Protein Sequence
Protein Accession #: NP_061155.1

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1      11      21      31      41      51
|      |      |      |      |      |
|      |      |      |      |      |
MDPPTKELLE RTAPRENLOI RMAERPTAA PRSMTHAKRA RQPLSEASHQ OPLSGEREKS 60
CTKPSGPKKR CSDNTEVEVS NLENKQPVES TSAKSCSPSP VSPQVQPAQ DTISGVAVP 120
ASLLGMRKGL NSRLNATAAS SVKTRMQKLA BORRRWMDND MTDDIPESLL FSPMPSEKA 180
ASPPKPLLSN ASATPVCRGK RLANLAATIC SWEDDVHNSF AKQNSVQBQF GTALCRKFS 240
AGCAAPAINI SVQKQIATC SQRDDQDSLH KALSSADADA SLNNAISGQ VYATSPKST 300
TSITDAKSCG QGNPELLPKT DISPLKTGVS KPIVCKTSLQ TVPSKGLER EICLQSGKD 360
KSTTPGOTGI KPLFERKGR CGEHSKESPA RSTHRTPII TPTNKAIQER LFKQTSSTST 420
THLAQQLQKE KOKELACLGR RPKDKINWSA EKGZNSKSGK LETGQETQC STPLNQHQGV 480
SKQGLPYT KPTGKPTGK HSTPKPGKT ECKMKGSSPL KITLLEEDL SLATKSDYK 540
EKQKIEVIREI EMSVDODDIN SKSVINLDSV DVLEEGEELM EKQSEMDQA LAESSEQED 600
ALNHSNSSLI APLAQTVGVV SPESLVSPTP LELKDTSRSD ESPKPKQFOR TRVPAESGD 660
SLGSEDDLL YSIDAYRSQR FKTERPSPK QVIVKEDVT SKLDEKNAF PQVNIKQRM 720
QELANEINRG QTVYQAGQA LKCCVDEBG KSGLEENAE RLLLIATGSR TLLIDELKL 780
KDEGPORNIK ASPSEPMSV KGSVTLSEIR LPLKADFVCS TVQKPDAAVY YULILKAGA 840
ENMVATPLAS TSNISAGDAL TTTTTFTLQD VSNDFEINIE VYSLVQKQDP SGLDKKETS 900
KSKAITPKRL LSTITTKENI HSNVMSAPQG LSAVRTSWFA LWSVTSLS SVNMTKVLQ 960
KVFPLSELGK HYLKIKQV NSVSEERGL TIFEDVSGQF AMHRHWVLS GNCISWTPY 1020
DEDEKXPFG KINLANCTSP QIEFANREK ARMTFELIT VPKQREDDRE TLVQCRDTL 1080
CVTKMLASD TKEREDLMOQ KINQVLVDIR LMQPDACYKP ICKP 1124

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Seq ID NO: 222 Protein Sequence
Protein Accession #: Q9H8V3

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1      11      21      31      41      51
|      |      |      |      |      |
|      |      |      |      |      |
MAENSVLSTI TURTSLADSS IPDSKYTEIS KEMLLIGTS VYEEBPOIE TRVVLQDAG 60
KQELTKALK DITQPVUME SVPEFGLS PFENVPVVT DQDSVDFDL VKALKVIGP 120
PVVLNCSQKG EPLFVSCRLP YCTSNQHLVL CFTGFRKKE LVRLVLVNH MGVIRKDFN 180
SKVTHLVANC TQGEKFRVAV SLGTFIMKPE WIYAKHERNN BQDYAAVDD FRIEFKVPF 240
QDCIPLFLGF SDEKTNHSE MTHQSGKYL PLQDERCTL VVEBIVKDL PFEPSEKLY 300
VQGMFNGSI QHDAKGETH YLYEKATPE LKVSQHLSL NTWNNKSR PLASTLAGLS 360
RDTVSFPFPF KRKPSAKSL SIGSLDISN TFEESINQDV TPKSKTSKX STVPVPSQS 420
ARQVAKELY QTESNYVIL ATIIQLFQVP LEESQORGGP ILAPEIKTI FGSIPIDFV 480
HKKIDGDEL LVWDSKRS IODIFLAKSK DLKVTYTPPV NFHFMBKTI ICCERKZRF 540
HAFKINMAK EPLKQFSGE LLTPVQLVPL LMLKALDNTA KATKATKAT STLEKALKE 600
KRWTHNED KRTEAQOI PDVVVEVDCP PAILLSKRS LVQVETISL GENPCDRGQ 660
VTLFLPNCLC EARKRKHVI GTFRSPHQGT RPAALRHHI LMLSQIKIV LDIRETECHI 720
NAFVLLVRPP TEQAVLLSLF QNTSEDLPEK HMLKMLCRHV AMTCADAEK NLIYADPES 780
PEVNTKENDS TLGRASRAIK KYSKYTRAF SFKSTPKDL RDAUMTSHG VECRSPSND 840
KNVSLBST SSLACIPSS VLSPSPFER RHTLSRST KLI 883

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Seq ID NO: 223 Protein Sequence
Protein Accession #: NP_002488.1

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1      11      21      31      41      51
|      |      |      |      |      |
|      |      |      |      |      |
MPSRAEDYEV LYTIQTSYGV RQKIRRKSD GKILVWKELD YGSMTEAKQ MLVSEVNLIR 60
ELKHNPVRY YDNIIDRNT TLYIVHEYCE OGDASVITK GTRBQYLDE EFLVLMFTQL 120
TLALKECHRR SVCKTQVVR DLEAVNPLD GRQNVLDGP GLANLHMT STFKTPTPT 180
YVMSPEQWHR MSYNKSDIW SLGCLLYELC ALMPPTAFS QKELAGRIE GKFRIPTRY 240
SDLANEITR MANLADYRP SVEEILNPL IADLVADQER RNLDRGRQL GEPEKSDSS 300
PVLSELKAE IQKQREBAL KAREERLEQK EQELCVRBL AEDKLARDM LLNLSLKEA 360
RFLVLSAMP ELLALUSSEV KANVHFSQES KKHNRSEN SGLTSRSKC KDLKKRLRKA 420
QLRQAQSLDI ENYQVLSRQ ILGRN

```

Seq ID NO: 224 Protein Sequence
Protein Accession #: Bos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
|      |      |      |      |      |
DISIENYNN SSWIPGSHV SPSSLNMAN QQLPLQLQG PANSWIPFSS GILQXQQQAQ 60
IDPLSPYSLA ALQFAGAGVH RQILPDEGAS FAGQAQNOY DPGLTQVTP TQPSHIME 120
YVFSEHCE QCMQVTPV YWVLPFQEG QTVPSRQD PQQYEQEDP FVAQGVPIQ 180
LAREPISQZ QQLAFDQLG TAFEIAVNST GEIPIYQKE AINPRDSAG VFMPSTSKP 240
STTVTYSAG DQITITPELE EDKDTLSRE P 271

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WO 03/025138

PCT/US02/29560

Seq ID NO: 225 Protein Sequence
Protein Accession #: eos sequence

1	11	21	31	41	51	
5	RGKEHRSRMV	QIFLFRSRSK	IYTYIMKIII	LIGFLGATLS	APLIPQRLMS	ASNSMELLNN
	LWNGQLPLQ	LQGLPLNSWP	PFGSILQDQO	QAQIFGLSOF	SLSALQOFAG	LWHPQILPTQ
	EASFAQAQA	QGVDFQLQOT	PQTOFGPSP	VMPYVFSFKM	POEQCMFOY	YFVYVWLPME
	QPGCTVPSL	QITRQOQVEE	QIPFYAQGVY	IPLQALPAIS	GGQQQLAFDP	QLGTAPETAV
10	HSYGEIPIYL	QKEAIRNFMD	SAGVFMGSTS	PKPSTTNVFT	SAVDQITYPE	LPEKDKTDS
	LREP					

Seq ID NO: 226 Protein Sequence
Protein Accession #: NP_003970.1

1	11	21	31	41	51	
15	NATVYDQGR	NGLKSXYRL	CDKAEWGVV	LETVATAGVV	TSVAFMLTLP	ILVCKWQDSH
	RHMPLPTQL	FLGVGLQPG	LTFATILGLD	GSVSPREFEL	PGLPISLCFS	CLLAAHNVLT
	KLVEGRKPLP	LWVILGLAGV	PSLVQGVJAI	EYIVLTWMSK	WNVVFSLSA	PRHEDVILL
20	LTVLVLMAL	TFIMSSFTFC	GSFTGKRRH	ARIYLTMLLS	IAIWANITL	LMLPDFUREN
	DDTILSALA	ANGWVFLAY	VSEFNLTK	QRHMDYFVE	DAFCKPQLVK	KSYGVENRAY
	SQEETIQGFE	ETGDTLTATY	STHFQLQMQP	PQKESFIPRA	HAMPSYKDY	EVKKEGS

Seq ID NO: 227 Protein Sequence
Protein Accession #: NP_116575.1

1	11	21	31	41	51	
25	MPKIVLNGVT	VDFFPQPVKC	QOEYMTKVLE	CLQQKVMGIL	ESPTGTGKTL	CLLCTTLAWR
	EHRLDQISAR	KIARAEQEL	FDRLALSNG	NAAAAGDPI	ACYTDIPKII	YASRTHSQLT
30	QVINELRATS	YRPKCVLAGS	REQLCHPEV	KQESNHLQI	HLCRKVKASR	SCHFYNNVEE
	KSLDQLGASL	ILDIIEVILVS	GSFKHVCVPY	LSRLAQDQAD	IIPMFINYLL	DAKSRABNI
	DLKQTVVIFD	EAHVVENKCE	ESASFDLTH	DLASGLDVID	QVLESQTKAA	QOEHPFEFS
	ADSPSPGLNM	ELEIDIAKLM	ILLRLEGAD	AVELPDDDSG	VTKPGSYIFE	LFAEAQITPQ
	TGKCILDSLD	QIQLHLAGRA	GVFTNTAGLO	KIADIITQIV	SVDPSESGPS	SPAGLGAQGS
35	YKVIHHRFAD	RRTKARQSD	WSTTAARKKQ	KVLSYWCSP	GSHMELVRY	QVRSLLITSG
	TALPVSSFAL	EQI:PPFVCL	ENPHILDKIQ	IWGVVVRPGP	DQAGLSAFD	RFSEBCLSS
	LGLKALNTAR	VVPYGLLIFP	PSYPVMEKSL	EFWRARDLAR	KMEALKPLFV	EPRSKGSFSE
	TISATYARVA	APGSTATFTL	AVCRKASBSG	LDPSDTNMRG	VIVTGLPYPP	RMDPRVVLKM
	QFDDKRLQGL	GAGQDFLSQ	ENYRQASRA	VWAIIGVIR	HRQVYGAUFL	CHHFAFADA
40	RAQLPSKVRP	JRVYDYNRGS	VIRKDAQFFV	VAERTWAPRA	PRATAPSVRG	EDAVSEAKSP
	GPFFSTRKAK	SLDLHVSFLK	QRSSGSPAG	DPRESSLCVEY	EOEPVPAROR	PRGLIAALEH
	SEQRAGSPGE	EQARSCTSLT	LSEKRPAAE	PRGRKKIRL	VSHPEEPVAG	AQTDRAKLFM
	VAVKQLQSQA	NFAITITQALQ	DYKGSDDPFA	LAACQLPLFA	EDPRKHLNQL	QVYQVPRPH
	KQCFEYICIQ	LTGRCGVPR	ESISPRQRRA	QVPLDPTGT	APDFLTVST	AAAGQQLDRQ
45	HLNQGRPHLS	PRPPTDQDGP	SQPQNGSGVP	RAGKQGMNAV	SAYLADARRA	LSGACGQILL
	AALTAYKQDD	DLDKVLAVLA	ALTTAKPEDF	PLHHRFSMFV	RPHHKRFQSO	TCTDLTRGPY
	PGMEHPQCE	ERLAAVPPVLT	HRAPQGPSPR	SEKTOKTQSK	ISSFLRQRRA	QTVGAQGEDA
	GFQSSSGPPH	GPAASEKGL	HGRDLAQDQA	TAPQGLPFLA	GCVQSCGSAE	IRVPPQCPAC
	DFQRCAQWQ	RHLQASRMCP	ACHTASRKQS	VMQVVFPEPH	KOHEGAGGAR	PVAJAVPGGA
50	ACPAAGAGCT	RGRNRTHLP	AGRRDRGAA	VCPVPRHLIC	AAJVPFRQPH	DWMPVSTAPL
	HAVLELPGAL	FLIQRPLRGA				

Seq ID NO: 228 Protein Sequence
Protein Accession #: NP_057518.1

1	11	21	31	41	51	
55	MPKIVLNGVT	VDFFPQPVKC	QOEYMTKVLE	CLQQKVMGIL	ESPTGTGKTL	CLLCTTLAWR
	EHRLDQISAR	KIARAEQEL	FDRLALSNG	NAAAAGDPI	ACYTDIPKII	YASRTHSQLT
60	QVINELRATS	YRPKCVLAGS	REQLCHPEV	KQESNHLQI	HLCRKVKASR	SCHFYNNVEE
	KSLDQLGASL	ILDIIEVILVS	GSFKHVCVPY	LSRLAQDQAD	IIPMFINYLL	DAKSRABNI
	DLKQTVVIFD	EAHVVENKCE	ESASFDLTH	DLASGLDVID	QVLESQTKAA	QOEHPFEFS
	ADSPSPGLNM	ELEIDIAKLM	ILLRLEGAD	AVELPDDDSG	VTKPGSYIFE	LFAEAQITPQ
	TGKCILDSLD	QIQLHLAGRA	GVFTNTAGLO	KIADIITQIV	SVDPSESGPS	SPAGLGAQGS
65	YKVIHHRFAD	RRTKARQSD	WSTTAARKKQ	KVLSYWCSP	GSHMELVRY	QVRSLLITSG
	TALPVSSFAL	EQI:PPFVCL	ENPHILDKIQ	IWGVVVRPGP	DQAGLSAFD	RFSEBCLSS
	LGLKALNTAR	VVPYGLLIFP	PSYPVMEKSL	EFWRARDLAR	KMEALKPLFV	EPRSKGSFSE
	TISATYARVA	APGSTATFTL	AVCRKASBSG	LDPSDTNMRG	VIVTGLPYPP	RMDPRVVLKM
	QFDDKRLQGL	GAGQDFLSQ	ENYRQASRA	VWAIIGVIR	HRQVYGAUFL	CHHFAFADA
	RAQLPSKVRP	JRVYDYNRGS	VIRKDAQFFV	VAERTWAPRA	PRATAPSVRG	EDAVSEAKSP
70	GPFFSTRKAK	SLDLHVSFLK	QRSSGSPAG	DPRESSLCVEY	EOEPVPAROR	PRGLIAALEH
	SEQRAGSPGE	EQARSCTSLT	LSEKRPAAE	PRGRKKIRL	VSHPEEPVAG	AQTDRAKLFM
	VAVKQLQSQA	NFAITITQALQ	DYKGSDDPFA	LAACQLPLFA	EDPRKHLNQL	QVYQVPRPH
	KQCFEYICIQ	LTGRCGVPR	ESISPRQRRA	QVPLDPTGT	APDFLTVST	AAAGQQLDRQ
	HLNQGRPHLS	PRPPTDQDGP	SQPQNGSGVP	RAGKQGMNAV	SAYLADARRA	LSGACGQILL
75	AALTAYKQDD	DLDKVLAVLA	ALTTAKPEDF	PLHHRFSMFV	RPHHKRFQSO	TCTDLTRGPY
	PGMEHPQCE	ERLAAVPPVLT	HRAPQGPSPR	SEKTOKTQSK	ISSFLRQRRA	QTVGAQGEDA
	GFQSSSGPPH	GPAASEKGL				

Seq ID NO: 229 Protein Sequence
Protein Accession #: NP_054622.1

1	11	21	31	41	51	
80	MPAPAPRATA	PSVRGDEAVS	EAKSPGFFFS	TRKAKSLDHL	VPSLKRQSSG	SPAAGPESS
	LCVEYDEQPV	PARQRPRGLL	AALDHSQRA	GSPGDEQNIS	CSYTLSLSEK	RPAEPRGRGR

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	KKRLVSHPE	EPVAGQTDK	AKLPPVAVKQ	ELSQMFAFT	TQALQVYKGS	DDFAALAACTL	180
	GPFLAEDPKP	IKHLQGYFYQ	VRPHKQKQE	EYCIQLTGRG	COTYRPEHSIP	RROKQPVLD	240
	PTGRTAFDPK	LTVSTAAAO	LDPOEHLNAG	RPHLSRFPFP	TGDGSGQPN	GGGVPRAGQ	300
5	GQHAVSAYLA	DARRALSGAG	CSQLAALTA	YKQDDELKV	LAVIAALITA	KPEDFPLHR	360
	PSNFRMHK	QRESQCTGL	TGRPLPQHEP	FGQERKLAV	PPVLTHRAPG	PPGRSRKGT	420
	TKQKISSTI	KQRPACTVLA	QEDDAGDSG	SGPWRGPAS	EMGEFGERDI	AQQATQAGQ	480
	GPLSAGCVQ	GCUGAEVVPF	QCPACDFQRC	QACWQRLQA	SRMCPACHTA	SRKQSNQVF	540
	WPEPQ						545
10	Seq ID NO: 230 Protein Sequence Protein Accession #: NP_003814.1						
	1	11	21	31	41	51	
	MRALEGPGLS	LLCLVLALPA	LLFVPVAVRGV	AETPTYPWRD	AETGERLVCA	QCPGTGFVQR	60
15	PKCRDSPTTC	QCPCFRHYQT	FMNYLEKCRY	CNVLGGERKE	KARACHATIN	RACRCKTGFF	120
	AHAGFCLERH	SCPPGAGVIA	PGTFSQNTQC	QCPCTPTFSA	SSSSSEDCQP	HNCTALGLA	180
	LNVPQSSSHD	TLCTSGCTGF	LSTRVQARE	CERAVIDYA	PDIDSIKRLQ	RLQLALEAPE	240
	GMQPTFRAGR	ALQQLKLRK	LTELGLAQDG	ALLVRLQLAQ	KVARNPGLER	SVREPLFVN	300
20	Seq ID NO: 231 Protein Sequence Protein Accession #: NP_116563.1						
	1	11	21	31	41	51	
	MRALEGPGLS	LLCLVLALPA	LLFVPVAVRGV	AETPTYPWRD	AETGERLVCA	QCPGTGFVQR	60
25	PKCRDSPTTC	QCPCFRHYQT	FMNYLEKCRY	CNVLGGERKE	KARACHATIN	RACRCKTGFF	120
	AHAGFCLERH	SCPPGAGVIA	PGTFSQNTQC	QCPCTPTFSA	SSSSSEDCQP	HNCTALGLA	180
	LNVPQSSSHD	TLCTSGCTGF	LSTRVQARE	CERAVIDYA	PDIDSIKRLQ	RLQLALEAPE	240
	GMQPTFRAGR	ALQQLKLRK	LTELGLAQDG	ALLVRLQLAQ	KVARNPGLER	SVREPLFVN	300
30	Seq ID NO: 232 Protein Sequence Protein Accession #: NP_000584.2						
	1	11	21	31	41	51	
35	MAELLASAGS	ACSMDFPRAP	PSFFPPAASR	GGLOQTRSF	PHRGAESFRP	GRDRQGVVE	60
	MASSCRAPR	CKCKLPQSL	AMGLTVLLLL	ADMVLRTAL	PRFSLVPT	ALPLRNVAV	120
	GLSRNAVML	GACGLVRATV	GSKSRNAGAQ	GMIAHLKFLA	AALGLALPGL	ALTRELISWG	180
	AFQSDASTEL	LWQSGSRTPV	VVSYAALPA	AALMHKLGLS	WVFGQQGSGS	NFVRELGLCL	240
	QSETRLSLF	LVLVLSSSG	EMAIFPFTPR	LTDHILQDGS	ADTFTRMLT	MSLITIASAV	300
	LETVQDILN	NTWQFMSHL	QSEVFGVLA	QESTFQYQ	TONHSLISVE	DTYFSLGDS	360
	ENLSLFLMYL	HLGLCLZIM	LWGSVLSLTMV	TLTLPLPL	LPKKVQWQV	LLEQVRESL	420
	AKSGQVAIDA	LSMPTVBSF	ANVEGEAKQF	REKLQKITL	NQKRAVAVAV	NSMTTISGM	480
	LLKVGLIYIG	QGLVTSAGVS	SONLVTFVLY	QWQFQAVEN	LSSTYPRVKQ	AVGSSKEIFE	540
	YLDRTPKCP	SGLLTFLALE	GLVQGPQDSF	ATYNEPDVL	LGSLTITFLP	GVETVALAV	600
	GGSEKTAAL	LQWQYPTG	QULLQCKPLP	QYSEVHLRW	VAWQSQEOP	FGRLSQENIA	660
45	YGLTKPTME	SITRAAAVSG	AHSIFSGLPQ	QYDTEVDEAG	SQLSGQQRQA	VALARALIRK	720
	PCVLILDDAT	SALDANSQQL	VEQLLYSEFE	RYSRVSLIT	QHLSELQDAD	HILFLEGDAI	780
	REGGTHQML	EXKQCTWAV	QAPADAFE				808
50	Seq ID NO: 233 Protein Sequence Protein Accession #: NP_002414.1						
	1	11	21	31	41	51	
	MRLTVLCAVC	LPFGSLALPL	PQEAQMSLE	QWQAOYDLK	RFYLYDSETK	NANSLSAKJK	60
	EMQKFGPLPI	TQMLSRVIE	INQPKRCQPV	DVAEYSLFP	SPKMTSKVVT	YRVSVYREL	120
55	PHITVDRLVS	KALNHWGIEI	PLMFPRVYWG	TADIMIGFAR	GAGGDSYFPD	QONTLAAAP	180
	APOTGLODA	NTEREDNTE	QSGDITNLYI	AATHELOSL	QWQSDPNA	VWYPTVQGD	240
	PQNFKLQDD	IKQIKLKYK	RSNGRKX				267
60	Seq ID NO: 234 Protein Sequence Protein Accession #: NP_061144						
	1	11	21	31	41	51	
	MPBIVCKIK	FAEEDAKPES	KFAGDBOSLL	GAVAPGAAPR	DIATFASTST	LHGLGRAQSP	60
	GPHKRLKTLV	ALALLSTPLA	GLVQAGLARL	GYLTERPMLVA	HPAPAAVPA	GFPVATLQNI	120
65	NFRSRALGD	ADTFELANLT	GLQEDQDCK	BAQLRYTPE	DWVDILNRTO	HLQALMLKSL	180
	NFSQMHCSAS	NFVSVYTRYQ	KCYTFNADPR	SSLSPRAGQM	GSQLEIMLD	QOEVELPLWR	240
	ETNETSFEAG	IKWQHSQEE	PPYIHLQFGP	VSPGPTQVVS	CQEQRLTYLP	OPWGMCRAS	300
	ELBEEFQCEP	SATVSASCLL	CEKEAVLQKR	CHRWWRMPG	NETICPTNHY	IEDAGWLDGS	360
	QDQTEDEPCT	CYFCNLTFR	GKEISWRHPI	NKQSAAYLAR	KYRWNETYIR	ENLFLDYDT	420
70	EALTSFAMEQ	RAAYGLSALL	GLDGLQWGLF	IGASLITLLE	ILDYIVESW	DLRKKYVRRP	480
	KTLPTLSTOG	ISTAGLQELK	EQSPCPSLGR	AEQGVSSLEL	PNHHHPGHP	GLGFEDFAC	540
75	Seq ID NO: 235 Protein Sequence Protein Accession #: BAC03567						
	1	11	21	31	41	51	
	KVSSSPSPAQ	RIRKRRKPPV	QQPAQGVQVQ	PPSPSGTAGD	PKGLSDPPVP	PRGSLALGD	60
	PSSDPACQSS	GPMEAEBSL	PRQEDSAQL	QOEKPSLYIG	VRGTVVRSMQ	EVLNTRLEEL	120
	POPLVSEEVY	EGIALGIEAA	LMNLTQOTNG	RYKTKYRSL	PHLDRPRLD	LFLKVVHGVQ	180
80	DTYVLWHS	KLAPLQELAR	WKEQEKRLG	HTEDQCEEP	CLPASPQHTH	KGEVEIORDH	240
	QDTYLLDLYG	QALPFASTDT	TOGHWHHPLD	PKWYICQWE	PSNELLGLG		300
	ANACQDMIT	QKALQSTDP	AMPMKPTREL	SPTEPQEQEP	PSGLRVPAAP	TKALCLPTPW	360
	BQVLDLFSIK	RFRARQALWS	GHSCLRLVAL	PTVIRISAGCI	PSNIVMDLLA	SICPAKADYD	420
	CVVRLCPHGA	SDTONCKILY	SYLMDQKHG	LASVHEGMW	LLPLFAPOPL	PTRLKPLGG	480

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GLEVTHSSLL LAVILPKRGL PYTAGSSNWL GKQGMVSN SKVEKRYTP DNMHPWPLK 540
 GTPPGQACM QGQRGSIAP RGISAMQRP RGRGLMPEP ENMHPGRQ WPPEGLRQS 600
 QMPSVAPAG HGFGRGHFN RDSCPQALL RHLESLATMS HQIQAALLCQ TKSSIPIRIQ 660
 HISSALAAPE PGGPARDSSL GPTDEAGSEC PFPKKA 696

5

Seq ID NO: 236 Protein Sequence

Protein Accession #: NP_005282

1 11 21 31 41 51
 | | | | |
 MSKSNWAGS RKPPREMLKL LMSFDSQSMH GLEVAFPGLI TNPISLATQD QOQETPLERM 60
 LEASFYLLDF ILALVHTLIA LMSFDRHKS GTPANVFLMH LAVADLSCLV VLPRVLRYHF 120
 SQRMWPFGEI ACRLTGFLEY LMYASIFYFL TCISADKFLA IVHPVKSLEK VLPRYLIAHC 160
 APLAVYVAVA MAPLVSPQT VQTNHTVACL QLYHEKASHI ALVSLAVAFY PPFYITVTYC 240
 LLTILSLAQD LKVESEHPTK AVNMHTAFLA IFLACVTVVH VRSVTVVH SHGACATQ 300
 RILALANRIT SCLTSLNGAL DPMTFFVAV KFRHALCHLL CGRLKGPPH SFEKTNSSS 360
 LSAKSEL 367

15

Seq ID NO: 237 Protein Sequence

Protein Accession #: NP_061113

1 11 21 31 41 51
 | | | | |
 MKRTRMGILL WMLVSELSEA ATKLTSEKYE LKSKQTLQVK CQVTLKFAIS SQEAWOIIDR 60
 GEMPTLACT ERPSKNHMP QVGRILEDY HDHQILARVM VNLQVDSGL YQCVITOPPK 120
 EPIDLFDRIR LVVTKFSQT PGMSENSTQ VYKIFPTTK ALCLPLTSPR TVTQAPPKST 180
 ADVSTPDESI NLNVTVDIIR VPVFNIIVLL AOGFLSKSLV FSVLPVATLR SFVP 234

25

Seq ID NO: 238 Protein Sequence

Protein Accession #: NP_003458

1 11 21 31 41 51
 | | | | |
 MDSISYSTD NYTEEMSGSD YDSMKPCFR EEMANFKIF LPTIYSIFL TGIVQNGLVI 60
 LVMGVOKLR SMTDKYLRHL SVADLLFVIT LPFNADVAVA NMYPONFLCK AVHIVITVNL 120
 YSSVILAFI SLDYLAIVH ATNSQPRKL LARKVYVGV WIPALLTPI DFIFANVSEA 160
 DDYKIDRFP PNDLVVVPQ FQHMVGLLL FOIVLSCHC IISKLRSK QGKKRNLKT 240
 TVILLALTA CNLGLLEET MCGCEPTEI NWSISITLH AFPPCCALPI 300
 LVAFIAKFK TSAQAULTSV SRSSLSKLS KQKRGGHSV STESSESSPH SS 352

35

Seq ID NO: 239 Protein Sequence

Protein Accession #: NP_036338.1

1 11 21 31 41 51
 | | | | |
 NHPQWVLSL LKHLADSVAG SVKVGGEAGP SVTLFCHYSQ AVTSMCHNR SCSLFTQMG 60
 IVWMTWTVR VRSVLSQVSL QSLQSRVSL TIENTAVSDS GVYCCRVDR GMNDKMTV 120
 SLIEVPKVTI TPIVITVPI VTVVRTSTV PITTIVPTTI VFTTMSIPT TVPTTMTVS 180
 TTVSPPTTS IPTTSEFVT TVTSTFVPM FLRQNHFP AVTSPSPQA ETHPTTLQA 240
 IREPTTSSL YSYTIDQNDT VTSSSDGLAN NMCTOLPLEH SLTANTHTQ IYAGVCISVL 300
 VLLALGVII AKKTYFFKEV QQLSVFSSL QIKALQAVE KEVQADNIT IENSLTAD 359

45

Seq ID NO: 240 Protein Sequence

Protein Accession #: NP_004923.1

1 11 21 31 41 51
 | | | | |
 MRYTVFLLL PHVQPYPTL STPLSKRTSG FPAKKRALEL SHSKNEIAR SKSMWNNQF 60
 FLLEETGSD VOYVQKLSD QRGDGSILKY LSGDGADEL FINEINTGI QATKRLDRE 120
 KPVVILAAQ IRRKTRQVE PESEFIIKH DINDHPIPT KEVYTAIPE MDSGTVPVQ 180
 VTATADDET KNSASVSV ILQGPQFVY ESTEITLTA LAMGERME QYOVYIQAD 240
 MGQWQGLSG TTVNITLTD VNUNPAPFP STYQFKTES SPQPTIGRI KASDADGSI 300
 AEIETSIDQ EDLMDFOVIT DQETQEGIT VKKLLOFEKK KYVTLKVEAS NYFVEPRELY 360
 LQRFDSATV RIIVEDVDEP PYSKLAVIL QIREMQINT TIGSVTAQD DAARNPVYS 420
 VNMDTMDI PIDSQHSI FSKLLDREI LMMNTVIA TEINMPQSS RVFLYKLD 480
 VNQNAPEFA FYETFCVKA KAKULQTLN AVDKDDPYSG HQFSSLAPE AAGSNTFTQ 540
 DNDKTAGIL TRNGYNRHE MSTYLLPVY SMDYDPVSS TGTVTVRVC CDMHMQSC 600
 KASALIHPTQ LSTGALVAIL LCTVILLTV VLPALRRQS KKEPLISKE DINDIVSYN 660
 BEGQDESDT ADYIGTLAN FLAIDENLRV DITFALPL RTTFYACMT DVIDENLR 720
 KENDTDPAT PYDSLATYAT EGTGSVAUSL SSLESVTTDA DQDYDVLSD GRFKKLAIM 780
 YGVGVSDKDS 790

65

Seq ID NO: 241 Protein Sequence

Protein Accession #: BAB14227.1

1 11 21 31 41 51
 | | | | |
 MRRLTRRLV PVFGVAMTV LLEFMYRKK LEVTPQPGV TPKNVSLFK VAGMSWAPQ 60
 VPSVTPPYQ RHLPTQSHL ANCHFCCLQ EAQPLQTV FLQVTRLLN YCTDLPTTSI 120
 ITTPNREAS TLLRTSRV, NKTPTHLKE ILLVDPSND PDDCKQLIKL PKVKLRNNE 180
 RQCLVRSRIR GADIAQGTIL TFLDSHCEVN RMLQPLLAR VKEDYTRVC PVIDIINLOT 240
 PTVIESASEL RGGFMSLHF QWDLSPQEK ARRLDPTPI RTPIAGGLY VIDKAMFYL 300
 QKYMDCMIL GGNELIFP VAKCELSLI VKCSNIGVF RSKPYFVDF CMANTYIHT 360
 KRTAEVWDE KYQYIYAAR PALERPGMV ESKLDLEKNI ROCSFKWYLE NITPELSIPK 420
 ESSIQGNIR QROCKLESOR QNQBTPNLK LSPCAKVGK DAKSOWAFT YTOQLQEEL 480
 CLSVITLFG APVVLVLCN GDDRQQWTK GSHIHIASH LCLDTMFQD GTENGKEIVV 540
 NKCCSLMSQ HNMVSS 597

80

Seq ID NO: 242 Protein Sequence

Protein Accession #: AAI10659

WO 03/025138

PCT/US02/29560

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31     |      |      |      |      |      |
41     |      |      |      |      |      |
51     |      |      |      |      |      |
MRRLTRRLVL PVPGVLNITV LFFVVTKKR LEVPTGPEVO TPKPSDAADMD DLMQDPDERR 60
YLNAKMMRWG DDPYKLYAFN QRESERISS RAIPOTRHLR CTLLVYCTDL PPTSIIITFH 120
WEARSTLART ISVVLWRTPT KLRREILVLD DPENDPDCK GLALKPKVKC LBNMKQGLV 180
RSRIKADIA QTTTLFLDC KCTVORNLQ PLARVKEVY TRVCPVIDI ISRLTPTTIE 240
SASELRGGDF WSLFQWEOQL SPQKARRIA PTERPITPII AGGLFVIDKA WEDYLGKYM 300
DMDIWGGENF EISFRVMWG GSLEIVPCSR VGHVFRKGHP YVFGHANTP YIKMTKRTAE 360
VHNDIEQYTY YAARFPALAR PFQNVESBLD LKHLRLQCSF KWLFLNIYFE LSIPRESSIO 420
KWHIKQKQK LSRQKQNGE TPLKLLSPCA KYGGEARQD VNAFTTQOI LQELSLAVI 480
TLPQAPVVL VLCKNGDDQ QMTKTSKIE WASHACLDT DMGIGXTENG KEIVNPKES 540
SLMSQMMQV SS 552

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Seq ID NO: 243 Protein Sequence
Protein Accession #: AAM10659.1

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51     |      |      |      |      |      |
MRRLTRRLVL PVPGVLNITV LFFVVTKKR LEVPTGPEVO TPKPSDAADMD DLMQDPDERR 60
YLNAKMMRWG DDPYKLYAFN QRESERISS RAIPOTRHLR VLNRTPTHLI REIILWDFS 120
NDPDCKQLI KLKPKVCLRN NERQGLVRSR IROADIAQGT TLTLFDSICE VNRMQLPQL 180
NRKVEYTVR VCPVIDIHL DTPYIESAS ELRGGFDWSL HFOWGLSPSE QKARRLDTEP 240
PIKTHIAGS LPIVDKAWDF YLQKVGEDMD IGCERPFES FHWKQCSGL EIVPCSRVGH 300
VPRKPIPTT PGMNTATYK NKTETASVM DEKYKYTAA RFPALEPFG NVESRLDKR 360
NLRCQSPKW LENIYFELS I PRESSIQKN IRQRKCLCS QRQNNQSTPN LKLSPCAKVK 420
GEDAKQVMA FTTTQOILE ELCLSVITLF PGAPVVLVLC KNGDDROQMT KTGSHEHIA 480
SHCLDITDF GDGTENGKEI VNVPCSSLMS SQHMDVSS 519

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Seq ID NO: 244 Protein Sequence
Protein Accession #: NP_078848.1

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NMGKVMGSGP PGALTSFRAH SDFLDSRCEV NRDNLQPLN RKVEDYTRVV CVPIDIINLD 60
TPTYIESASE LRGGFDWSL FQWGLSPED KARRLDTEP IRTPIIAGGL FVIDKAWFYD 120
LGKYDMMDI WGEHFEISF RVWHGCSLE IVPCSRGRV FRKHMPVVF DGMNTYIKN 180
TKTAYDNGE EIKQYVYAR PFALERFQW VESLRLAKN LQCSFHWGL EDIYFELSPT 240
KESISQKGI RQRKCLCSQ RQNNQSTPN LKLSPCAKVK EDKASQWAF TTYTQOILEE 300
LCLSVITLF PGAPVVLVLC KNGDDROQMT KTGSHEHIA HCLDITDFG DGTENGKEIV 360
VNVPCSSLMS QHMDVSS 378

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Seq ID NO: 245 Protein Sequence
Protein Accession #: NP_001209.1

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MPRSLAAHA VLLLVILKEQ PSSPAPVNS IWTYFGPDGE NSMSKKYPSC GGLLQSPIDL 60
HSDILQYDAS LTFLEFGQYN LSKNQPLIT NMGKSVKLN PSDHIGQLQ SRYSATQLML 120
HMGQPNPDHG SEHTVSQGHF AELHIVHYN SDLYPDASTA SKSSEGLAVL AVLIEMGSPN 180
PSYDKIPSL QRVKYKQGEA FVPGFNIEEL LPERTAEYR YRGLSTTPFC HPTVLMTVFR 240
NPVOISQGL LALETALVCT RMDPSRPM DMFRQVQCF DERLVTYSPS QVQVCTAGL 300
SLGILSLAL AGILGICIVV VVSNLFRK SIKKGNKGV IYKPATMET EAA 354

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Seq ID NO: 246 Protein Sequence
Protein Accession #: BC00278

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1      |      |      |      |      |      |
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51     |      |      |      |      |      |
MPRSLAAHA VLLLVILKEQ PSSPAPVNS IWTYFGPDGE NSMSKKYPSC GGLLQSPIDL 60
HSDILQYDAS LTFLEFGQYN LSKNQPLIT NMGKSVKLN PSDHIGQLQ SRYSATQLML 120
HMGQPNPDHG SEHTVSQGHF AELHIVHYN SDLYPDASTA SKSSEGLAVL AVLIEMGSPN 180
PSYDKIPSL QRVKYKQGEA FVPGFNIEEL LPERTAEYR YRGLSTTPFC HPTVLMTVFR 240
NPVOISQGL LALETALVCT RMDPSRPM DMFRQVQCF DERLVTYSPS QVQVCTAGL 300
GILGICIVV VVSNLFRKS IKGNKNGVI YKPATMETE ARA 343

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Seq ID NO: 247 Protein Sequence
Protein Accession #: NP_006623.1

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1      |      |      |      |      |      |
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51     |      |      |      |      |      |
MQVDELIPR KGPSLCSARY GIALVIAFCN FTIAAQVIM NITWAMVNS TSPQQLNDS 60
SEVLQVSPG GLSKAPKSLP AKSILQOQF AIWEKMGFP ERSKLCSIAL SGNLGCPTA 120
ILIGCFISET LQWPFYPIF GAVQVCCCL MFVVIDYDFP SPWISTSEK EYIISLKKQ 180
VSSRQPLI KANLSLPM SLCGCSGMO WLSSTVNYI PTYISVNYI WIDKLLSA 240
LPFIAMVIG MVGGYLAFLP LTKERFLITV AKIATILGSL PSALIVSLP YLMSGYTAT 300
ALLTSLGSL TLOCSGIYV VLDIAPRYSS FLMSARGFS SIAPVIVPTV SGFSLSDOE 360
FGWRNVFFLL FAVNLGLLF YLIFGADVQ EWAKERKLT L 401

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Seq ID NO: 248 Protein Sequence
Protein Accession #: NP_003049.1

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1      |      |      |      |      |      |
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31     |      |      |      |      |      |
41     |      |      |      |      |      |
51     |      |      |      |      |      |
MPTTVDDVLE MGEFPHFQK QMFLLALLS ATYAPYVGI VFLGFTPDNR CRSQVAELS 60
LRQCSPAEE LNTYTPGPG AGEASRQCR RYEDVMQST FQCVPLASL DTRNSRLPLG 120
PCRDGVYET RGSIVTEFH IVCANSHMD LQSSVNVNG FIGNSIGVI ADFRQELCL 180
LYLILWIAA QVILSILFH TMLITFLQI GLSKAKMLI GILITFPGV RYKWTGIF 240
YQVATYGLI VLAGAYALP HWRQLQTYA LNPFFLLTY WCIPEPRML SGNQNAEAM 300
RIIHKJAKN CKSLPASLR LRLKETGKK LNPFLDLVR TPIQRHIMI LMYNFTSSV 360
LYOGLTHNG LAGDNILYDF FYSLAEFPA AMPLITDR IGRYVPAAS NNVGAACLA 420

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SVFIPDQLW LKLIISCLGR MCHPAYEIV CLYNARLYPT FIRMGLVNIC SSMCDIGIIL 480
TFPLVYVLTU IMLEPLIMYF OVGLGVAGGL VILLIPETGRK ALPETIEEAE NMQRPEKKE 540
KMILYQVQL DIPIN 555

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5 Seq ID NO: 249 Protein Sequence

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Protein Accession #: E05 sequence
1 11 21 31 41 51
| | | | |
MORAIQWVF EDLPSPSP LTPRHGIGLA NVQYDENIA VRHEATLLPH QEDLSIMSG 60
LGLIKVYKSI LKLEIQLDL LCQ3DQVYV LKPPVCSSEI KDDAASGPFK 120
ADNTNANFLM WCRDIGVDET YLFSEGLVL HKDPQGVLC LLEIGHIVSK YGVEPPVLV 180
LEKELELEET LMTSPDEDS ISIPESCRR ELIAEAVKHI AEDPPSCSH RFSIEVLSG 240
SYRLGKILIF IRLMKQRMV VRVGGWDTL QGLIKYDPC RILQFATLEG KILAFQWVS 300
NESVFGSPAR TPOFENRPL SAVNKKFOM KSPVQVPIV KSEKQVPSL 360
CZHLGSSNVS SLFNSPAS SHPLKESKO ITKKQAPSIN NASSSLASLN PVGKNTSFA 420
LPTAPCISE SPRKCISSN TPKAKVPAQ NSADLEESTL LPNKSCKTKO PYLKGKHIS 480
SRDNANSHLA AISMSSKCP KLPIANIPVR KPSFQSSAK MYTKSTKITA TOLGTQEQS 540
DGAPQAPFVP AQLIKSALAL NQPSVESVS PSKATQSKD STKGEPRBSK TPASIAKPPS 600
GRSSLSKOR TLLIEVLQV SSTKTQAPK SAQTVAESQM STKGEPRBSK TPASIAKPPS 694
SVKDAUSGOK KPTAKKEDD DNYFVMTGK KPRK

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25 Seq ID NO: 250 Protein Sequence

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Protein Accession #: NP_001035.1
1 11 21 31 41 51
| | | | |
MSKSKSVGL MSHVAPAKE PHAVGKVEE LILVLEQNV QLTSTLTNP KSPVPEAGR 60
ETWKGKSLV LKVLQGLD ANVDFPYLC YKGGGATLV PTPMPVIAG KPLFYMEAL 120
QQFNREGAAG WKVICPLKG VGFTVILSL YVGFYTNVIL AMALKLPSS FTTELPHNC 180
NHSNFSNCS DAHPDSSGD SSGLDNFTGT TPAAYFERG VIALKHQKHI DDLGPPRMQL 240
TACLVLVLVL LYPILMKQVK TSKRVNMTA TPFYVVLTAI LKRGVLPGA IDGIRATLV 300
DFTLCLDNY KIDAATQCF SLGQWQVLI AFSYTHFTN KCTDAIVTT CIELSTFSS 360
GFVVFSLYQ NAQKNSVTO DVAKDGLGI FIIFYEAIAT LPISBAMAVV PFIMLTLGI 420
DSAMGSHSV ITGLIDEPQL LKHKRELFTL FIVLATFLS LFCVYNGOY VFTLIDKFA 480
QGTSLTGLVI EAGVAVFTG VQGFSDDIQO MTQGRPSLV RLCKWLKSPC PLLFVYVVIS 540
VTFPRPRTA TIFPDMAAL GHVIATSDMA MVIYANYKF CBLPGSFREK LATAIAPED 600
RELVDEREV QFTLEMLKY 620

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40 Seq ID NO: 251 Protein Sequence

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Protein Accession #: NP_071356.1
1 11 21 31 41 51
| | | | |
MPLGHIMELD LKIALEYIV PCILHEVGFCY LDMFLGVGV DCVLERYKQL KCTGALRQQ 60
LAGPRAQVK KHLRGDITV IGHGDEBCA ISFLLESLID LKVLQGLG KTYVEKBSA 120
WVACQDNT CYVRNDDNMW GDSCTCTCY VLKNDMLK HSGILRIFPE OKSFIADVP 180
IFDRLLEFMS DRANKHEVQ SATRYAMTV WYFDAERAE AKKFRILTR KTESALTD 239

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50 Seq ID NO: 252 Protein Sequence

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Protein Accession #: NP_647475.1
1 11 21 31 41 51
| | | | |
MKGAPTAGAA LMLCAATAVL LSAQGPVQS KSPFASNDP MVLNHLQLQ LQQLGRBAE 60
KQVQDALE RLKAGCCDA QOTEGDLP LAPSEVPPE VMLHQLQK AQNSIQQL 120
HKVAGQKRL KEQKRLIQL QSQFOLLNKH KLDKEVAKPA RKKLPEMAQ PVDPAVRYS 180
LHRLPRDQE LFQVQIERQS LPEIQPGQS PFLVNCMTS DQGVYTIQR HDGSDVRNP 240
WEATYAGQV PHQFVGLGL KVSITQDM RLAVQLKRM DSNALQLPS VHLGDEYAT 300
SLQATPAVAG QLQATVVPVS GLQVPPFSD QNDKRLQR CAGSLGGDW PUTCNSHML 360
GVYRSTPQK ROKLKGIVP KTWREGYPL QATTMLQPM AEAAS 406

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60 Seq ID NO: 253 Protein Sequence

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Protein Accession #: NP_001207.1
1 11 21 31 41 51
| | | | |
NAPLCPSMWL PLLIPAPAG LTVQLLSLL LMPVHPORL PRMQEDSLG GSGGEDOPL 60
GEDLPSEED SPREEDPGE EDLPGEDLP GEDLPFVKP KSEEDSLAL EDLPVEAPC 120
DQKQCNAN KQEDKQCNW KMYQDFPFP PDSACAKRY GSPDILRPL APTCPALAP 180
ELLGQCLPPL PELRLNRRNG SVQLTLPPGL EMALQGREY RALQHLHWG AAGRPSERT 240
VEGHRFPARI HVVHLSTAFV RVDEALGRPG GLAVIAATLE DQPEINSAYE QLSRLERT 300
EGSEIQWPG LDISALLPSD FSRFYDESS LTTPCAQGV IWTYVQTM LSAQLQTLT 360
DTIAGKDSR LQIAGLQVW LKGVSIENF PACTDSPEFA AEPQLMSCL AAGDIALIW 420
GLIFAVTSA FLVQNRQNR ROTKQGVSR PAEVAETCA 459

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75 Seq ID NO: 254 Protein Sequence

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Protein Accession #: NP_003030.1
1 11 21 31 41 51
| | | | |
MBQDQSKKE GRITIVLALA TLIAAPSSS QYGVVAAVN SPALLNQFY NITYYGTGE 60
PHEDPITLL NSVTVSMFPF GGFISGLLV PLVWFKRKS ALLNWFISI VPAIACSR 120
VATSELI II SLLACICAG VRSVWVYPL GELAPNLEIG ALGVVPLQFI TWGLIWAIV 180
KIRMLNANDW GMPILIGITL VPAALQILL PFPFSEPTL LQKKDEAAE KCAIOLIRGW 240
DSYDREVAEI QBEDAEAKA GFISVLKLF MSLNWLQIS IIVLMQOQL SOWNAITYVA 300
DQITLASQVP EBYQVYVAG TQANVWTFE CAUVFVLEIG RLLALLQPS ICLACCVIT 360
AARALGCTVS WHPYISIVCV ISVIGHMLG PEPVAILIT KIFLQSSSPS APWQSDVM 420
LSNFTVGLIF PFIOELGVP SFIVFAVICL LTTIYFLIV PETKATFIE INQIFRQK 480
VSEYPEKE KKLPPVTE Q 501

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Seq ID NO: 255 Protein Sequence									
Protein Accession #: NP_001243.1									
5	1	11	21	31	41	51			
	MPEEGSCSV	RRRPYGCVLR	AALUPLVAGL	VICLVVCIR	FAQAQQQLPL	ESLQMDVAEL	60		
	QJNHNTQQDD	PRLYWGGPA	LQRSFLHGPE	LDEQQLRIHR	DGIYVNHVQL	TLAICSSSTA	120		
	SRRHPTTIAV	GICSPASRSI	SLRLSLPHQG	CTIASQRILP	LARGDTLCTN	LITGLTLPNRN	180		
	TDTEFFQVQV	VRP					193		
Seq ID NO: 256 Protein Sequence									
Protein Accession #: NP_060562.2									
15	1	11	21	31	41	51			
	MLFTSFVEQK	KXAGVFEIT	KTHGTITGIT	SGIVLVLLII	SILVWQVQPR	KXWACKTAF	60		
	NKTFQVEFVD	PHYELFSLR	DKEISADLAD	LSEELDYOR	MRRSSTASRC	IHDHOGSSQA	120		
	SEVKGRETHL	SMHELPLAND	FAQPQMKTF	NSTFKKSSYT	FKQGHCEPDQ	ALEDVRHREI	180		
	PCETIYKGRS	DSNOASISID	F				201		
Seq ID NO: 257 Protein Sequence									
Protein Accession #: Eos sequence									
25	1	11	21	31	41	51			
	IIAATINIAS	MTSPIDNAGL	AADFQKQIAS	LQTQISTDAE	AVSSAKSEIM	ELKQVLQSLQ	60		
	HELQGLVMAQ	SSPQGTADT	EAGYVAQLSE	IKMYISILRE	QIQQIGETE	YQNTVEAQLQ	120		
	DITRLLEVEI	ETYNHLLQGE	GQSEAREAES	RG			152		
Seq ID NO: 258 Protein Sequence									
Protein Accession #: NP_003256.1									
30	1	11	21	31	41	51			
	NRQTLPCIFY	WGLLLPFQML	CASSTTKCTV	SHEVADCSKL	KLTVQVEDLP	TNITVLNLTN	60		
	NQLRLPAAAN	FRYSQSLTSL	DVGFTTISKL	EPELCQKLPM	LKVLNLQHRN	LSQLSDKTFA	120		
	FCNTLTLEHL	KMSISQIKLN	NPFFVKQDML	TLDSLNGLS	STKLGTQVQL	ENLQELLSEN	180		
35		NKQALKSEIS	LDTFANSSLR	KLELSSQIKR	EFSPQCFHAI	GLPLGLFLAN	240		
	LCLELAITSI	RNLSLSNSQL	STTSNMTFLG	LKVTNLTMLD	LSYNNLAVDG	KDSFAMLPQL	300		
	EYFFLENNYI	QHLFSHSHQL	LHWVRYLMLK	RSTFKQSISL	ASLPKIDDFS	PQWLKCLBBL	360		
	NHEDNDIIGI	KSNMFTGLIN	LKYLSSLNSF	TSLRTLTNET	PVLSLMSPLR	IMLITQKIS	420		
40		KIESDAPSL	QHLSEVLQGL	VEIQEQLTQD	EMHGLDHFTE	IVLSYNYLQ	480		
	SLQRLMLRVR	ALQVYDSSPS	PFQPLRLITI	LDSLHNNIAN	INDMDLELE	KLEILDQGN	540		
	NLARLWQHAN	PGQPIYFLQG	LSHMLILMLE	SNQDFEIPVE	VFKDLFLKI	IDGLLNLNLT	600		
	LPASVFNQVQ	SLKSLNQLGN	LITSVEKCVF	GAFFNLITEL	DHRFNPFDCI	CESIANNVNW	660		
	INETHNPIPE	LSGRHLNTP	PMYQGFPHL	POTSSCKESA	PFELFFHMTT	SILLIPIFIV	720		
45		LLIHFGWEI	SYFNVSVHR	VLQPKEDQ	TEQFEYAVY	IHAVKQKDW	780		
	DQSLKFLCEE	RDFEAGVFEL	EALVNSIKRS	KRIIFVITHL	LKMDLCKFR	KVHNAVQQA	840		
	EQMLDSILVL	FLEBIPTYKL	NHALCLRRCH	FKSHCILAMP	VQKREIGAFR	NKLQVALQSK	900		
	NSVH						904		
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Protein Accession #: NP_000570.1									
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	LKSMYTDIYL	NLAISDLFFL	LTVPFWAHYA	AQMDFQMTN	COLLTGLYFI	GFFSGIFFII	120		
55		LLTIDTRLAV	HVAVFALKAR	TVTFQGVTSV	ITMVAVFAS	LPQIIFRFSQ	180		
	HPFYSGQPM	NKHTQITVLI	LQVLPLILHM	VICYSGLIAT	LIRACNKKR	HVAVLIFTI	240		
	MTVFLFWAP	VNIVLLATTE	QEFGLNCS	SNRRLDQAM	VTTGLHTNCK	CINPIIYAPV	300		
	GKRFNRLLVL	FPQKIIAKRF	KCCCSIFQRE	APERASSVYT	RSTQGERISV	GL	352		
Seq ID NO: 260 Protein Sequence									
Protein Accession #: Eos sequence									
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	PGQPPQPGI	PGAKZELGLP	CAVDIGKGG	FKQKQKDPGE	PGPAGLKGEA	EGKELSLGLP	60		
65		ADQLKGEKE	SASDSLQESL	AQLIVERPGP	GPDPQPPGMP	LQIQPKPKGL	120		
	GERGSPDLPG	PVGPGLGLIG	PQTKGEKGRF	GEPLGLDFFG	PRKRGDRSE	RGEKGERGVP	180		
	RGKGVQKQKG	EPGPPGLDQ	CPVQPDGLPV	PGCHMK			216		
Seq ID NO: 261 Protein Sequence									
Protein Accession #: NP_004852.1									
70	1	11	21	31	41	51			
	MLPPQKXPE	SNAGLVILGA	LFTSFLLIYV	SYAVVPLNAG	LASTTPEARA	SCSPPALEWE	60		
	AVIANGSAG	ECQPRRMVIF	LKTHKTAST	LMILIRFQGG	KHRLKAFAN	GRNDPDTPT	120		
	FARSLVQVYR	PGACFNQIN	HMRPHYDEVN	GLVPTNAIFI	TVLRDPAFLF	ESSPHYFGPV	180		
75		VPLTNKLSAG	DKLTFEFLQD	DRYVDPMGN	AHVLRNLAF	DLGYDNLSDP	240		
	EVERREHGL	LQYVDESLV	LADLLCWEL	EDVLYFTLMA	PRDQVPRLS	GLYGYRATN	300		
	NMLDSHLYHR	FNASPRKVE	AGREHMAKE	VAALAHANER	MRTICIDQCH	AVDAAAIQDE	360		
	AMQVPLQGT	KSILGYNLAK	SIGQRHQAQC	RRLMTEIQT	LMDLGNLHV	TKLMKFIQDP	420		
	LWR						423		
Seq ID NO: 262 Protein Sequence									
Protein Accession #: NP_061130.1									
80	1	11	21	31	41	51			

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MAVLSLRLG	KRSLLGARVL	GPSASEDPSA	APPSEPLEEG	AAQPFPTTSD	DTFCQEQPKK	60
VLKAPSTSGL	QQQAFQPOK	VYVYVGGQEC	TGLVEQHSNM	EQQVTVMLLE	QKLGQVCRCVE	120
EWMLAEQLQP	QKQAPFLIEG	AQALAYHPUS	KNIDVKKKS	DAVMDKEMMA	AMVLTSLSGCS	180
PVQGFQFQGT	ALFASASRAAC	DPWKSQDLS	DGSSSTTSKH	WSSSDVSTP	SPFPAQSPKK	240
YLGDAFGSG	THGFTFDPO	PFLLDERAPK	RRKSNYKMY	KCLMPHCQV	LBSLVQIKKH	300
VKALMLGQTV	DSQDFKRRER	FYTTVQVQKE	ESAAAAAANA	AGTPVPGTPT	SEAPATPSMT	360
GLPLSLPFP	LHKAGSQGE	HGPESSLFS	QALSKSAPGS	FMHQAURAY	QALPSQIPIV	420
SPHIVTSVM	AAAPSAACSL	SPVSRSLFS	SEPPQAPAPM	KSHLIVTSPS	RAQSGARKAR	480
GEAKCKRVY	GIDHRQWCT	ACRWKACQK	FLD			511

Seq ID NO: 263 Protein Sequence
Protein Accession #: AB058765.2

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1	11	21	31	41	51	
MEENYETLVS	VGTAELEPLS	AFLSPESEGR	AVGGSGINDE	QREFAGCQDP	QQQQRHSLIN	60
LTALVQLVKE	IEPFLFGVK	GAMDSPESES	RGASLDGERA	SPFAAAREP	CTLRGLLSCL	120
WPGFTSQRL	ATTIDTSSCS	SOPTGDOVOG	SPLPITAKD	PWFTKKEGS	ALGSESPPT	180
NSPSEKSKR	QJERQTSAG	ISPGNSPLOG	LINCLKEILV	RGPHRPETSP	SFLPLPLSLG	240
TSRLTRADLG	PGSPPPWAKT	EAVSGDCPIQ	GLMLCKELP	EAQDRHPFS	GVGNRLQEN	300
PGANKRGSGQ	PGVLLTFPH	FDLQAGLLS	VMKNSHWQS	PPQFASCPQG	HQPLSPATG	360
DTRGVPGVSH	GVEQAASAS	SSPLALEAAC	LRGIPFMSS	PGQLPTFSCS	QHPQDQRS	420
QKPELQPHS	NEIATREPV	LPQLQGCVR	DGSEPLAPE	GTPIFSFSSS	STDMQDFGS	480
PVGNQGNQPG	KSGPPGGSPL	QGLNCLKEI	PVEVLRPAW	CESAANDGR	RAEPRHWAD	540
KEGLRARECE	SARLGQGRGE	APTRSLHVS	PQVTTSSCPV	ACHQRPKDP	GATREFQVMN	600
LPFGSAPFVS	PLMLLSLAR	GLIPVRLFL	ACVGGSPSP	SPGSSSSFSG	SGDEGRPEP	660
ELMKPLKJR	DLRPGCKPV	PLGCKGZTT	ACGSSGSPG	DPRHTEPCV	SGLGATGAD	720
FCVVSQLEKX	PRVSEASRLG	SLWGRPRVA	AKTKEELLQ	GPPELSESE	PFELPPPEAA	780
PFVLPASSIL	PCCHCQRFQ	QELKSLQAL	AEKLDRATA	LAGLQEVAT	MRTQVHELGR	840
RFGQPFHQZ	ASHMTLFRG	PRNAGHQRH	MLFTWQKQF	TRPKPLIBG	QGSCEAGDL	900
QGLSGTAR	NBLPLPOAP	APFGLNCS	SQLGLSTPS	CHAAPPAHL	LAHTQDRGS	960
LFPLVPAAL	LQNASPPAAS	ADADVPTSGV	AFDGIPEFK	SPSLGQGVQ	RALQEELMG	1020
EHRDPHGAH						1030

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Seq ID NO: 264 Protein Sequence
Protein Accession #: AL631935.1

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1	11	21	31	41	51	
PAGCGDPQGG	PRHSLMLTA	LVQLVEKPE	FLFGVEKGM	DPSEESRGA	SLDGERASPE	60
AAAREPCPLR	GLLSCLPDOP	TSQPHLATT	TDSGSSGPT	GDGQGSPLP	IKTADKFWPT	120
RKEGPGALGG	EPSPPTHTSP	RRKSHBQER	OTSEAGISGP	NSPLQLGLNC	LKEILVQPR	180
HFPTSPFLP	PLPSLTGSL	TRADLGPSF	PNWKTENVS	GDCPLQGLLH	CLHELPEAQD	240
RHPSPGVSH	KRLQGLSMG	KXGSGGPOIL	LTFFPRFGL	AGDLELYME	NSHVGSPSP	300
ACQCPQKPL	SPSATDTGK	VQPSWQPEA	QANASGKLI	EALCAKLGK	PFHGSFSQL	360
PFTSCSNFQ	PGDSRSQKPE	LQPRSHSEE	ATREPVPLG	LQSCVRDGS	RPLAPRGTP	420
SFSSSSSTDM	DLDFGSPVNV	QQHNPQKGP	PGSSPQLGLE	NCLKEIPVIV	LRPAWPCSSA	480
ADRGPRRAEP	RHTADKESG	AKPKPLMKL	ESALGILLV	RPLFAVCQVG	SPSPSPSGS	540
SFSSGSGED	PRHPELAKF	LPQERDLPS	CHFPVPLSP	PGDTFAGSG	GFPGEDPRT	600
EPFYCSGLGA	GEFGVS					616

Seq ID NO: 265 Protein Sequence
Protein Accession #: A029071.1

55
60

1	11	21	31	41	51	
KTRGTGRGL	RSQWMLPLAE	AGALAQGGP	SATEMACILR	RKTPRKQPT	LLWVRSRES	60
QKTSVAVLQ	RGQTRVPLA	TEVLLPLGA	SLGREKGRF	LAPRSHKVM	LRTRGRTKM	120
VQTLARMSR	TROPVERAAA	AAAAAAGDGA	GHAPFTPPA	ADGARAPESP	QQVTPGLRL	180
RLPREFSLR	GLCRPLRLPL	GFRESDSAKP	ASRLRLQHTP	SARMRYRIAG	ARLMSENYPP	240
PLSSAALEGA	GPTRRN					256

Seq ID NO: 266 Protein Sequence
Protein Accession #: NP_002095.1

65
70

1	11	21	31	41	51	
MTKFSFSLF	FLIVGAVNTH	VCFMHEIIG	KEVSPSRHFP	MASIQVQGHM	VCGVLDIPQ	60
WVLTAANQY	RFTKGQSPV	VIGASHLSKN	EASKQGLEIK	KFFPSRVTS	DQSDIMHVL	120
KLQTAALKAN	HYVMHLIRSK	ISLASQTKK	VCMGATDPO	SLRPSDLRE	VTVTVLSRL	180
CNSQSYNGD	PFITDKMVC	GDAAQQKDCS	KDGSQGLPIC	NOVPHAVSG	GHECQVATP	240
GIYVLLTKY	QIVKNSLVP	PRTH				264

Seq ID NO: 267 Protein Sequence
Protein Accession #: NP_443179.1

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85
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1	11	21	31	41	51	
MQVNTLFETS	QVPDSDPPQ	VQVQTVRET	ISCSQMFAPS	EPAGEESPPT	GTTTISFNL	60
GGVKNENASL	AQSEKVPCT	QHQREQKQD	RKCNIPNFR	EDLKVRQIS	EMDRWTSFG	120
VFSHLPLDA	RAHREYVPL	SPASFPPTT	ALTLDKQK	PRDEKAVCM	ECEASDQT	180
CFDTIDSLG	TPVDNYSQE	ICSVDTLAE	QGNKYSDLCS	SNDKTLEVF	QTQVSTSVS	240
TKSSSDKGS	VNSPLFISTF	TLNISHTASE	GATGENLAKV	EKSTYPLAST	VHAGQKQSP	300
SNISQDLDET	LSSSENPLM	QFKGQKQSP	SPSAADITAT	PASTSYTSEV	PMKPTVTLIA	360
NSGKQATRE	VYTATVHYV	AKLVASVPE	DKMAGTQVF	PRASHREKS	QPSQGVQNM	420
ILSKATIKST	KELLGRAPHS	NOVPHVLQ	PECEGFCNS	PLQVNLMSG	SKQVTDNRD	480
RYEYENFQR	QSTKQGVQ	QSLSQQSLS	APDFQSLPT	TSAAQERNL	VFTAPSPASS	540
REAGQKSGW	GTRVSVVART	AGEEDSQALS	NVPSISDILA	EESKTRPGN	WENGLNKIT	600

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TLASASBIV PPRLTNSBS KASDGLIIP DKNAVHSEL KADAVVPELA PSFIAALAHS 660
PEDASGALAD SRESHGKEEP TIOVIMRSLS SRGFSQPRLL BSSVDPIDEI ELSVDTSLSA 720
ASETCGKEMV NVYSQDQEBK OLOMDHTAFF KKLFTCPKIL BSSVDPIDEI SVIETTRACK 780
PEPSETTVOQ AREQGGQSTQ NKHMEAEIQS AIIQVPCIQ TILSENRISS SQRSMKROKA 840
TOIOPENANT AIHQVLQPLAS QDERIPBQCS IQGIESSSQ SLASAEQSK DDAE1SPIS 900
PLSSCLPMT HSLGLQDTIB STQIHDHVE MOIVFERKQ VYVFPQKRG TIHERGKPL 960
PSSPOLTRFP CTSSPENVTJ DFLISNMHE PKIEVLQIGE TRKPPSSSSG AKTLAFISICE 1020
RELEKAPKLL QDPCKGTGLG CAKSRERER SLEARAKGSP GTIATVIGSE EVKRRKPAFG 1080
SGHLDADYVK KILDRVAALL LKLEKEDNIR KNEAPLOKMP KLETSLSHTE EQQKPKPSC 1140
KRRUNAPWLL KIQDANRPE KSGRWLGLCO PAHIEHSTI CFTDKSKIA QVQSGAGNS 1200
TSFVAIWGAS PKDGLGIYCC IKSYSKYVTA RPNLTARVIL QLSRQDTKS CEIEFISOLI 1260
KFEDFLDSY FGRLRGGQIA TSELHFGGV HRAAFSTVM HOLMPVFKPG KACVLKVBNA 1320
IATVGRNDEI LIQNYQLAS QCYQNTAR YAKIYAAQA QPLESGEVP EIIIPFLIHR 1380
PENHPIATY ERLGLQKQIM STYRDKKIM FLHREKQAOO ACTPQWMT QTSOGLLMT 1440
DNQGVGMLT DVGITATLAK YKGFKNCSM TFIPOFKALH QNKYCKMLG LKSLQNNKK 1500
QKQPSIGSK VQTNMTVKK AGPETPGEKK T 1531

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Seq ID NO: 268 Protein Sequence
Protein Accession #: NP_602293.1

1 11 21 31 41 51
| | | | |
MKQNSKLRP EVLQDLREIT EPTDHELQW YKGLKDCPT GHLTVDEFKK IYANFFPYGD 60
ASKFAKMFVR TFDTNGDTI DFREFIALL VTSRKLEQK LKMAFSMYDL DQNGYISRSR 120
MLEIVQAIYK NVSSVMQKPE DESTFEKRT KIFRQWDTNN DGKLSLEETI RGAKSDPSIV 180
RLQDCPFSSA SQF 193

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35

Seq ID NO: 269 Protein Sequence
Protein Accession #: NP_002140.2

1 11 21 31 41 51
| | | | |
MKQNSKLRP EVLQDLREIT EPTDHELQW YKGLKDCPT GHLTVDEFKK IYANFFPYGD 60
ASKFAKMFVR TFDTNGDTI DFREFIALL VTSRKLEQK LKMAFSMYDL DQNGYISRSR 120
MLEIVQAIYK NVSSVMQKPE DESTFEKRT KIFRQWDTNN DGKLSLEETI RGAKSDPSIV 180
RLQDCPFSSA SQF 193

40

Seq ID NO: 270 Protein Sequence
Protein Accession #: NP_003937.1

1 11 21 31 41 51
| | | | |
MGNQAPRSE TIDREKRLV ETLQADSGLL LDALLARGVL TGPETEALDA LPDAERRVRR 60
LILLVQGGKE AACQELLRCA QRTAGADFPA WDMQNVGSG RDSYDPPCP QHMTPEAFGS 120
GTTCCPLGRA SPDDEAGPSE GSEAVSQSTP REPFELEAE ASKEAPEPE PEPELEPEAE 180
ARPEPELEPE FDFEPEDPFE ERDESEDS 208

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Seq ID NO: 271 Protein Sequence
Protein Accession #: NP_004198.1

1 11 21 31 41 51
| | | | |
MGAQVVDGEP TGKAPDGGN GWAVLFGCPV ITGFSYAFPK AVSVFFKELI QEPGIGYSDT 60
AHISILLAM LYGTGPLCSV CVMRFGRFVR MLVQGLPASL QMAASFCSR LIQVILTTGV 120
ITGLGALNRP QPSILHMYRI FSRKRRPMANG LAAGSPVFL CALSPGLQL QRGYHMGDF 180
LILGGLLNC CVCALMBRL VTAQGGSGP PRSRLLELL SVYRGRFPL TAPASGWWL 240
GLVFFNPPVVF SYAKDLGYVD TKAALFLTLT GFIDIFARPA AGFVAGLKV RPYSVLYLFS 300
SKFFNGLADL AGSTAGDYGG LVVPCIFPGI SYGMQALOP EVLMAIVOTR KFSSAIGLVL 360
LMAEAVLVNG PPSQGLKIDA THVMYVFLI AGAEVLTSSL ILLGNHFFCI RKKRKEPOPE 420
VNAJEEELKL KFPADSGVDL REYERFLAKE PERNGEVNMT PETSV 465

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Seq ID NO: 272 Protein Sequence
Protein Accession #: NP_060705.1

1 11 21 31 41 51
| | | | |
MAALTTLFKY IDENQDRIY KLAQVVAIQS VSAMFEKRG EIRRMMEVAAA DVKQLGGSVE 60
LVDIGQKQLP DQSEIFLPII LLGRIGSDQK KKTVCIVGKL DVQPAALSDG WDSEPTFLVE 120
RBDKLVKRGS TDGKFPVAKI THALAEFORT QRTIPNVPF CLECHRESSR BOLDLIFAR 180
KTFKFRVDY VCTSDNVWLG KKKCFITVL RQICVPFVLE ECKNSLDHSG VYQGSVHEAM 240
TDLILLMGL VDKRCHILIP GINEAAVAAT ERENKLYDDI DDFIEFAKD VQAQILLASR 300
KKDILMHRN YPSLSAGIE GAFSGSGAKT VIPRXVKGPF SIRLVNMTF EVVGEQVTSV 360
LTKKFAELRS PNEFKVYMK GGRPVMSDES PHRYLAGRA MKIVGVGEVD LTRGGSIPV 420
TLTPQATQK NVMLLPWGA DQASBSQEK LKRYVYIGT KMLAATLYEV SOLKD 475

75
80

Seq ID NO: 273 Protein Sequence
Protein Accession #: AF258592.1

1 11 21 31 41 51
| | | | |
MAALTTLFKY IDENQDRIY KLAQVVAIQS VSAMFEKRG EIRRMMEVAAA DVKQLGGSVE 60
LVDIGQKQLP PNVNIFLDEG MEESGSGGLD ELIFARKDTT FKDDYVCIS DNTWLGRKXP 120
CTFELRQDC YFFELFQVGL KLASGSDYQG SVIENATOLI LKASLVEKX GRILIKIWE 180
AVAAATEEEN KLYDDIDFDI EEFKADQVQA ILLASHKKDI LMBRWYPSL SLNIGEGAFS 240
GSKACTVYPR KVVKGFSIRL VPMNTEPVVG EGVSTLYTK FAELRSNPEF KYVMGHGQK 300
WYSDSHKPY LAGRKAMKTV RGVFHLTRE GGSIVPTLTF QEATGKNVWL LPVGSADGGA 360
HSQNEKLRYL NYIESTHMLA ATLYEVSLDK D 391

Seq ID NO: 274 Protein Sequence
Protein Accession #: NP_060871.1

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1      11      21      31      41      51
MGGRHSKPP VFDNEEVNF DHFQILRAIG XGSPGKVCIV QKRDTKMYA MYKYNKQKI 60
EREDEVNVPF ELIQMGGLH PFVLNMYSP QDEDEPMVVF DILLOGDLRY HQQNVHFTS 120
GTVKLVIYEL ALAEVYGRY HIIRHDKPD NILDHGRHV RITDNIATV VQGNABRSM 180
AGTKPMPAPE VQTVYDGRP GSYVDNMGH LGITAYELLE GWRYPEINSH TIDEDIANQ 240
KVERVYHSST WCKGMVALLR KLUTEDPESR VSSLRDIQSV PYLADGNHDA VFKKALMPGF 300
VPNKORLMCD PTFEELEML ESKPLMKKK KLAKNWSRDG TKDSCLPNHG LQHCLETBRE 360
EPIIFNREKL RRQGGGSGQL LQDTSRGGQG AOSKLGQGCN NHLLTCTCTR GCNS 414

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Seq ID NO: 275 Protein Sequence

Protein Accession #: NP_004198.1

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1      11      21      31      41      51
MGGAVIDEGP TGKVAKGGGW GNAVLGCFV ITGFSTAFPK AVSVFPKELI QPFGIGYSDT 60
AMISSILLAM LYTGPGICVS CVNRFGCPV MLVGLGASL GMAVASCRS IIQVYLITGV 120
ITGLGLAINF QPSILMGRY FSKRRPWANG LAAGSPVPL OLSPLQQL QRRTPMGST 180
LILGZILLNC CVCALMRPL VFAQPGSCP FRSRLILD SVFRGRFVL YANAASDWL 240
GLTFVFPFVA SYAKDLGVPD TKAALITLI GFIDIFARPA GAVAGLGVK RPYSVYLSF 300
SHPFNGIADL AGSTAGUDYG IAVFCIFFGI SYGMVQALQ EVLMAIVGTH FKSSAIGLVL 360
LMEAVAVLWG PPSGGLKIDA THVMYVFIL AGEAEVLTSSL ILLAGFFCI RKKPKRQFE 420
VAAAEERKLH KPAADSGVDL REYEHFKAE FENSGEVNHT PETS 465

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Seq ID NO: 276 Protein Sequence

Protein Accession #: NP_006589.1

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1      11      21      31      41      51
MPTNFTVVPV ENAHAGGQDE TAERTBAQPT PEGPEPERFS PQDNPRENS PFLNNVEVQ 60
ESFFEGQDMA LFEEDKSNP MVSSILAKLA HTNLSQGVV EHEDEBSRR KEAKAPMGT 120
FIOVLVLCIQ NIGLVILFR LTNIMVAVG LESFLIVMC ICTPTMAIS NSALRWVPT 180
PAGSYPMIS RSLGRQDA VOLCYLTGT FAGVILGT IETILTYSF GAALIRAKA 240
GGEAANLNRH MRYVQCTLV LNALVVFVG KYNNKLALVF LACVLSILA IYAGVKSAP 300
DFDIPVLCIL GNTLSBRFS DACVKAIGH NNSATBALMG LFCNGSQPSA ACDEYFIQNN 360
VYIQTGPQA ASGVFLEBLW SYTAGAGAP EKKQVSPVVP AESSASTLP TVLTIDAST 420
TLVWITFYS VYVDNIDEN FTERTEKQNS IPTGILALV SVFSGRSLV VPCADICD 480
VLREDKGEAL QNLVIGMLA WFSNPIVIG SFFSTCGAGL QTLTGARLL QAIARDGIVP 540
FLQVPGHKA NGEPFWALLL TVLICETGIL ISLSDSVAP LSMTFLMCTI FYNLCAVQT 600
LRTPNNRFR FKFVWTLFS LQSLCLALM FICSNVYALS AMLAGCTYK YITYSARKR 660
WQDLKRLSL NARYVALLV EBPQPHYRM FQVLMMLAL DAKVAHSLR LSLFQJKA 720
QKGLTIVGVS LQGTLDXHM EQRAREENIR SLMSEKTKG FCQLVSSSL QDMSHLQGS 780
AGLQGLKQDT LAMWAPSMK QEDNPFWMN FVDTVRDTTA AQHALLVAN VDSFPQDER 840
FOGHHDVNW LVHIDGMGMG LPEFLRGHQ WRCEMRITPT VAQVDNHSPT HRDQLQELY 900
HLRISAEVYR VQVNDIDEN FTERTEKQNS QKQKAGQW LSKVQKGLS GLHDSHVAS 960
HYAAARQDA PPTPDQVQT WTEKLLAIK YRSQDTSLSG FIDLFSMKED QSNVRKMTA 1020
VKLGVVLNKK SQDAQLVLLN MRQPPNRRG DENYMEFLV LTEGLNRVLV VRGGREVIT 1080
IYS 1083

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Seq ID NO: 277 Protein Sequence

Protein Accession #: NP_004576.1

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1      11      21      31      41      51
MASHPQEPKP GLIEIFRLQ YEMWALYGD GYVILAPPS EYDQAGSSV PSVLNSAEV 60
KQRLDVGWG GCRYNNSLN DHEYQRPVE VISSAKEMV GQMKQYISV RNCHEFVAQL 120
RYKSRCKQV EKAKVEGVA TALGILVVG CSFAIRRYQK KATA 164

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Seq ID NO: 278 Protein Sequence

Protein Accession #: NP_004687.1

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1      11      21      31      41      51
MKKSGKQVP YTKTLQGMG MYVYHFFVL MYVYNKHTK PALTVPVFOE ERTSESQIG 60
WIGSIMSSLR FCAGPLWAI CDILGKETS LGAFVVTGQ YLISSWATS PFLCVTMGLL 120
PQLGSAFLYQ VAAVVTYKFL KYRLALSTAI ARSQNLTLFL LAPTFTLID LYDWTGALIL 180
FGAIALNLVP SSMLLRINI KSEHNSGINK KQSSLSNMGF EAHATETHCH RTESTIKDS 240
TQKAGLPSK NLTVSQNGSE EPYKQPHNRH LLASDESDS KVIWQCKQL FQISLFRFP 300
MYIKKYVYRK STYLICQTH LLAFLATPLF LMTYTICFA IFAGQTLALI LPVILDCRN 360
STVNRFLQLA SFFAGMAVLS GPFIAGNLVD YTYQYNSGF FSGICVLLSS VSPFFVPLAR 420
RWKNSLT 487

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Seq ID NO: 279 Protein Sequence

Protein Accession #: NP_000349.1

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1      11      21      31      41      51
MALFVRELLA ALALALGPA TLACPAKSPV QLVQLHSRLR GRQGHNVCA VQKVIQNRK 60
YFTNCKMYQY RKIGCKSTVI SYECCPGYEK VPQEGCPAA LPLSNLYTL QVGSYTTQL 120
YTRTEKLPK RPENIGKSTVI TAPSNEWAS LPARVLSLV SNWIELLAA LYNNVGRV 180
YTDLSKQNT LPSVQRENI QHMYPMGIV TYNCKALLKA QHAKTQGVV LIQYISITI 240
INIQIIEIE DTFTLEAAV NASCLMTMLE QNCQYTLIAP THRAREKIPS ETNLRLGDP 300
EALRDLNMRH ILKSNACADA IAVGLSVTL EOTTLEVGCS GDMLTNGKA IHNKDLIAT 360
NGVHITDEL LIPSAKATP ELAERSDST AIDLFRAGL QHLSGSISRL TLAPLMSYV 420
KQDILKQNT KSLAKSLYK HQETLETGS KRLRVYVYV SLICNHSICIA 480
AHDKRYVQT LTRKRVLP PCHTVMDWLK QDNRFSLVA AIQSAGLST LRRQDYTVV 540
APTHAFRAL FRPERSLLO DAKELANILK YHIGDEILWS GIGCALVELK SLQCKLEVS 600
LKNNVSVNKK EPAVEDPIKA TNGVVIVITH VLQPPANRQ ERODELADSA LEIQQAQAF 660

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SRASQRSVRL APVYQKLLER MKH		683
Seq ID NO: 280 Protein Sequence		
Protein Accession #: NP_663623		
5	1 11 21 31 41 51	
	MEGSGGAGGE RAPLLGARRA AAAAAAGAG AGRRACGAV LLETLLERAA FYGITSNVL	60
	FLNAGPFCWE GAQASALLL FMGLTYLGSF FGNLADARL GRARALLSL ALYLGLMLAF	120
10	PLLAAPATRA ALCCSARLTM CTAFQPDAAA KCCSPATFAG LVLVLGLVAT VKANITFFGA	180
	QVYKRRGRPA TRVYFNFMF SINGLALSL GGIATYQWY SEPTOTALPT VCGLAFYVF	240
	LCQSGVITK PFDGSAFTM KILTYISCCS QKRSGRQSM GRGIGVQQS SKQSLFHSCK	300
	MSHGGPTEE KVEDGVKALV IVPVELALIF YMYVFQMQT TVVLQSLMLR IPELSNITTT	360
	PHTLPAAMLT MEDAVLILLL IFLKDLVDV ILRRHLLPS SLERIAQWQF FMCSAFAPAG	420
	ILSRSLNLD KEXTNQTIG SINGLALSL LKHWYKQSL IGTISEPAST ACGLAFATPA	480
15	PKSHQSAIMG LFFFFSGWGS FVSGCLLALV SIKAIQWMS HTDFGNINQC YIANYFFFLA	540
	AIQGATLLLF LLIISVKYDHH RDHQRSRAG VPTSRRA	577
Seq ID NO: 281 Protein Sequence		
Protein Accession #: NP_001241.1		
20	1 11 21 31 41 51	
	NURLPLOCVL MGLLTAVHP EPTACREKQ TLINSQCSSL CQPGKLVSD CFTEFTETCL	60
	PCGSESLDT WNRHTCKQH KYCEPNLGLR VQKGTSETD TICTCEKSMH CTSACSCCV	120
25	LHRSCKSGFG VKQIATGSD TICEPCPGVF FSNVSAFKE CHMTSCETK DIAVQQAQTN	180
	KTDVVCQCPD KRLALVPIPI IFGILFAILL VLVFIKKVK KFTNKAPRK EPQEQINFPD	240
	DLRGSNTAAP VQETLNGCP VTQEDGKSR ISVQERQ	277
Seq ID NO: 282 Protein Sequence		
Protein Accession #: NP_003833.3		
30	1 11 21 31 41 51	
	MEQRQGNAPA ASGARKRKGP GPREARGAP GLRVPKTLVL VVAAVLLVS AESALITQD	60
	LAQQRAPAQ QKRSSPSEGL CPGHNIHSD GRDCISCKYG QDYSTRNDL LFLRLCTKCD	120
35	SGVELSPCT TRNTVQCEG EGTFRREDSF KMCRCCTQC PRGVNVGDC TMSDIECVH	180
	KESDTSSDE APVETTS SPTCPAPCS LQTIIGVTV AAVLILVAF VCKSLAKWV	240
	LPYLKXICSH GGGDFKVRD SSQRGAEND VLMIEVSLQ PTQVPEQME VQEPAEPTGV	300
	NMLSPGESH LLPEFAERS QRRRLVPAE EGDPTETLRQ CFDFADLVF PDSMEPLRK	360
	LGLDNEIKV AKABAAGHRD TLTYMLIKWV KMTGRDASVH TLDALETIG ERLAKQKIE	420
40	HLSSGKPMY LERADAMS	440
Seq ID NO: 283 Protein Sequence		
Protein Accession #: NP_671716.1		
45	1 11 21 31 41 51	
	MEQRQGNAPA ASGARKRKGP GPREARGAP GLRVPKTLVL VVAAVLLVS AESALITQD	60
	LAQQRAPAQ QKRSSPSEGL CPGHNIHSD GRDCISCKYG QDYSTRNDL LFLRLCTKCD	120
	SGVELSPCT TRNTVQCEG EGTFRREDSF KMCRCCTQC PRGVNVGDC TMSDIECVH	180
	XESDIIGTV AAVLILVAF VCKSLAKWV VLPVLGICG GGGDFKVRD SSQRGAEND	240
50	NVLMEVSLQ PTQVPEQME VQEPAEPTGV NMLSPGESH LLPEFAER QRRLVLVPA	300
	NEGDPTETLR CFDFADLVF PDSMEPLRK KGLDNEIKV AKABAAGHRD TLTYMLIKW	360
	VNKTGRDASV HTLDALCTL GERLAKQKIE HLSSGKPMY YLERADAMS	411
Seq ID NO: 284 Protein Sequence		
Protein Accession #: NP_002002.2		
55	1 11 21 31 41 51	
	MRLLALLGV LLSVGPVPL SLEASEVEL EPCLAPSLEQ QRDELTVAGL QPVRLCCRA	60
	ERGRHXYKE SRLAPAGRV GWRGRLEIAS FLPEDAGRL CLARGSMVL QNTLITGDS	120
60	LTSNDEPDP KSHRDLNRH SYPQAQPYVT HPQMEKKLF AVPAQTVKFP KCPAAGNPTP	180
	TIRNLKQGA FNGENRIGI RLRIHQNSLV MESVVPDRG TTYTCLVENA GSIRVNYLLD	240
	VLRSHRPI LQGLPANTT AVUGSDVELL CKVYSADAPH IQMLKHIVN GSSGQADGP	300
	YVQVLKTADI HSESEVELY RVVSAKDAGE YTLCAHNSIG LSYQSAWLV LPFEDPTTA	360
	AAPEARYTDI ILVAGSLAL AVLLLAGLV RQALGRHP RPAATVKLS RFPLARQSL	420
65	ESBSGKSSS SLVGRVRLS SGPALLAGLV SLDLPLDFL EPPFRDLVQL KPLGRCQPG	480
	VVRARANDM PARPQASTV AVNKLKDNAS DKDLADLSE MEVMLIGRH ENIINLQVC	540
	TQGPVLIVV ECAAKGNLR FLRARPPGP DLSPDCPRS EGPLSPVLV SCAYVARGM	600
	QYLESKCIH RDLAARNVL TEDVVKIAD RGLARGVHH DYYTKNSCR LPVVKMAPEA	660
	LKRVYTHGS DVNSGILLW ELFTLGSPY GPVPEELFS LRRGKHMRD PFCFPELYG	720
70	LNRCKWAP SQVYFKGVY SALQVLLAV SRVYLURLP RGPVPSGSD ASSTCSSSDS	780
	VFSIDPLPLG SSSFPFGSQ QT	802
Seq ID NO: 285 Protein Sequence		
Protein Accession #: NP_075252.1		
75	1 11 21 31 41 51	
	MRLLALLGV LLSVGPVPL SLEASEVEL EPCLAPSLEQ QRDELTVAGL QPVRLCCRA	60
	ERGRHXYKE SRLAPAGRV GWRGRLEIAS FLPEDAGRL CLARGSMVL QNTLITGDS	120
80	LTSNDEPDP KSHRDLNRH SYPQAQPYVT HPQMEKKLF AVPAQTVKFP KCPAAGNPTP	180
	TIRNLKQGA FNGENRIGI RLRIHQNSLV MESVVPDRG TTYTCLVENA GSIRVNYLLD	240
	VLRSHRPI LQGLPANTT AVUGSDVELL CKVYSADAPH IQMLKHIVN GSSGQADGP	300
	YVQVLKTADI HSESEVELY RVVSAKDAGE YTLCAHNSIG LSYQSAWLV LPCTGRPHL	360
	TCSLIPAGR TSKFLQSL ESBSGKSSS SGPALLAGLV SLDLPLDFL EPPFRDLVQL	420
	EPFRDLVQL KPLGRCQPG VVRARANDM PARPQASTV AVNKLKDNAS DKDLADLSE	480
	MEVRLIGRH ENIINLQVC TQGPVLIVV ECAAKGNLR FLRARPPGP DLSPDCPRS	540

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8DPLSPFVLV SCAYQVARGH QYLESKCIH KDLAARHVLV TEHNVMKLIAD PGLAROVNHI 600
 DYTAKTSMGR LKPMKAPRA LKRVKTHGVS DVMKPGILLH EITPLTGSPY POIIVPELFS 660
 LRLBGRKRCR PHMCPPELGY LMRKXWHAAP SQRPFTKQLV KALDKVLLAV SKRTLDLRIT 720
 FGYSPPSGGD ASSTCSSSDS VFSMDPLFLG SSSPFGSGSV QT 762

5

Seq ID NO: 286 Protein Sequence
Protein Accession #: NP_002836.2

1 11 21 31 41 51
 10 HSGLOTCLAT LAQLLLTAAG YFSSGKCLFD KPYSTCGYSQ IGGDDFNWEG VNTLTKPTSD 60
 PMMPSSGLML VNASGRPEGO RAHLLLPQLK ENHTICIDFN YFVSSKSNPS PGLLNVYKRV 120
 NNGPLGNPIM NISGDPTRTW NBAELAISTF WENFYQVIFE VITDSQKCYL AIDENVKVLGH 180
 PCSTRPHFLR IGVNVNAQGO FATPQCSAIV RTVAGDRMLV QGIDVDRDAPL KRIKVTSRR 240
 FIASPVNVTI TEGDAGKYRC MIRTGGVGI SYATLKVVRRE PPVLIAPPOL ASVATPLTAI 300
 15 QLANSHIND GPTFVYVSSV TTAGASTRAD PQMDSTSYKI GHLDRTIYE ILSVLTKEPE 360
 GGTGSGPQAL RTRTKCADPM RGRKRELVVE VKSRQITIRW EPPGVNTRC KSYMLTVHYC 420
 YQVGGQQRVR BEVSMTEHS HPQRTITNLS PITYMVSVELI LAMPEGRKES QELIVYDDED 480
 LPGAIVPTESI QGSTFEKELI LQMRPTQTY GVITYLKITTY KAVSFHPEI DLSNQSGYS 540
 KLGNETHPLF POLVPTIYS FTIAGSTRAD PQMPADQIT TKLSAGMFA YELTEPLNGT 600

20

DNTVTMLPKR AHSKGAPVES YQIVVEEREP RRTKKTTEIL KCYVPIHFQ NASLMSQYI 660
 FAAEFPADSL QAAQPTIGD KNTGVYNTV PLLPYKSYRI YFOASRANG ETKIDCVQVA 720
 TKGATPKPV PEPEKQTDHT VKIAGVIAGI LLFVYIFLGV VLYNKKRLA KKKRTHSST 780
 RQNTYVNRW KQSTAJAQGT KCDAPFMDV TMLKLRVRS EPPSPHMTN TLSTVPSNY 840
 YPDETHMAS DTSELVQSHI YKOREADVP YOTGOLHPAI RVADLQHIT QMKCAGYGF 900

25

KEEYESFPEG QSAPOSACK DNRNMKNRYG NIIATDHSRV RLQTIEDTN SDIYNHNYD 960
 GYHRPHRYIA TQCPQETTY DPNRMWHEN TASIIWTHL VEGVRKCKC YMDIOTHYIK 1020
 DIKYLILTE LAAYVIRT AVRGQVHIEI KRIKQNFQTC WPMQVPMFA TOLLOPQRY 1080
 KSKSPFQSNR LVYKCSAGAG RTQCFIVIDI MLDMAERGV VDIYVCKREL RSRKRVNQT 1140
 30 REQYVIRIDA ILEALCGDT SVAPSOVRLS YDMMKLDQO TNSSQIKREF RLANVTPTL 1200
 RVEDCSIALI PRNHEJRNH DIPLPDRCLP PLITIDGESS NYINAALMS YKQPSAFIT 1260
 QHPLNTVYG PWRILGDYHC TSHLMDLVY PAQLCTQVMP ENCRHREPI QVETYSADLE 1320
 EDIISIRPRI VYASRPOQY RWOQFOFLG WPMYREDTPS KRSFLKLRQ VDKWQEEYIG 1380

30

GEPPTVYVCL NGGGRSGTFC AISIVCEMLR HORTVUVFHA VKTLERHKNP MDLSDQYKF 1440
 CYEVALEYLN SG 1452

35

Seq ID NO: 287 Protein Sequence
Protein Accession #: NP_057635.1

1 11 21 31 41 51
 40 HPIQLQLIYA VLASEHURVAG AAEVPMQNSR GLIEFSVGKF RYFELNRPPF EAILHDISS 60
 NYTFLPIQIH SQVQNTVSF SPILLNSSE TOTASGLVPI LRKPDSCTVM YLQTSQIQPV 120
 QNMALILEYS ERDPVPGGNC LEFDLDIDPN IYLEYNFET TIKFPANAG YARGDVPPPC 180
 DADGTQDSNR RLQDYQYQF IPEHDLTEEN LKRLHQWVS VPOVKASAKL VYTLANDKT 240
 SVFSSSLRQO QVITVIVVD PLFMSAYI PMWYACSTF AGRESKALG RYSSVFTPL 300
 45 PALLGPFICF GHRFRNTEL FFIQFIIISF FFYILITRLT PIKYDMLIL TAVTSGVGM 360
 FLVAVWRFQI ILISCHLCVG LVGLFSLIS 7ZFTPLONLK IPKDDGVFVY TFSCIALIIP 420
 VVPMGICRLI NLITCGVIGS YSVILAIDSV WTSLSLYTL NVLKRALNKD PHRAFTHYFF 480
 QTNDFIILAV NMLAVSGSIT LQIDREKQD PFFPHPYKLM KQERKRRVTN ILDFSTHIFP 540
 50 LRERLYRLT QIKGLPQRQ DAGERTPLL 570

50

Seq ID NO: 288 Protein Sequence
Protein Accession #: NP_003811.1

1 11 21 31 41 51
 55 MEPPGDWGPW PRSTPRTDV LRLVLYLTFL GPCYAPALP SKCBEDYFVG SECCPKCSG 60
 YRVKACGSEL TOTVCEFCPP QYIHLANGI SKLQCCQCD PAKHLASRN CSRTBVARCO 120
 CSRQHFVICO QDHCALACA YATESPQRY QWQTESQDT LQNCPTOTF SPNQTLEQCO 180
 HQTKCSLVLT KAGACTSSHS WYWFLESL LVIVICSTVG LIIICVKRRP RGVAVKVIYS 240
 60 VQRKQBAEG EATVIBALQA PPVTTTVAE ETIISPFGRS PNH 283

60

Seq ID NO: 289 Protein Sequence
Protein Accession #: NP_000943.1

1 11 21 31 41 51
 65 MEPEDSHMD SEPRYTLFPI VYSIIPVLGV IANKYVLMVF ARLVPCKKFN EIKIPMNLT 60
 MADMLELITL PLHIVYQNO GMLLPKFLC NVAGCLFFIN TYCSAVLGV IYNNRQAVT 120
 RPIKATQANT KKKGISLSLV INVAIVGAAS YFLILDSTNT VPDSAGSNV TRCFBIYEGK 180
 SVFPLIHIIF IYVFFVLVFL IILPCNLIIL RTILMOPVGO QBRNAEKHRA LAMWCVTLAV 240
 70 FLICFVHVS VGLPMTYHIL GDRSKSHRA HADANVQLC LSTKCVLPD VIVYLTKEF 300
 RKLHTEKFS HESSKCSRA TIDFTVTEVV PFHQIKNSL KN 342

70

Seq ID NO: 290 Protein Sequence
Protein Accession #: NP_003262.1

1 11 21 31 41 51
 75 GCIGAIKENK CLALLTFLLG LLVFLLEATI AILFEYATTK IDRYAQQDLK KGLHLYGTGQ 60
 NVGLTNHMSI IQDFRCQGV SNYTHDFEY KATRVPDSCC LEFSKCOLM APQWNAKPC 120
 YETVKNLQGE NLGAVIGFOL CTALQVILGL TPNMTRQCV WRADTYCA 168

80

Seq ID NO: 291 Protein Sequence
Protein Accession #: NP_005620.1

1 11 21 31 41 51
 MAKKSASNGI YSVSGDEKKG PLIAPQDGA PAKGDGPGVL OTPGRLAVP PRKTNTRQMD 60

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5 FINSQVQAF GUGNWFEPY LCYRNGQGV LIPVVLIALV GCIPIFFLEI SLQGMWAGS 120
 INWNIICPL KGLTASQNI VPCNTYTYM VLWQGFYVL KSFITTLPA TCGRTMTPLD 140
 CVEIFRHEDC ANAGLANLTC QDLADRSSPV IKFBNKVLK LSGGLEVPGA LNEVTLLCL 180
 ACHVLVYFCV MKGKSTCKI VYFATTFPV VLWVLVRCV LLPGALGDI YLKKPMKSL 300
 GSPQWIDAG TUFPFSYAIK LGLATAGSY NRPNNKCYD AIIIALIDSG TSFFAGFVFL 360
 SILGPMWAG QWLSQVWAS GRLALDAPY RAVTLAPVAP LMLALIDSG LQVLEDSQIV 420
 QVDFQITGL DLLPASYFR PQREISVALC CALCFVIDL MVTQSGHYVF QLDFFYSAG 480
 TLLWQAFGE CVYAWYGA DRIMDIACH IGYRCPWPK WQSFYPLV CMGIFINWV 540
 YEPFLYNNY VYVPMWAGM GWAFALSSML CYPHLLGLCL LRAKOTHAER WQHLTPQMG 600
 10 LHLELYRAQD ADVRGTLTIT PVSSSKSVV VRSVM 635

Seq ID NO: 292 Protein Sequence
Protein Accession #: NP_037464.1

15 1 11 21 31 41 51
 | | | | |
 MKHVLNLYL GVLLTSLIF VRVMESLEGL LESPSPGTSM TTRSLANTE PTKGLPHPS 60
 RSM 63

Seq ID NO: 293 Protein Sequence
Protein Accession #: NP_064527.1

20 1 11 21 31 41 51
 | | | | |
 MGASLGARF YRQIKRHPGI IPMIGLICLG MCSAALYLLR LALRSPOVCM DRKNPFEMN 60
 25 RLSPNDQYKF LAVSTDYKK KDRDPF 87

Seq ID NO: 294 Protein Sequence
Protein Accession #: NP_002195.1

30 1 11 21 31 41 51
 | | | | |
 MGQPSRAPR APRMLCALA LVAAGQGVV SAPNLETRFL VYKAGNPGS LFGYSVALMR 60
 QTERQRYLL LAGAPRELAV PDQYTHRTGA VYLCPLTANK DCCERNHITV KNDPHHIE 120
 DMHIGVTVAS GQPAQRVLVC AHRYTQVLMS GSEDQRHVG KCTVKGNDLE LQSSDQMTY 180
 INHECNSNTD YLETGMCQLG TSGQITSTNY YTGAPAGYNM KGNSTMIQRK EMDLSEYSTY 240
 35 DPEDQNLVI QTYWQGSFI LHPCHITTVT GAFRRHNGA VFLLSQBAG DLRRQVLEQ 300
 SOVQATFQSA IALADLNQD WQDLVGAIFY YPERKEEVGG AIVYFMWAG TSFAPMSLL 360
 LHQSPSARF LSVASIGDIN QOQFDIAGV APFELGKIVY IYHSSKGLL RQPOQVHGE 420
 KGLGPLATF GYSLGQGVV DENFYDLLV GSLSDHIVLL RARPVNIHV KTVLVRPAVL 480
 DPALCATSC VQVELCFAYV QSQGNPYTR NITLAYTLEA DRDRPFRIL PAGESAVFH 540
 40 QALENTEVC PQKECPGNK CESNLQMRRA PVSQQQKLS RLQYSDRVK LLLSINVTV 600
 RTERSQEDA HEALLTVVP PALLLSVRP RQACQANETI FCGLNPFKR NQRMELLAF 720
 EYIOVTLTR DLQVQLQSLT SHIQDLNPM LITLLVDYTL OTSLMNRH LQSPFGGVN 780
 GESMKTVDV WSPKLVEYF VQPMGGLVG LQTLVLGLEM PVEYSNGKML LPTFTYVHG 840
 NQSWCPKPP DLINPLNLTL SDQDRPSSP QRRRLQLOFP GQOQPPVTL AAKKAKSET 900
 45 VLTCAQRAH CWLECPIDP APVYNVTVK ARWNSTFIE DYRDFRRVW NQATLEFRT 960
 SIPTINMENK TTWFSVDIS ELVEELPAEI ELMLVLVAG AGILLGLLI LLNKKQFFK 1020
 RARTRALYA KQKAKMSQ PSTRTSLTD Y 1051

Seq ID NO: 295 Protein Sequence
Protein Accession #: NP_005492.1

50 1 11 21 31 41 51
 | | | | |
 MGQPSRAPR APRMLCALA LVAAGQGVV SAPNLETRFL VYKAGNPGS LFGYSVALMR 60
 QTERQRYLL LAGAPRELAV PDQYTHRTGA VYLCPLTANK DCCERNHITV KNDPHHIE 120
 55 DMHIGVTVAS GQPAQRVLVC AHRYTQVLMS GSEDQRHVG KCTVKGNDLE LQSSDQMTY 180
 INHECNSNTD YLETGMCQLG TSGQITSTNY YTGAPAGYNM KGNSTMIQRK EMDLSEYSTY 240
 DPEDQNLVI QTYWQGSFI LHPCHITTVT GAFRRHNGA VFLLSQBAG DLRRQVLEQ 300
 SOVQATFQSA IALADLNQD WQDLVGAIFY YPERKEEVGG AIVYFMWAG TSFAPMSLL 360
 60 LHQSPSARF LSVASIGDIN QOQFDIAGV APFELGKIVY IYHSSKGLL RQPOQVHGE 420
 KGLGPLATF GYSLGQGVV DENFYDLLV GSLSDHIVLL RARPVNIHV KTVLVRPAVL 480
 DPALCATSC VQVELCFAYV QSQGNPYTR NITLAYTLEA DRDRPFRIL PAGESAVFH 540
 OFFSPMERC QKLELLWEM LQDLRPLIII SMYSLPLRM PDRPLGLRS LDAYFILAQA 600
 QALENTEVC PQKECPGNK CESNLQMRRA PVSQQQKLS RLQYSDRVK LLLSINVTV 660
 65 RTERSQEDA HEALLTVVP PALLLSVRP RQACQANETI FCGLNPFKR NQRMELLAF 720
 EYIOVTLTR DLQVQLQSLT SHIQDLNPM LITLLVDYTL OTSLMNRH LQSPFGGVN 780
 GESMKTVDV WSPKLVEYF VQPMGGLVG LQTLVLGLEM PVEYSNGKML LPTFTYVHG 840
 NQSWCPKPP DLINPLNLTL SDQDRPSSP QRRRLQLOFP GQOQPPVTL AAKKAKSET 900
 70 VLTCAQRAH CWLECPIDP APVYNVTVK ARWNSTFIE DYRDFRRVW NQATLEFRT 960
 SIPTINMENK TTWFSVDIS ELVEELPAEI ELMLVLVAG AGILLGLLI LLNKKQFFK 1020
 RTRTYIMPK YHAYRIREE RYPPGSLP TKHWIWSQD TRDQY 1066

Seq ID NO: 296 Protein Sequence
Protein Accession #: NP_003777

75 1 11 21 31 41 51
 | | | | |
 MDALQOSGL GSKFWSNLS VITENPDLP CFQNSLWAV PCIVLWALP CTYLLSRHC 60
 ROYILSHLS KLVWGLVLL WCVSNADLYF SPFKLVHRA PARFVFPTVL VQVUTMLAT 120
 LIYVYRGLS VQSSQGLVY WFLCVCAIV PRFKILALX AGELEDFPR FTTFYHAPL 180
 VLSALILACF REKPPFFSAR NVDPNYPET SACFLSRIF WMTQMAIYG YHRLPEKDL 240
 80 WSLKEEDRSQ MVVQQLLEAV RQKEQOTARH KASAPAGNA SDEVELLGA RPPRPFSFL 300
 KALLATFGSS FLISACPLFI ODLSFINQF LSLILIRFS NRPAPRMPR LQVGLNICS 360
 HQGLLQHY YHLYLQVY FETGNIQYI KRAYITNIV KRASTVQEI LNMWDQAFQ 420
 MDLAPFNLL WSAPIQLILA IYFLWNLQF SVLACVAGV LLIPLNGVA VKMRAFYKQ 480
 MKLSDRIKL MSRLINQIK LKLYAMEPSF LQVQEDVQK ELQLLRTAY LHITTFVTM 540

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CSPFTVLTIT LAMVVVVFPM NVLDAKFAIV SVSLFNILHL PLAMLPQLIS NLTOASVSLK 600
 RIQPPQSQGE LDQPQVERKT ISPOYAITIH SGTTFMAQDL PPTLHSLDQI VPEKALVAVV 660
 GPVGCQKSSL VSALLQDEMK LEGKWNKGS VAVYFQQAWI NCTLQENVL FGKALNPKRY 720
 QUTLEACALL ADLMLPGSD QTEIQRKGIH LAGQOQRVRS LARAAYSADN ILFLDPLSLA 780
 VDSHVAGHIF DNVIGPQDVL AGKTRVATVH GISPFLQYDF LIVLAAQOVS NRPFTPALQI 840
 EUGSFANFLC WYAFEDQGH LEDSNALAES ADEKALALIE DTLNHTLDT DNDPVTTVQQ 900
 KQFMRLQSL SDSDGQGRF VPRHRLGPSE KVQVTEAKAD GALTQEEKAA IGTVLESVFM 960
 DYAKAVGLCT TLAICLLYGV QSAAGAIQAN WLSAMTNDAM ADSQRNNTSL RIGVYALGI 1020
 LQGFALMLAA HMAAGGIGQA ARVLQALLHI NKIKSPQSFP DTPFSGRLHA CPKSDITVFD 1080
 EVLARVILML LAGTAIST LVMIMASTFL FTVTILFLAV LTTQLQRYFA ATSRQMLEKE 1140
 SVSRSPYISH FSKTVTAJG IYAVNRSDF EIIISDTKVA DNRSCYPYII SNRMLSIGVE 1200
 FVGCNVCVLA ALFVAGIRSS LNPGLVGLSV STSLQVTFFL NMMIRMSDL ESNIVAVERV 1260
 KEYSKTEETA PWVIGSRPP GOWPGRGIVE FMYSVSVYRP OLDLVLRLSL HGVAGGKGV 1320
 IIVORTGAKS SNTLHLEID LAKKEIRID QLVADIGLE DKSQITLII QPILFSGTLL 1380
 RMHLDPFQVS SEEDIMWALE LSHMLTVFSV QPAGLDFOCS EGGNLSVVGQ RQVLCLARAL 1440
 LRKSRILVLD EATAIDLET DNLIQATIRK QDFTCTVLTl AHRIMTIMDY TRVLVLQKGV 1500
 VAEFDSPAHL IAARGIFYOM ARDAGLA 1527

Seq ID NO: 297 Protein Sequence
 Protein Accession #: NP_002692.1
 1 11 21 31 41 51
 | | | | |
 MHFYRLFLGA TRRFLLPENK GEIDNMCVTV LLSLLPFKQI SQDIKALQKE LEQFAKLKQ 60
 KRITLQYQTA DVOLTLGVLF QHYVSQTTIC RFBALQLSPK NMCKLRPLLO KMVEADNNE 120
 NLOEIOAKST LVQARKKRT SIENRVGRHL DNLFLQCPKP TLQOISHIAQ QLGLEKDVVR 180
 VNFCHRRQIG KRSSDAQGR EDFEAGVSFF SGGPVSFPLA PGHPGAPQY GSPHFTALYS 240
 SVFFPDEAF PPSVYTLGS FLHSH

Seq ID NO: 298 Protein Sequence
 Protein Accession #: NP_005449.1
 1 11 21 31 41 51
 | | | | |
 MASPSRSGQP QRPPIPPPPPP ARLLLLLLLL LLLPLAPGAM QMARQAPRP PPSPLPISG 60
 LWFPLKEVAK GSGIQRVLPA VELAIQIRH ESLRLPYFLD LRLDPTCDM AKGLAAFYDA 120
 IYQYDNRHML PCGQVQVQVS IIAVQLQGM LVQLSFAAT PRPLDQKAI YFFRTVSRM 180
 ANPAPLKLK KXVQKRVQVT LTQDQVRFS VNEDLTVGLV GEDIESDTE SFSDNPTCSV 240
 KKLKGNQVRI LIGQDFQDMA AKVFCAYEE NYVOSKQYI IPGWYPSHW QDVTEANSS 300
 RCLNLALAA MEGYIVDFPE PLSSQIKTI SKPTQVQYER EYNNRSGVG PSKHGTATD 360
 GIVVIAKTLQ KAWETLASS RHAGLQYPT DMTFLFTHI NAGVSTFIE VTGVGVYER 420
 ERMTQITFTY PQDSREKVG ENYAVADTLE IINDTIRFQC SEPPKQXTII LEQLRKISLP 480
 LWSLSALTI LQHMNASAFI FNIKRNQK LKNMSPPM NLIIQLGMLS VASIFLFDL 540
 GSPVSEKTFE TLTCTVTHIL TVGYTTAGA MFAKTRWRHA IFPNVWKKK IIKQKLLVI 600
 VQGHLLDLIC LILCWQDQD LKRTKXYSN RFPQGRDVS IRLKLRCBM DMTVTLGV 660
 YAVGILLMLF CQFLWETRM VSPALMDSK YIOMSVYMG IMCLIGAANS FLTRDPPVQ 720
 FCIVALIIF CSTITLCLVF VFKLITLRTN PDAATQNRH QFTQNKQED SKTSTSVY 780
 NQASTSLELG LQSENRHLRM KITELDIDLE EYTMQLQDPT EKKTYIKQH YQELNDILHL 840
 QNFTSTGGG KAILORHLQ NPQLQWTTIE FSKTCKDPIE DINSPEIQR RLSLQPLIHL 900
 HAYLPSIGGV DASCVSFVS PTASPRHRIV PPSFRVWVG L 941

Seq ID NO: 299 Protein Sequence
 Protein Accession #: NP_055632
 1 11 21 31 41 51
 | | | | |
 MEARALRLLL LVVCOCLALP FLAEPVCPER CDQHPQELL CTNRGLRVVP STSLPSPHD 60
 VLTVSLQGHF ITMTATPDIH RFLQRRLRLD QYQIRSLMP KTFEKLRLLE ELYLQRLNQ 120
 ALAPOTLAF AKULIYANO HESILSRGS FSLSESLVQL ELQWALGAL FQVTFPLGN 180
 LYLHLESNR RFLQKQNAFA QLOKLFRLHL SANELQPSLR HATTFAPLAS LSLILSANS 240
 LQHGIRPFIQ HFLRLGLLSL RGNOLTHLAP EAFWOLEAR ELRLGHRLS QLPTALLEP 300
 HSEALQDSG NELASALPAT FQHLGRLEL SLANHALSAL SDIIFAASPA LYRLDLDQNG 360
 WTCCRLRGL KRWKQWHDG QDLTVFVVC RHPFLAKQYI RLYLDLQQLQ HSCDAPSPF 420
 ASLTADRERQ PLPTAGCEIM TPFAQLAEEL PPQLOLQOQG RFLAGVAMQD AARELVNRS 480
 ALRLSRGPG FLSPQSVVAA AAGPAPQSLD LHKXPKQRGF TRADPALAP TPTASPOSAP 540
 SPAGPQWRA TKHRLTEHQ ERAAGSDGCA GLPPLVSPDC DNFKFILOH TLEAVADGA 600
 SVRYAVRHR SPFLQGLGAR RLAQRDFOQ WFRHFRVFLP ESDSSTALAE LQDTVFLVC 660
 VCVYLGQVC PVWQDHQHC LYLTPAAGER DQDVLQILT ALLYNNALV LLAIAAASR 720
 MWRLKLRAR GAGPAGVVRH MYSTRPLES MGTGVSAFDS GFQSHRPRTT VCALSADLI 780
 EFPCCDFMDS AGGQAGGSLR REDRLQRF A D 811

Seq ID NO: 300 Protein Sequence
 Protein Accession #: NP_001783.2
 1 11 21 31 41 51
 | | | | |
 MCRIAGALKT LPLILALILQ ASVEASEGIA ILQCTPFQDM YSAVLSKRVH DGQPLAVKF 60
 SNCKNGKKVQ YESSPADPF VEDCMYAV RSPFLSSEA KFLIYAQKE TQEKVQAVK 120
 LSLKPLTEE SVKSEAEVIE IVFFQFQSKH SGLHQRKRD WVIFINLPE NSRQPTQEL 180
 VR:IESHDNR LSRYSVYTF GADQPPGTGIF IINPISQGLS VTKPLDRDI ARFLHARNAV 240
 DINKQVNSP IDIVIVNIDM NEMRPFELAG VNGKTVPESE EKYTVTQPTI AIDAHNML 300
 NQMLRYRVS QASTPSFRM PTINNETGDI ITVAGLDRE KVQQYTLIIQ ATOMCHPTT 360
 GLNSTATAVI TVTDNDNPF EFTAMTYGE VPENRVDIIV ANLTVTKDQD RHTPANNAY 420
 RISOQDPTOR FAIQIDPNS DGLVTVKPI DFINTENRVL TVAAENQVL AQKIDHPPDS 480
 TATVSVLID VNSRVRFL RFLGRGEL KACTLEPTEI AQDPRYKQD NIVYLSLV 540
 ANWELIDPYN QSTTIAYLD RESNVRKNI YNATIDASE GIPFMSGTOT QLYLVIDND 600
 NAPQVLQDEA ETCTDPDPS INITIALDYDI DPNAGPFAFD LPLSPVTKR NMTIRLNGD 660
 FAQLNLKIKF LEAGIYEVPI IITDSNPPK SNHSLKRVY QCQDSNGDCT DVERIVAGL 720

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GTGATIAILL CIIILILIVL MFTVMHRRD KEMQARQLLI DPSSDVRINI LKYNDEGGGE 780
 EDQDYIDLSQL QPDOTVEDPA IKPVGIRMRD ERPIHAEQY PVRSAAPHP DIGDIFINEL 840
 KAACNDPTAP FYDSLILVDY EGSSTAGSL SSLASSSSGG EDDYIDYAND GPRFKKLADM 900
 YGGDID 906

5

Seq ID NO: 301 Protein Sequence

Protein Accession #: NP_058637.1

1 11 21 31 41 51
 | | | | |
 10 MVSPRMGSLI GQTVILALIF LQTPRAGVF LQIHSPFGP PQGAPRSPG SARLPCRLFP 60
 RVCLKPLSE EAESPSCALG AALSAGKPY TRQKAPAPL LPLDGLQLV PFRDAMPRTF 120
 SFIIETWREE LGDQIGGPAN SLULARVAGRR RLAAAGPMAR DIQRAGAMEL RFSYARCEP 180
 PAVGTACTRL CRPMSAPSRK GPGLRACAPL EDECEAPLVC RACQSPHGF CEQKGRCNEL 240
 EOWTQCLTY FVSTPSLSPG AGPSIATGTC LVKVPQDGO NPGACGSCS ETPRSECTC 300
 15 PRGFYGLRCE VSGVTCADGP CFNGSLCVGZ APDSAYICH CFPFGQSMC EKKVDKCSLQ 360
 PCRNGLCLLO LGHALRCRCR AGFAGRCRCH DLDCCAGRAC ANGGTCVGG GAHRSCCALG 420
 FGGRDCKERA DPQACAPCAN GRQCYAHFSQ LVACAPGTH GARCFPPVHP DGASALPAAP 480
 PSLARPCQPR TLLPFAIGLH VAGVAGACAL LVWVRVRGH SUBAGSLLA CTPEFVHAL 540
 DPLANILKTO EGGDGRGSE VKNRPFEDVD PQCIYVISAP SIYAREVATP LFFPLATGRA 600
 20 QQRQLLFPT PSSILSVK 618

Seq ID NO: 302 Protein Sequence

Protein Accession #: Egenes prediction

1 11 21 31 41 51
 | | | | |
 25 MCQAFIVLGL TLWLJANRAC LQPIYFPMHQ SCLISEANQG QALQPLQWVK WPLHASELS 60
 KSLERKYPFL LMGIEAQCIC KTSSELPFC DLVTADGSTE VTISEMLPAV GFHICQQQDS 120
 HVBMGNISK ASSGQM 136

Seq ID NO: 303 Protein Sequence

Protein Accession #: NP_079088.1

1 11 21 31 41 51
 | | | | |
 35 MCGCGSRADA IEPYRYSWT RETESTWILY TDSDDAPPSAA APDSGPEAGG LIHSMLDEGL 60
 PBNVYFPIIA PQPIPIYFPIA TQPIQCCNHP QLSGGPLTQ KQNGLQTTEA KKDARMPAK 120
 EVTINVIDS1 QQDREBRIT KNCVH 145

Seq ID NO: 304 Protein Sequence

Protein Accession #: NP_040550.1

1 11 21 31 41 51
 | | | | |
 40 MDADGETVVL KNLIGINLI LLSGMIKPE QLEWVITER QRSVESEG IANYNTSKE 60
 QVVYFRIYIN INVPLDNLCS SGLSAGDGE VSRDGTALR VMQTSRSHS QVTFIRHIF 120
 PKACPKASS AQVQLLELR IFMLREYSYV LKQCNMCC QSAATQGLD YIFPCSGKN 180
 45 FFESEGCCIC KNEWGKNCES EPHYCPLGCS RGVCVGQDCI CDEYSGDCC SELRCPTDCS 240
 SRGLCGDGRV CDEEPTGDED CRELRCPDCC SOKGRCANOT CLCEBYGVE DOQQRCLMA 300
 CDRGRCCEBG LVCCEBOTGQ PCDSAVAPPE DLKAVGISDR SILEWGDPM AVTEYVISTQ 360
 PTALGGLQLO QRVPQKSHV TITELPGLT WISYPAVIS NISLPIATAK VATHLSTGO 420
 LQKFTITETT VEVCHEPFSF SPCMEISFI PKMNEGVVIA QVSDVTSEN QCLKPGEEK 480
 50 IYRVVALKEQ ASRPPTSAGV STVIDGPTQI LVRDVSOTVA FVEMIPPRAP VDFILLKVLG 540
 VQGEGRITTF KLPPLSUSYS VOALRQSGSY EVSVSAVROG NESDSATTOT TTEIDAPNHL 600
 RVGSRATSL DLRDMSGAE VOEYKPYST LAGSQYHEL VSRGIGPTTR ATLTLVMTG 660
 EYGVGISAWK NSQSGVPATH NARTELDSPR DLMVTASSET SISLWTKAS GPIDHYRITF 720
 TPSSGIASEV TVPKDRSTSY LTDLEPGAAY IISVTAERGR QQSLESTVDA PFGFRPISHL 780
 55 HPSHTSSSV WITSDSPESP ADRLILNYSF KRESEEMNEV SLQATRHAV LQALQIPATY 840
 IYMLVAMQOT VTGSLGSI TCEIOPDGI TI DVTDKDVW TMSYSPVVAS DYVTSYSTR 900
 TQVRLDSSV VPKVTYFTFI TRLPATETE ISLMSVGRGE ESERICTLHV TANDVPDLI 960
 ATNITPTAEL LQWAPGVGE ENYIVLTHF AVAGETILD GVSEERFLVD LLPSTHYAT 1020
 MYATGPLPTS GTISITNSTL LPPANLITAS EVTRQSALLS WQPRACIEN IYVITYKSTG 1080
 60 SKELSLVDAS DYTIRISALL RQDTYTVLLQ LAGDTWGGSI ALRATFTGGR VFFHRQDQ 1140
 HMLKDTLGE YPIPLKNGEL SGLQWLCYM TDDGSDMVF QRRKQZOTF PRQWADRVG 1200
 FQNVDEPHL GLDNIHRITS QCYELARVM RDKQQAAPAS YDRFSVEDSR NLTKLRIGST 1260
 NOTGADSLSY HQCRPFSTED RNDVAVTMC AMSTYKAMWY KNCHRTNLNG KYGSRHSQSG 1320
 65 IYHVHKGHE FSIPFYEMHM RPYMHRMLAG KRGQSLQF 1358

Seq ID NO: 305 Protein Sequence

Protein Accession #: NP_005874.1

1 11 21 31 41 51
 | | | | |
 70 MASSVAPVEQ LVKQFALKLA ENSHLQELR DNSSHLKLE TETSGMKVEL KHLQCKLQE 60
 ARVLVSQQT EVLEQLKALQ MDITSLYHLK PQPPTLGPE AARTPGSEV HSGSPKSGP 120
 GLSRATILIE LEELDEBQCT LMLIEIKREK EKLMYTSGLQ GLSKRLDELQ IYVTOFSPQM 180
 DLINQLEPFE AQTLKESKEL RYTSRDEWQK PQPTASLRL QIDKLELQAG DYVTSYSTR 240
 75 LLAVKSPVD EDETEVEPTI PEDOTPQPN SKVEYFVML SMLATRQED TARTLLAKSS 300
 SPSCVAMRR SGCLPILLQI LQTEAAAGG RAGAPGAPGA KDMRMANNA LBNIVFSPQ 360
 QGLARKEMVR LHWLQIGIRAT CETCDWJGA EDKGPBEKGA GSAPIPIEPQ ICQATCAWPK 420
 LSFLDGLA NMLGSGALL AELQGLDYIM HWYRDEGLWL AKQAAATVRL TRLTDEGVR 480
 KATLCARRCG MEAIVQAQAS DSEKLIQVVS SILRLMSRA DINSKVLKLE AGSVTALQC 540
 80 VLKATKSTL KSVLSALMLH SAHSTENKAA ICQVDGALGF LVSTLYTKCO SHSLAIIESG 600
 LBNIVSVSL VATRDYRQV LWDNCLQTL LQHLTSHSLT IVSNACOTLV HNSKASAKQ 660
 ELLMDLGAH HMLKESGAL HLEKQNSMA LKTLAHLRA WQAAATVAS POSCVPSLV 720
 RQRLAEATL DAKHLQAQLE HLEKQFPFRA EAATKKPLP LBLHLDLQAG VLDSSGCTDD 780
 DAPSLAAGA AATGEAPASA ALSLPLGSPF LQQAQALRPT FTRRGKRAE KOTSCAAVA 840
 AKAKAKLALA VARIQDQVED ISALHTSSDD SPFLSSGDPG QEAPRKGRAQ SCSPCRGPEG 900

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	GRREAGSRAN	PLALKAANA	SLNDNSLNSG	SASDGYCPRE	HMLPCFLAAL	ASREEDPRCG	960
	QPRPRDLDD	LPOCCAEPPA	REATSADARY	RTIKLSPTQ	HVPLLEGASR	AGAPPLAGRG	1020
	ISPGARKQAM	LPADHLRKVP	EKLAAAPLVS	ASKALQKLA	QEOPLSLSHC	SSLSLSSSAG	1080
5	IKPQSGKGLD	GDSSLSHLEL	KKAGPSEAEI	DSTWRAPGAT	SLPVAIPAPR	KRRSGGLQVE	1140
	DATPSSSSSH	VYQSTFVMSL	KCSVSSVGLG	VSFSPSLASS	PSFPCSCQGS	GTTFSELEDD	1200
	SPQSTMPFPR	SKTPALALAP	QGPSTATQFS	LQWSTVGRF	LOJADCHERC	PLRSELDAQS	1260
	VRTFVEKQPE	NTPSCASSLSA	LALMHYVQO	DVELRLLPSSA	CPEKGGGAG	AGLIFAGHRR	1320
	REEGPAPTS	RFRGAADQEL	ELRLRCLGAA	VVARLRKVAS	ALVPGRRALP	VPVYMLVPAP	1380
10	APAQEDDSCT	DSASGTFNPF	SSAASLSDET	LQCPREDQGG	QFAGKQRQPT	RFTTSRQAQC	1440
	HNUKAGQAG	SARGSCGAG	VRAGLELPLI	RPPGAPADD	GSPKRTGG	CALQSLCLIT	1500
	PTTEAVICFY	GNDSDKEEPA	AAPTTHRTKT	SAIPRAFTR	RPOGRKEAPA	PSKAAFAAPP	1560
	PARTOPSLIA	DETTPCYSLS	SSASSELPE	PSKPPAVHPR	GKRPVTKDP	GPOGKSDSP	1620
	SPRAAEELQ	RCISSALFPR	RPVSVSLRRK	PRATKILDER	PAGDSREGE	EAAGSDRASD	1680
	LDSVWRATC	EDAPALWEL	NQAALNTRFA	SSGSSSLTGF	USGLQSVSTI	QPPKURKGR	1740
15	AEQEGSSAR	PKKGAASVCK	TSGSPRSFAG	FEKPRQTQK	TGQVPAVLRG	RTVIVVPSPA	1800
	PRAQPKTGP	PRATPRKVP	PLCAQAPAA	KVPSPOQGRS	RSIHRFAKTS	ELATLSOPPR	1860
	SATPPARLAK	TPSSSSSQTS	PASQPLPRER	PPVYTAAGAL	PGPCASVPK	TARTLLAQQ	1920
20	HKTGRSPVI	PMKGRPARQ	PPPLARAVPE	PPKPRACETE	AGPCARGRL	GLVPLASGL	1980
	SGSSSDRSQ	FRNOLTFKE	SGLERRARE	LSASASAQA	PGASPRKRC	PALPAVFLCS	2040
	SRCEBLAAAP	RQCPAPARQ	PFAARSPQRE	RFARITTSSE	PSRLPVAPRA	ARPEVVKRYA	2100
	SLPHLSWRR	PGVAPAPAA	SADAARSSD	GEPRFLKPA	AGCTTMRIR	DEDVHILRES	2160
	LTALATALFLR	GSTPEADAPG	PPKRTSDAY	VOTGEPAAPK	TNSTSTSLSE	TREPPCAPAG	2220
	QQLSLLSDSN	DOPLARAPI	SAPFVHGDLG	WAGGTFPASR	HGSPRSARV	PFYNYVFSM	2280
	VVAATIDSA	EKAPATASAT	LLE				2303
25	Seq ID NO: 306 Protein Sequence						
	Protein Accession #: NP_006356.1						
	1	11	21	31	41	51	
30	MFILTDLLTF	MLANLILLPL	VESSFSFGAG	GFCTTLPSFT	LAVDGRATSS	TTDSRAPFSS	60
	PFKPGTSMCK	DISTRETCRE	LCVLPLRTSQ	VPIVWAFQHD	QEKFMIDAYS	CLCKSPSMNN	120
	QQLYQYSTSS	LALGLAWLHM	ETTKKNVLLIL	VGDLSD			156
35	Seq ID NO: 307 Protein Sequence						
	Protein Accession #: AB32726.1						
	1	11	21	31	41	51	
	MASTRSIELE	RFERKDKHPR	KSGRGAPSS	SGGSSSSGPK	GNGLIPSPAH	SAHCSFYTRK	60
	TLQALSHREK	AKXALFYNG	YSGKGLFVA	DSSTSDSTO	ALLILHLESL	SHVNLVLPQV	120
	RTIYITDGSR	KVTSLEDELE	GESVYCASNE	PFKRYDYTN	INRHSVNIK	GTTSRALAAA	180
	SSKSEVKES	KDFIKPKLVT	VIRSGVKPK	AVILLNKKI	AHSFQVOLD	ITEAIKLDGS	240
	VVKRLCTLDG	KQVTCLODF	GDDVFVACG	PEKFRYAQDD	PVLDSHCVK	LKSYTSRSHA	300
	KVTSYSGSKP	PSRRSRAQ	VACTPQDLS	TKWTSKSSSS	SPTSQSGFR	LKI SANGRES	360
	SVNKGELD	KCTSEEDVNG	NKCSSESTLL	EKVIKGVIV	DGNFVVKEC	DRSTOKFEA	420
45	KLIIKDACC	KGERLHNEV	SILRKVKFPM	INLVEHEMT	ATEFLVLMEL	VKGGLDFDAI	480
	TSSTKYTERD	GSNMYNLAN	ALRYLHGLSI	VHRDIKPNL	LCVETPDGT	SLKLGDFOLA	540
	TVYRPLVTV	CGPTTVVAPE	IIAETGVGLK	VDINAGVIT	YILLCGPFF	RSBNLQGLD	600
	FQQLLAKLSE	FPAYVWYIT	DSAKELISDM	LQVNEASCT	AGLISHPWP	SDASQSRMM	660
	QAEVYGLKLG	HFNALPKQK	STTTGVSVIM	FDLTV			695
50	Seq ID NO: 308 Protein Sequence						
	Protein Accession #: NP_055978.2						
	1	11	21	31	41	51	
55	MBNMEELCK	PVQGSFYREF	IIILPCSNLC	QACANRILVO	TPSESPOSH	KAAGSOVEY	60
	DTLDDSHML	TSADATYNG	YGGPARAPIT	POKSPMPVR	VPPFMAPPA	THLSPALAPV	120
	PRNSCTCTPO	CHRSLLDOR	GLGFPFNRK	LEGVIDRYQ	SKAALAKQL	CEKAPKEATV	180
	MCEQGVFYC	DCPLRLCHPP	ROPLAKHRLV	PPAQGRVSR	LSPRKVTCT	DHELNDNSMY	240
	CVQCCHPVCY	QCLSEGRSSS	HEVALKAGM	KLHKSQLSQA	INGLSIRAKE	AKFLVQLGNS	300
60	WQOGLIYR	EFACELVAC	DALDLDMLRE	KAGLLARNNK	DRHKLKVR	DOIISCTYVL	360
	ROTLGLMEYC	LEVIKENSDS	GFLOISDALI	RVHVLTEQD	GKGTLTPTMT	TFDPLSLDS	420
	PLLQSHQLD	FVQVKASSVP	PATPILQLEK	CCTHNSNATL	SWKQPLSTV	PADGYILELD	480
	DONOGQPREV	YGVETKTCV	DGLNFIKNTQ	ARVKAANKTO	VSPTKSTLVL	QTSVAMPAP	540
	DPGASNDII	LSKRLTCTV	PSYEDRVGLQ	KYPSGKSHY	QALQWKSQV	HYPKAPVAF	600
	MVWKMDSML	KDKKAWATY	DNRKSPFMAN	NSHTWREDS	ITKATGVOL	LDLNRKMLT	660
	FINDEQGPPI	AFDNVEGLTF	PAVSLMRNVQ	VTMLTGLVP	DFYSSASIA		710
70	Seq ID NO: 309 Protein Sequence						
	Protein Accession #: NP_118025.1						
	1	11	21	31	41	51	
	MEDLSHVRK	IVDETLDFOG	LSFSDSREEE	DTYLVTPER	FLRKLSHRS	DPNAVAPAQ	60
	QVRLSLGFLS	PEGLRLVLEI	ANGLAAQLQ	CLQKQKSGH	RELGPFRVK	SFRRTFVLE	120
	DSPVEDLPT	VNGLSTRSTP	PSSLTPRLRS	NDRKGSVAL	RATSGKPSFN	MKRESPTNL	180
75	FPASKSPASS	PLTRSTPTVR	GRAGPSGRAA	ASPTPTIRSV	LAQFSTNSG	QRLPFGQGA	240
	AKSSGLPLP	SAIPPIASRM	PLTRESVFPQ	RGALPDSLSS	TRKGLPRFT	AGHRVRESQ	300
	KVPVSQLRL	PVWKAIRSNL	QPRKRVAVPG	PTR			333
80	Seq ID NO: 310 Protein Sequence						
	Protein Accession #: rat XP_166946.2						
	1	11	21	31	41	51	
	KGSDSLRFPM	REKSGOOKAG	WGALLAEVK	NGQLKLCSMM	LVJKAELVEW	YTSVIVQOQG	60
	HLRLKDLAKE	RHRKYLQPK	IKRCSGLMGL	NNSLRFAISS	SLPARSQKH	HGAKRGNGVK	120

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ALSFRLRLK KRPPTPPSQA KSWRCRTGSA ADSPGAAMAA VQALLSTHP FVPPFGOSGP 180
 DGLGAPVAL DKGALLS GARGGVFRA TRMLSFDS ASMLTALAD 200
 KPKSKSRKON KRNAPTVAAP NHCKVAPRE ASQAAAASL QSSSLAALFD SLRHVPKGAQ 300
 PAGOGEVAPR AGGLGAGTQD AGGDVAPAG ATAIQDARK PLRARNLPSF FPTEPSRAQG 360
 GCGCGPGSDV SLGZLEKGAE AVIEFFELLGP DTGNGTEAV LLAELPLDFV PAGAIVLRSP 420
 PELKGLPDS PNAKGVRLN PUNHGVKPS FTXSSTLTP AGGLTLMPL SPYLAAPAS 480
 GPGSECRGHL ASFAFPFPCD ALPPTPPPHQ VSDYSAGYS RTAYSSILMRS DQWKGARK 540
 EGJNRD 546

Seq ID NO: 311 Protein Sequence
 Protein Accession #: NP_071406.1

1 11 21 31 41 51
 | | | | |
 MAPTKPSFG DPSKRLRLQA LRKSSPDAA RSRGKENTF FTELAKLPL PAATTSQLOK 60
 ASIRITLTV LKMDPFANG DPFNLMEDG PPFYTSVKCA QRSSSPALSA IEVFRMILGS 120
 HILQSLDGFV PALMGQKFTL YISETSYTL GLSQVELTGS SVDTVIRPG NVMADQLGM 180
 KLPGRGLLS QCTADEGAS ASSSSQSETP EPVESTSPFL LTTNTWTLRS FFIRMKSTLT 240
 KRGVHISBG YVHIVITGRL ELKRVLSRGK TVPSITMLV VVAHAPPT IEVTRIDCM 300
 FTVRVMLGL IYCNELRIL DMELTPDIV QKRCFTFHA EYVSEIRSH LOLLAKQCV 360
 TKYRMKMNQ GYIWIQSSA TIAINAKNAN EKNIWVWYL LSNHYKYETD MDIAQLPLP 420
 EKTSESETTS DSSISDSKOTS GITEDNENSK SDEKQWSEN SEDFPEDRK SGNAQMDNMN 480
 CNDGHSRNN PGRSGSDSFH SHGDFENHKA GHDGFGALGA MQIKVETVE SSDDLALQC 540
 SLSLTSNAD SDSAQJAGQ ASGSHQKKE PRHQVGGGA SRRLSSSSS PGDLALGLVE 600
 PRLLSLSPNS ASVLKIKTEI SEPINTDMS SIWYIPNRE ISRNSPYSM TKPPSEHNP 660
 SPQCGGGGCG GGGGLVAIPI DSVLTPPGAD GAAARKTFQG ASATALAPV ASDPLSPFLS 720
 ASPRDKHSD GCGGCGGGCG AGCGGSPASH SLTYTDLGLA LQLQKQHTV PLFHVIRVTP 780
 LAATSTAKR VTCCTGSAI PACYLANAG NLLPAHAAH PLYMNSGTF LDVTFHMLG 840
 YHVYRLNMS GFFGAGVMSA SLTQMPAGNV FTIAELFST LPPFVYSNGI NAAGLTLRKG 900
 D 901

Seq ID NO: 312 Protein Sequence
 Protein Accession #: NP_005797.1

1 11 21 31 41 51
 | | | | |
 KQSDASLVSE PPSSEFDDL PLPARKSGS GAFTTOOTVS STTPSDCPPE LSALACAMQ 60
 SAGAKRMLD GSGCFKSSRS STSSSTSSAA ASSTKIDKKQ MTEPEQLQLR LKINSRERK 120
 MHDLIANDQ LREVPYAHG PVSRLESKIA TLLLRNYIL MLTNSLFPMK RLVSFIYGH 180
 HAGPIHSPAC GLAHSAPLPA ATAHAPAAAH AAHPHVVHNP PLTPAJAANA AAAAANAAS 240
 ASLPQSGPLVS VGSIRPHGL LKSPSAAAAA PLGGGGGGSG ASGGFQHMGW MPCPCSMQCV 300
 PPFHRSVSAK GAGSLKRLTS DAK 323

Seq ID NO: 313 Protein Sequence
 Protein Accession #: XP_045127.3

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 70
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1 11 21 31 41 51
 | | | | |
 MTVLEESSIS LMSSVVADFS EFEDDPQVFN TLFPSPPIVP LSSRSMEISE TSVGISAEVD 60
 HSBVTTTQV PAHGRGLVPA SLDPQAGSL VAPTQVTPSS VTTAFVSVIT SILLDSFSFV 120
 IANKVTFSLR VDDPSFTPT SLRVPSSEL PQCGRSRPS EHKPRCALQF ASSTFTPTPL 180
 ELKSGISBS EAPASLELMP SLSLPTPSQS FSLVETFTL FDSLDQSGQ LSLPSTMLE 240
 FSQOLQPSSEL PLMTIMLLPS RSEVSWSFF FSDSLFVEA STVSLTDESA HFTSAFIET 300
 SYLESSLISH ESATVALVPP GSESDILTA QIATSPILT VHTTPTLTS SLFSTLTPD 360
 DQTSALDQIV SYLASFHAI PTOTYLITDA TLFSGSPVS SATVPLPTE LTVQVSLTP 420
 TEVLNLTETE VETTSIGAT GGLDSTLAD DAASGSPFE SAAPFLSLR PVTAFTLEAT 480
 VDTPLATAK PPVCDITVP DAYLITTVLA BRAVQYIIT AIKEVLEINH NRAVELKYVE 540
 LFTDFTLATV SGPPVYTAIS VINVLINSLK VRDQTEPLS VKPSFLWPS RFQVQTVLQF 600
 VFPVSVDTPF NTFGRLEKL HTALVEVRKH NQOTDMLQI LMITIISGR VTPARQPMH 660
 IFPAVSTQCF LKGSVSELL RLKLVPSFT VLOYPLQIA EFPVQGLML SGLKLSMKR 720
 TVLLGQNEKQ LQNEVFQLEM ERKLQQLLSE VSTRRRMWR ATVAAGNSV VQNVNLSLEG 780
 DNNFVQLIYF VEDQDGERLS AVKSSDLINK MDLQRAAIL GYRIQGVIAQ PVDRVKRSP 840
 EBSGNSLNVV VGVVPLVLV MVYIVILWIK LCKTDKLDQ PRTVANHQR GLQIVPSHG 900
 FTFAPQKQLO KHKGLTIN HEPALPQKQ DHTTSDKNG VPSRSPKISF NVYHVRKIS 960
 PEDADTSVE SESEKEDAGK TPAUNDGRS NRPAGSGPL PEGSNQJMS ASIPEHVDRI 1020
 SPPEASRVR PSKILQIAMQ PIAPPPVQRP EPAURVAEN KINKIKOTAL RKSEIEBUR 1080
 NIKIRLANKR GHYEFVVDV LSGDCTKERH RVYRAQMCI DKILDPTAV HSVPIFRKS 1140
 SLIKSVKVR KSHQVNGCA DAKKRLTITL DSDQYKTFV QVNNASVTC PSDQLPAJN 1200
 QTPSSVELGR FYALPFPASQ YIFQPSIEE ARQTMHSLD DAFALVAPS QVASTAGVGP 1260
 GVVPLPIANS TSQDEERAT QWGSFYSPAQ TANMPCSKYE DYGMTPTGP LPFGFGGGL 1320
 LQSTLEVLTP PQQPAQASAE PFAARGIYSE EMSVAPRPP VQOTTGSOIQ MLTVOGIASR 1380
 LQAGVVEIIP BRGSGQNGR WPKGIDEAG ERSAPVWRSQ ERSAPVWRSQ WPKGIDAGGL 1440
 GVTFSSSTDL QPCHSSASLI KAIKEELRL ELKQKSTQNF HS 1482

Seq ID NO: 314 Protein Sequence
 Protein Accession #: BAC04820.1

1 11 21 31 41 51
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 MAPPLGLPIV LALOGAAAVL GGVLFILWKT YFGGRERRR DRGAWWGAE AARLPEDKEM 60
 DPEDEEPEP ALLELRQREV LVGLSDGAK STFLRVLSGK PLEKRLPIW GFNSVRLPTE 120
 DFNVLQIIG GRBLPLVH EPVRSVPLV PVGQABRL LPWAGDELAK LKQDPLPV 180
 VVANKQDLS KAMSGELQR ELGLQAINQ REVFLLAASI APAGFTPEP GTVIRIMKLL 240
 ELLS 244

Seq ID NO: 315 Protein Sequence
 Protein Accession #: NP_066563.1

1 11 21 31 41 51

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MARRAGARM FQSLLLFALL AAGVAPLND LPEPESBASK IIVHSRQHLM ATGMFMGKKS 60
LEPSSPSGAG QLTPTPLRQD RIQLSHDLIG ILLALKALGV SLSPAPQIQ YRRLVLQIQ 120
K 121

Seq ID NO: 316 Protein Sequence
Protein Accession #: NP_002046.1
1 11 21 31 41 51
| | | | |
10 MERRRITSAA ERSYSSGDM MPQGLAPGR LQGTSLSLA RMPPPLPTTV DFLSAGALNA 60
GFKETRASER AEMLEMDRF ASYIEKVRFL EQQNKALAA IQLRAKEPTV KLDVYQAL 120
RELRLRLDQL TANSARLEVE RDLNADQLAT VRQKLQDRTN LRELEANNLA AYQEADENT 160
LARLDLERKI ELEEIEIFPL RTHHEEVRE LQQLARQGV HVELDVAKPD LTALKEIRT 240
CYANASNNH HEAEVHSK FADLTDAAR VALLAKRKA EANDYDLSR ELTCDESLR 300
15 CTNSELQRQM RQEEENHRE AASVQELAR LSEEQSLKD EMARHLQPYQ DLAVNKLAD 360
LEIATYRKLK EGRNRTIIP VQTFNLIQIR RTSLTQSVS EGRLEKNIVV KTVNRDGEV 420
IKESQENKD VM 432

Seq ID NO: 317 Protein Sequence
Protein Accession #: AAA19191.1
1 11 21 31 41 51
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20 MRLSSLSGS SVSSDAEYQ PPIHKSYLTY LQGEAPFRKR IICPREVNR PKTYGEPHG 60
IISREQADEL LQGVGEATIL RESQRQPCY TLALRFQMT LNYLRFNDK HFVGEKRFES 120
IDHLYTDGLI TLYIEKAAE YISKMTNFI YEHIGYATLL RKKVSRRLER SKNEPRKTNV 180
THEETAVAK ESSLVRAAL TDGNHNYE KTHPFKVTTF RQPHMCITCA MFMGLLIAG 240
VRSCDGLPV HGCSEHNVN DCPGLGKIK KYTCGLTTL VQAMTQSPH VVICIEIS 300
30 ARGLSGELYI KVSQFTETIE DVNMAPDRG EKADISANVY PDINIITGAL KLYFRDLPI 360
VITYDTYSK IDANKSNAD ERLEAVHEVL MLPPNAYET LRYLMHLK KVTNEKDNFM 420
NAENLGIVPG PTMRPFEDS TLITLDMKY QKLIVQILIE NEDVLF 466

Seq ID NO: 318 Protein Sequence
Protein Accession #: XP_113553.1
1 11 21 31 41 51
| | | | |
35 MKRAHPEYS SDSELDETIE VEKESADENG NLSSALGSHS PTTSSQILAR KRRGIIIEKR 60
RRDRINNSLS ELRLRVPSAF EKQGSAKLEK AEILQMTVDH LQMLTAGKK GYDAHALAM 120
DYRSLQPREC LAIVARYLST IEGLDASDPL FVRLVSHLNN YASREAAAG KHLGLHLPW 180
GYVPRGRIPI AEILLPLQG HGNAGTASP TEPHQRGLQ SAHFAAPLA APSSSLGPV 240
40 LHYVTSASKL SPFLLSVVAS LSAPFFSPGS FHLLSPNALS PSAFTQANL KPYRPMQTE 300
IGAF 304

Seq ID NO: 319 Protein Sequence
Protein Accession #: NP_001927.2
1 11 21 31 41 51
| | | | |
45 MTTAKEPSAS GKSVDQDEE LVGSHFPQM MGIATALLV ILVICELIVT SVILLTAEED 60
NLSQKKVKT VEDLFSEDF IDGSEAWIS DTEFTYREKQ GTVRLMWKIT NSTYLIHQK 120
KIESLAIERY EISDPREYAL PSYNVEPIY HSYTQYVLS KIPHQDQSL DPPEVSNAL 180
50 QYAGWGPKQO QLIPIFENNI YYCAHVQKA IRVYSTOKEO VIYNGLSDHL YEEELKTHI 240
AHWSMDGTR LAYANINSGV VINHELPITT GSIFYPTVKP HYPKAGSEPH SISLAVIGLS 300
QYFHELDMP PDSPPHRYI ITWVKATST KVAVTMLRA QWISLITCD ATYQCTIKK 360
EDESEAMLER QNEEPFVSKD GRKFFIRAI PQGRGKGYH ITVSSQPHS SNDNIQSITS 420
60 GMDVTKILA YDEKGNKIYF LGTEDLPRR QLYSAMTVN FNRQCLCDL VENCTYFAS 480
FSHSDMFLP KCGQGVQWV TVMTTDRKK MFOLETENH KKAINDRQHP KUYEHDIEID 540
55 DYLPLGILK PATYITVPT PLLLINDPT GDSQVAFKE VSHETPHSS IGNAVVKCD 600
RSGSQOTKL LHEVRRRLQ LEEKQMEAV RYMLAEYID NTRVAVPGD YGYLYSTYL 660
PAKGENOGOT FCGSALSPI TDPLKASAF SERYLGLHL DNRAYMTKV AHRVASLEQD 720
60 QFLINIQAD EKIMFOHTAE LITQLRGKA NYSLQIYPDE SHYFTSSSK QHLYRSINF 780
FVECFRQDK LPTVTAKEE EED 803

Seq ID NO: 320 Protein Sequence
Protein Accession #: XP_007461.1
1 11 21 31 41 51
| | | | |
65 MLPLAALLA ANCLPPVKG GAADAPCLLG VPSNASVNAS SAASPSRGC WPRRPGPPS 60
ARARRRRER RRLCNISVR QMLSSLVRE GRPQFQCDL LLFSTNAHRG AFPAAPAMRV 120
GPPLLEHSG LAGGQAQDL ELCVQGVNR GRETGRLEPA AAFSAARATA GAFTALPAT 180
70 AAHSPFLML CGSEHVECL DFLSELRGE FNGLRKRTI ESTLVACNTE LVIVNSVAA 240
LHNFVPIAG FLRNGMEQRK TASTTAAFT AAYFACITAA AAAAAAANA AVTSQVATK 299

Seq ID NO: 321 Protein Sequence
Protein Accession #: NP_036393.1
1 11 21 31 41 51
| | | | |
75 MDLQGHQVPS IDRLRLVLM PTMAQIMAE QEVENISGLS TNPEKDFPV RENGTYCLMA 60
EFAAKITVY DVNANVGL TREQADIALT GDAVDEKRC HQSLEQLVPM VDRALAPL 120
PVKESIDNSK GREATHRLSK VQVYDVSSE THFDKVASG KHTANSBILE ALVTPAGSKY 180
80 ECQAQTQSL ASSDPKQTV MILGAVHIQ FDIISDPVPS EEMKCPVDR EQLLETPLLI 240
LGLILGLVIM VTALTYVNH KMTANQVQIP RDRSQYNNK 280

Seq ID NO: 322 Protein Sequence
Protein Accession #: NP_653187
1 11 21 31 41 51

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MVVLGIAATP CGLFLLPGFA LQIQCYQCEH POLNDCSSP EFIVNCTVNV QMCCQKYNVE 60
 QSAGIMYRKS CASSAAACLIA SAGYOSFCSP GKLANVCISC CHTPLCNGPR PKRGSSASA 120
 LRLGLRTTIL FLKALFSAH C 141

5

Seq ID NO: 323 Protein Sequence
Protein Accession #: NP_004685

1 11 21 31 41 51
 MTQKRLKCS YANVTETVDP QGQWAVAVS FPFVEVTVYQ IIKTFQVFPN DLMDSFNEGN 60
 SRISWIIISC VFVLTSAPL ATVLNRFPG KLVAMAGLL VSTGWAAFP SOEVSIMYVA 120
 ILIISGLGYC FSLPTVTIL SOTYFKRRI VTAVASTGEC FAYFAFAPL MALAKKIGWR 180
 VSLILPGLLO IAVIIPGALL RPIIIRGPAS PKIVIQENRK QAQYMLENEK TITTSIDSIDB 240
 GVLTSFSPH VHTHTMLRLE FVADNQGVLV KTSRPSSEBK APILLSPILK ERSICTYALF 300
 GLFATLGFFA FSLIITPLGI SLGIDQDRAA FLIUSTAIAE VFRIGAGFV LNRPEIRKLY 360
 IELICVILLT VSLFAFTFAT ENFLNMSCSI FFCNVGTIGT GLTFKLLCKH NSWALQKMS 420
 AAGVTIFIOS IAGLACPLLA GLLVDQSKIY SRAPYSQAG MALAAVCLAL VRPQWGLQ 480
 RHSGSKTVV SHRGKTLQDI PEDFLMDLA KNEHRVWVM EFA 523

20

Seq ID NO: 324 Protein Sequence
Protein Accession #: NP_004824.1

1 11 21 31 41 51
 NESKYKEILL LTGLNDITDE ELDRFKFFLS DEFNIATGKL ITANRIQVAT LMIGNAGVAVS 60
 AVMKTIKIP KINYMILLAKR LQEEKEKVDK QYKSVTKPKP LSQAEMSPAA SAAIRSDVAK 120
 GRAAPRVSF VKPQKQKWA QQSIRSEGO KCLUPMVWLK AKKPTFETO ESKQENFAT 180
 VATEKEFTFV KVDTLGKDL FIPKRIIJA RYVHSFGLF VMSARVLDM ISDQKWNPL 240
 NIIRKAGETV KINTLQTPRL GTVKNGLTVV QVYTKKXHI LFLDLSNTQK MEVLGVNED 300
 TMCKCEGDVY RLTNFTLSKN GELKOLTSQV HSTIKVIRAK KKT 343

30

Seq ID NO: 325 Protein Sequence
Protein Accession #: NP_005400.1

1 11 21 31 41 51
 MEVYKMAIAL LVILCATVQV GPMPFKRGK LCIGPGVKAV KVADIEKASI MYPSNNCKDI 60
 EVIITLAKNK QORCLNPKSK QARLIIRKVE KXNF 94

35

Seq ID NO: 326 Protein Sequence
Protein Accession #: NP_002553.1

1 11 21 31 41 51
 MPACCSGSDV FQYETNKVTR IQSHQWOTIK WFRFVIIISV VCFALVSKL YQKKEPVISS 60
 VHTYKQIAR VKESIVENDV KLVIVSEPTF ADYTFPLQCN SPFWNDFLK TEGQGRGCP 120
 EYFTRFCLS SEBGCKEKNH DQBGKIGTQ KCVHSEKMK TCEVSNACP I EAVSEAPPA 180
 LLSASRIFTV LIGNIDFPQ HMYTTRMILP GLMITCTFHK TQWQCPPIR LGDIFRETGD 240
 NFSDVAIQGG IMGIEIYDC NLRMFIRHCH PKYSFREELD KTNVSLVYPG VNFYAKYTK 300
 ENRVERTLI KVFGRIDFLP VFTQGGKDFI IQLMVYIGET LBSVGLAAVF IDPLIOTISS 360
 NCCSHVYPM CKQCPQCVTM EYTVKACDIS VIMPTFLYK VEFVDSHTR MNQGLLGS 420
 LQDVQKQVFP RPAWDFTLDS RLPLALHDPF PIPQGFEEIQ LKREKATPS RDSFVWCQCG 480
 SCLPSOLPES HCELEELCOR KKPACITTS ELFRKLVLGR HVLPFTLLYQ EPLIALVDGS 540
 TMSLRHCAY RYCATWRFQS QHADFALP SCRRMIRKE FFKSGQYSG FKSPY 595

50

Seq ID NO: 327 Protein Sequence
Protein Accession #: NP_001784.2

1 11 21 31 41 51
 MGLPRGLAS LLLLQVCKLQ CAASEPCRAV FREAEVTLIA GGABGEFQQA LGKVFQCCPG 60
 QEPALFSTDN DFTFVNGET VOERSLKER NPLKIPFSKR ILRHKRDVW VAPISVPENG 120
 KGPFPQRLAQ LKSNKORDTK IPYSITGPQA DSWPGGVAF EKETKLLLN KPLDREETAK 180
 YELFWAWEK AGASVEDPHN IGIIVTQGD HKVFKQCTG KGVSLBVLPL GTSNVGVAT 240
 DEEDAIYTV QVAYSINSO EPKDPRDLAF TIKRSTOTIS VISGLDREKX VPYETLTQA 300
 TEMDQGGST TAVAVVELLD ANENAPMFPD ORYEAHVPEV AVGHREVORLT VTDLAPNSP 360
 AWATYTLING GDDDHFTIT TIPESHQGLI TTKGQLDFA KNQHTLVFV THEAPFVLKL 420
 PFTSATVYH VEDVNEAFVF VPFKQVEVQ KGIYGRPCV VITADPQKE MGRISVYELA 480
 DPACGLWLP DSGQVATGCI LARDEQFVS NITYVWYLA MNQSPPTTG TSTLLTLTID 540
 VNDKGVPEP RQITICNQSP VRQVLNITK DLSPTSPFO AQLTDSDIY VTAEVNREGD 600
 TVVLSLKKFL KQTYDVILS LSDHGNKEQL TVTRATVDCD NGHVTCCPG WKGQFILFVL 660
 GAVILLFLFL LVLLLVHKK RKIKPELLP EDITHDNVTV YSGRSGEDD QGDVTQLR 720
 GLEHRYVYLW KWDVAPLIR TWVRRRPM FQIGIYFIIH MUKAMTDFD APYDTTLTVF 780
 DYKSGSDAA SLSSLTSSAS DQDQVDYILN SWGSRFKKLA DMYGQDEED 829

70

Seq ID NO: 328 Protein Sequence
Protein Accession #: NP_002562.1

1 11 21 31 41 51
 MDIPTQKDL ELPLKACTWK SMAMATNNIS IMATLKAPLR VHTLSLTPF EDHLEIVLWR 60
 WENNSCYBEK VLGSQVIVAN RATLLETDID NPLVLCQUT TTPIGSMQC 120
 YLARVLVEDD EIMQGFIRAF RPLRPLMWYL LQLKMEERC RF 162

75

Seq ID NO: 329 Protein Sequence LK66
Protein Accession #: NP_001318.1

1 11 21 31 41 51
 MQAGRGTOGT STGDADPGG PGIPDQPGGN AGGPGACAT CGRGPRGAGA ARASPGOGGA 60

80

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PRGPHGGAAS GLNQCRCGGA RCPSERLLEP YLAMPFATPM EAKLARRSLA QDAPPLPVPG 120
VLLEKFTVSG NULTRL7AA DHPQLQLSIS SCLQLQLSLM WITQCLPVPF LAQPPSQRR 180

Seq ID NO: 330 Protein Sequence LRK6
Protein Accession #: NP_066274

1 11 21 41 51
MQAEQGGTGG STGDADPGGG PGIPDPGPGM AGGPGEAGAT GSRGPRIKGA AKAPGPRGGA 60
PRGPHGGAAS AQDRCPCGA RHPDSRLQF RL7ADNRQL QSLISBCLQG LSLMLWITQC 120
PLPVPLAQP SQRR 135

Seq ID NO: 331 Protein Sequence
Protein Accession #: NP_008859.1

1 11 21 31 41 51
MDLVLRKCLL HLAIVGALLA VGATKVPRIHQ DMLGVSRLR TKAMRIQLYP EMTAQRLOC 60
NRGGGVSRLV SINDOPTILGA NASFSIALNF PQSQKVLPGD QVIMWNTII NGSQWQGGP 120
VYFQKTDGAC IPGGSGPCPS GSHGSHKSFV TWKTMQGM QVLAGQVQL SIOTGRMGL 180
THHTVYVYV RRGSRGVPVL AHSSSAFTIT DQVPSFVS QLRALQGNK HFLANQPLTF 240
ALQALDPSY LAEADLSYTM DFGDSEGTLL SRALVVTHY LEPGPVTAQY VLQAAILPTS 300
CGSSPVGTT DGHRIPEAP NTTAAQVPTT EVAGTTIPGA PTAEPSGTS VQVPTTIVS 360
TAPVQMPTAE STQTHKVPV VSRNMTLLA EMTPEATGM TRADSVIVL SGTAAQVTT 420
TEWVETARE LPIDFSGPT ASHINSTESI TCSLQILIG TATLRLVKRQ VPLQCVLRY 480
GSFSVTLIDV QGIESAEILQ AVPSQEGDAP ELTVSCQQLK PKRACHESS PQCPFAEVL 540
CQPVLPSPAC QLVLWQILKG GSGTYCLNVS LADTNSLAV STQIMPQGE AGLOQVPLIV 600
GILLVLNAVY LASLIYRRL MKQDFSVQL PHSSSHMLKL PRIFCSPQE EHSPLLSQQ 660
V 661

Seq ID NO: 332 Protein Sequence
Protein Accession #: NP_001913.2

1 11 21 31 41 51
MSPLWGLLL SCLOCKILKG AQGQFPRVCM TVDSLVNKEC CPRLGAESAN VCGSQQRGQ 60
CTEVSQVADRP MSQPTILIGA DDEELWPKRF RHCTCKCTGN FAGIMGDCCK FQWTHPCR 120
KRSPFQWHT HSLDGLAXK RYVQVPTT QMGLGLAN OTQTPAKES 180
VYDFFWFVLY YSVRDTLLPG GRFYRAIDFS HQGPAFVTM RYHLCLLER LQRLIGNESF 240
ALPYMFWATG RNECDVCTDQ LFGAARPDOP TLLSRNSRFS SWETVCDSD DYNHVLTLGN 300
GTVEGLLRAN QMGRNEMMLP TLKDIRDCLS LQKTFMPPFF QNTSFSPRA LSGFDKADGT 360
LDQVWMLHN LVISFLGHT ALPSSANDP LPVYLHSDTP AIFDEWNRK HPFADAWPQ 420
LAFIDSEMY SWYTFPPFV NEELPLDSQ LGYSVAIDL VSVKETQMP TTLVWVHGL 480
VALVGLFVLL AFLQYRRLRK GTTFLMETHL SKRYTEEA 519

Seq ID NO: 333 Protein Sequence
Protein Accession #: XP_059422.1

1 11 21 31 41 51
MNHLPFLLL ASVTLSPICS HYNPLSLEL GSNSTGIQVFN QIVSRPHDN IVISPHIAS 60
VLQMLQLOAD GRTEQLQWLV MYGVNWKV LKRIKMAV SKGRKDITV ANAVVDIAS 120
EIEVFYPTEN KDVFQCEVRN VKFEDPASAC DSNANVQNE TROMDNLLS FDLIDGLVLR 180
LVNLNAVYFK GLWKRFOPE NTEKRTFVA DOKSYQVML AQLSVFRCS TSAPNOLWYN 240
FIELPYNGKS ISMLALPTE SPTLSAIIH HISTKTIDSH MSIMVPRKV VILKPTATA 300
QTDLEKPLAV LGTDWFDSS KAFKATFS DLUNVSHLL KAKIEVSDEG TKASASTAI 360
LIARESPWF IVDREPLFTI RINPTGAVLF MQIIRKP 397

Seq ID NO: 334 Protein Sequence
Protein Accession #: XP_040512.2

1 11 21 31 41 51
MRQHDTRNGR IVLISGRSP CSIFSPLVPR DSTQVGDCLK DGRQSTGAV SLKEIIGLEG 60
VELGADKRV STYQFLPTM AGARLRWID STSPSQPRN LSHASLSGR ASCTQGLDT 120
QSGDLQPMY DWLLDDPM PCGSHKRVLL PSYVTTVID VYKPSDLKD NHTTKRFP 180
HIKLTLSKIR SLKREMKLA QEDCLKEPT VMAFVFYFK LALKGLNWQ NRKLCAGACV 240
LLAAKIGSDL KREVRKHLID KLEKFKRLNR RELIAPEFV LVALEFALRL PEHEWPHYR 300
RLVQSS 306

Seq ID NO: 335 Protein Sequence
Protein Accession #: AAI08826

1 11 21 31 41 51
MTTLGAVPR MNRPGPQNT PRSGCFLEVS TPLQCGRVNQ LGGVFINGRP LPNHIRHKIV 60
EMAHKIRPC VISQGLVSR GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKIKRY 120
KRENPNWSP RIMKLLKLA VCDENTVSV SISRILRPSK PGQGEERAD LERKEARESE 180
KRASHIDGI LSRSLAQQ RRGSDIDEP DLPLAKRQD QSLSTYFANG HLEDAEFT 240
HYDITREE LAQRKLTEA RYQVFNRR ARNRKQA CAN QLMAFHLIP GSPPTAMP 300
LPYQLSETS YQPTSPQAV SDPSSTVHRP QPLPSTVHQ STIPSNQSS SAYCLPSTRI 360
GFSYTDSPV PPSKPSMNM PTICNGLSPQ NSIRHNLSLH SKFIRVQNEG TCKSBWMLN 420
PRCKBCKSP RRDALANR RSTASRERA AKKASLQCG QSGADICPS QFSKSPASG 480
SHRCDPDM STTPRSTSN ASTISGRSP IMTEQDLCE GDVHSWVVP SANWASTLP 540
SLSEINPEN MENLNLML LSPSTSLTVS TQSSPTMQO GTPCYSPAP NTSLSNPSN 600
YQYTYQSSS MSPLPQPIQ TQDNSSSYG GMSQVNCAP LKLETTSDS PPRNDITVP 660
DKVADPMSR VQVPLSTQSG AGRNWRMS STTRPCDAQ TSANRPLV 720
HTVSTHPTS QVRLTQVT PQVPLNPMQ QMSALQDYS VSSCNCYGM CLJLQKRLS 780
DLQMPLEL DCMKESIIRN DLMQDTLDF NFNVLNQS PHSVKTTH SWVS 815

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Seq ID NO: 336 Protein Sequence
 Protein Accession #: NP_605752.1

	1	11	21	31	41	51	
5	MEVSRKRAP	RPRRPAAPL	LLAYLIALAA	PGRGADFPW	RSBQAIGIA	ASQEDQFVA	60
	SGSCLDQDV	SEHSLRSLG	RDGNACCTE	VSLAPFARR	PGSSPKLLI	PIYRQAGLG	120
	GLLITQTFD	SGACTFPIG	NLSBHELRG	TEVMSCHQG	STACVYVRAG	RNNRWLAVA	180
	ATVVLPEPT	ASRCNPAAD	MDTATALKD	EGRLSLATQEL	GRLEKCSAG	SLHFDAPLV	240
	NGSIVFPYF	YNYTSGAAT	WFSMARIAQS	TWLFQOQAS	LDQCHGFPG	RRLLLSSSLV	300
10	EALDVWAGF	SAAGAEQER	RSPTTATLC	FMHSLQARA	KRVSRDFTA	ESHCKSDGF	360
	ERWQYIASL	LHSDLTSPY	QTYVNRWTL	FLDTGQGLL	KVILQDLTS	NCFPIVEYLK	420
	EETPVPKVL	PDPPKNIVY	LTAGKEVRI	RVANCKRKS	CSECLATDP	HCONCHSLR	480
	CTPQGDVHS	ENLEMDLIS	SGAKKCKIQ	IIRSSKCKT	VTVNGSPSP	HSKCNWKNVD	540
	SSRELQKNS	QRHCTCTBI	PTBATYKDS	VWNVSPFS	WGLSDRENT	NCSLSAKCA	600
15	CYSTCAWCK	SARICINPT	ACQSPDYRM	QSCQPVAKK	TSSGQREKH	RQIRHTQAQL	660
	VFYIKSEIQ	KVSLTGSNV	IVTGANFTR	SNITMLWGT	STCDQVIOY	SHVLDNTHK	720
	FSLEPSRKN	KDVCIQDGG	NCSSVGSLSY	IALFHSLIF	PATTWISGG	NITMKRNFH	780
	VIDNLIISH	LKGNINSEY	CVATQCFLA	PSLKSRRVT	INTVKLVQD	TYLDCDTLY	840
	REDFPTTCV	VESEVDEIE	VKIQKSNDF	WSEKDEIT	LFNGKQQLM	CSFNITMQ	900
20	DLTTLCKIK	GIKTASTIAN	SKKKVRKLG	NELTYVEES	VFTSWYFLV	LPVLLVIVP	960
	AAVGVTRHS	KELSRKQSQ	LELSELRK	EIRDGFALQ	MOKLDVDSF	GTVPFLDYKH	1020
	FALRTFFPE	QGFTHPTFD	MRRDANDRH	ESLTALDALI	CHKSFLVTVI	HTLEKQKMS	1080
	WDRCLPASF	LTIATLTKLV	YLTSLELV	NOLMBQCSM	QPKMLARTE	SVPELRLTM	1140
25	MVCLGSLFL	ETWSEFILL	VTLLAQYLNK	GPVDVITCKA	LYLLEMDML	KQVFEFTVA	1200
	LVNVFIKPE	NESADVCRI	SVNVLDCDTI	QDAKEKIPQ	FLSKNGSPYG	LQMLEIGLE	1260
	QMGTRKELL	DIDSSVILLE	DGTTKLATIG	HYEISMGSTI	KVFKRIANPT	SDVEYSDMC	1320
	HLILDSWAF	QVQGRNRIG	KHFFPEVEM	LYLKLSTVA	INHVLEKLF	SIWLSNDR	1380
	PPAIFYTDF	LDQAQSKKI	TQDVFVIMK	TEHLERFNV	NILKQPFVF	DIKKTTHIDG	1440
	CLSVIAQFM	DAFSLQEQL	GEKAPTNNL	YAKDIPTKE	EVSYSKAIK	DLFPLSSSM	1500
30	BEFLTQESK	HNENFEVEA	LTEITKYIVK	YDEILANKL	REGLERBAQ	QLRWLVLPD	1560
	EKKKCKM						1568

Seq ID NO: 337 Protein Sequence
 Protein Accession #: XP_063670.1

	1	11	21	31	41	51	
35							
	MQRILEPAD	DCWSTRILL	TLEFIMSLQ	RTVPHSEKQ	RALSVPSSSY	PQLVGTSGE	60
	LALTFWHLLS	MPQFFIVSYG	FLTAFGRTLF	HLDLQPLMT	PSRFDTYGL	PIYIEKDLG	120
40	DFCPQSKVQ	ILEVLAMKV	ESATHTNDG	TAGEVENGT	SGTQGGGAA	RSRCREMEP	180
	TFEYVYVDV	KGLTLACPVF	LCLFLVMII	RCARVIMDY	SAIPTSWEE	QHLD	235

Seq ID NO: 338 Protein Sequence
 Protein Accession #: FGDNESH predicted

	1	11	21	31	41	51	
45							
	MEFHSQPTM	DMGNQERPA	ASPLKQDQR	QSAQSPLSA	GRGSPAPLGA	LTPAEPGLGS	60
	APRAPRARAP	VTQKRSRRS	AVALGSAAPQ	PGPRERTORA	SPALENSDL	LSKASAIATG	120
	TPPCDEBTHA	RYFLPPLTL	HEELWGTSG	LALTFWILLE	HPQFIVSYG	FLTAFGRTLF	180
	HLDLQPLMT	PSRFDTYGL	PIYIEKDLG	CHGSDPCA	OVNCTSYTR		240
50	GGGGAARSC	RENEEPTPE	VTVVDKGLT	LACPVFLCLF	LVMMIRCAK	VIMDFYSAP	300
	TSTWEEQHL	D					311

Seq ID NO: 339 Protein Sequence
 Protein Accession #: FGDNESH predicted

	1	11	21	31	41	51	
55							
	WQKDPKSTPT	KAMATQAKID	KDMLKLKSF	CTAKKTTIRV	WQPTBMEKI	FAIYSSDEGL	60
	ISRIETHPKQ	YIKKKTNPDI	NKQAKDMNRH	FSKEDIYAM	RHMCKSSEL	AIREMQIKTT	120
	TRCHLTVPKM	AIIKKSGNRR	TAEEDPKLRK	BAVSGEIEFR	FADGLDITLM	ILGLASLAV	180
60	GACPLMPLVF	LGPMNSHLIS	GCLMTNTTN	VQKCTQSEK	IAENMTLLTL	YVVGIGVAAL	240
	IPQVIOISLM	LITAAQRTK	ISQGFPHVL	AQIQWQSD	DIGELMTFTV	DDKIDISGI	300
	QDKALPQNM	MTSPSICLAV	GLVKMKLTL	VTLSSTPLIN	ASANACSRAW	ISLTSKELSA	360
	YSGKAGAAVE	VLSIRITVIA	FRAQEKELQR	YTONLKDAD	FGIKRTIAGK	VLGAQVYFM	420
	YQVWGLAFY	GTSLLWQEP	OTTIGTVLAV	FPVSIHSSYC	IGANVPHET	PAIANGAPH	480
65	IPQVIOISLM	ISLTSKELSA	ISLTSKELSA	ISLTSKELSA	ISLTSKELSA	ISLTSKELSA	540
	LVGLKMSH	YVWQLQRLY	DPEDGIMVD	ENDIRALMR	HYRNDIGVVS	QEVPLFTTI	600
	SNNIKIGRED	VTEDEMERAA	REANATDFIM	EPFNKFTLV	KEGKGQMSQG	QKQRIALARA	660
	LVRRPKILIL	DEATSLDSE	SKSAQAQALE	KDTPREYF			698

Seq ID NO: 340 Protein Sequence
 Protein Accession #: XP_166496.1

	1	11	21	31	41	51	
70							
	WQNDNIRAL	WYGHYDNIG	VVSQEPVLVG	TTISNNIKY	RQDVTEDEME	RAAREANAYD	60
75	FIMEFTFNKN	TLVGEKAQM	SGGQKQRIAI	ARALVRPKI	LILDEATSAL	DSKSKSAVQA	120
	ALEKDTPRYS	F					131

Seq ID NO: 341 Protein Sequence
 Protein Accession #: XP_166305.1

	1	11	21	31	41	51	
80							
	HEKFRVLDL	KYHSHSALG	GLVTLTLAGQ	KEIFSAVAFQ	CPCSAAHMLF	YGLVPLLVPA	60
	LALFLDGLVL	SRNTWELLTG	CCSSARASCO	SALRGSIVCT	QISAAALAP	LTVWAVALLG	120
	GAPYECAATQ	SAAFQRLCL	GRHSRCAEL	PLVPCQAKA	SDVQDLKDL	KAQSQVLQNI	180

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	LIADVITILL	IFTSTVTRCLS	FVSPFLQKQW	KYILEQBQOI	LKSKATEHAT	ELAKBNKICF	240
	FEHSHPKTW	TPSHKQKQI	SSLVITPNFKG	QTYMLKLYV	WRKEKTHSIR	STEGQTVIVP	300
	LQFVDSGGIN	STPEL					315
5	Seq ID NO: 342 Protein Sequence						
	Protein Accession #: NP_115587.5						
	1	11	21	31	41	51	
	MARSPATLF	LFLLLLGQPP	PSRQSLGT	KRLVGFESK	PEDGRLEVLH	QQQMGTVCD	60
10	NPAIQEATVA	CRQLQFPAAL	THASAKRQV	GGPILWLRV	QCVTESSSLD	QCCSHQSHV	120
	DCSHSEGVW	ICFPHREBY	LSTQVSHAL	PGQRLEEVK	LEKPLASAG	NSPVTGAVE	180
	VYKEGHWKQ	CDQGMWNIS	KTVQCHMGFP	SEVPDSSTHY	RKVMDLKMD	PKSKLSLTN	240
	KNMFVHQVT	CLTGETPHMA	QVQVAPARG	KLRPACFGM	HAVVSCVAG	HREPKTKPQ	300
	RHGSWAEPE	VRLHSGAQV	EDKEVLAKH	QWQTVCDHM	NLISASVVCV	QLQSHAREA	360
15	LFQARLOGGI	GPILHSVPC	ROYERTLSD	PALESQWQC	QENIAAAYC	WVVMGHPQO	420
	VRLAGGRIFE	EGGLEVQEV	NOVPRGSCV	SDNGLTEAM	VACRQLGQF	AIHAYKTFW	480
	WSQTPTAQE	VMSGVRCSGT	ELALQCGRI	GEVHCSHGG	RFLAGVSCMD	SAPDLVMAQ	540
	LVQETAYLED	RPLSLQYCH	EDNCLSKSD	HDMVPGYRR	LLKPVSTQIM	LQRTDFPRT	600
	GRDWSWQC	HRVHSIVVF	THYDLTLWG	SVASDHRAS	PLCUDTTCCT	GLQRYKACH	660
20	RSEQVTVGC	WQTVREHDC	QWVDITDVG	GNIFYQIVN	PRHYEABSDP	SNHMLQCRK	720
	YDGRHVLIN	CHTNSYFPA	AELSLBQER	LRLMLI			756
	Seq ID NO: 343 Protein Sequence						
	Protein Accession #: NP_001789.2						
	1	11	21	31	41	51	
25	MEHFQKVEKI	GGTVGVVYK	ARNKLTGFW	ALKKIRLDE	TEGVPTAIR	EISLLKELMH	60
	PHIVKLLDVI	HTNKLYLVF	EFLHQDLKKF	MDASALTGP	LPLIKSYLFO	LQGLAPCHS	120
	HRVLIIRDLP	QNLINTEGA	IKLADFLAR	AFGVVPRTYT	HEVTVLWYA	PEILLCKTY	180
30	STAVDINSG	CIFAEKPTR	ALFPQSEID	QLPRIFRTLG	TPOEVNFGV	TSHPDVKPSF	240
	PKNAQDPSK	VVPFLDEGR	SLLSQMLYD	PHKRIAKAA	LAHPFPQDV	KVPHRLR	296
	Seq ID NO: 344 Protein Sequence						
	Protein Accession #: NP_439892.1						
	1	11	21	31	41	51	
35	MEHFQKVEKI	GGTVGVVYK	ARNKLTGFW	ALKKIRLDE	TEGVPTAIR	EISLLKELMH	60
	PHIVKLLDVI	HTNKLYLVF	EFLHQDLKKF	MDASALTGP	LPLIKSYLFO	LQGLAPCHS	120
	HRVLIIRDLP	QNLINTEGA	IKLADFLAR	AFGVVPRTYT	HEVTVLWYA	PEILLCKTY	180
40	IFRTLOTPO	VWVPTQPM	DYVSPFFNA	RQFSRVVPP	LEDEGRSLLS	QMLYDPVKE	240
	ISAKAALHP	FQDVTKVPV	HLRL				264
	Seq ID NO: 345 Protein Sequence						
	Protein Accession #: NP_116127.1						
	1	11	21	31	41	51	
45	MKLGCVMAN	ALYLSIGVLN	VAQMLAASF	ETLQCEGFCV	TESSCHTED	DLTDAREAGF	60
	QVATRTFSE	PHLVSYDML	ILQGPAPVF	EDLLVLQKQ	AKQGNPLTV	FFYRDSALG	120
	FPFPRPREI	TVYQADSDH	YHCQIFQSF	GGCIPETASV	VAITVSELFP	AFILRAVPSA	180
50	EPQAGSPML	SCQTKPLQR	SAARLLFSYF	KDRIVQSRG	LSEEPQITA	SEDMISGYSVC	240
	EAATEDHVN	KQSPQLEIR	QGASSSAAP	TLMFAPQKA	APGTAFEPD	GFLPFPPTPS	300
	SEDFGSPFL	GMDFPHLYT	MGLLLKMDQ	VVLLGLHLM	ELRELSHGK	POTTKATAE	359
	Seq ID NO: 346 Protein Sequence						
	Protein Accession #: NP_002317.1						
	1	11	21	31	41	51	
55	MKIFPLVLL	ALLGVERRS	LACFSLNQK	SNLYCLKPTI	CSQDNYCVT	VSASAGIGNL	60
	VTTPYLSIKT	CSFACPIEG	VNVGVASMI	SCQSFCLNF	SAADQGLRAS	VTLLAGALLL	120
60	SLLPALLRFG	P					131
	Seq ID NO: 347 Protein Sequence						
	Protein Accession #: XP_113526.2						
	1	11	21	31	41	51	
65	MEDLGNTWV	LSTRLSIANP	ISORVEGSG	LDISTSARGS	LQNOYQOSHQ	LEERAEQIRS	60
	KSHLIQVER	KQMHLSHKR	ARVELRAAS	TSANRYERE	DRQELLTRI	RLQREAGA	120
	EKKMQDLER	WROCOQLNA	AKRLREKED	SLAQGETIN	ALGRISELO	MSWMDQNRV	180
	KRLSEKQEL	GGDLGLCKP	QKANGKLE	LQAQSEKAD	HQQJLQDLO	KLLAQQDA	240
70	IVQNMSSLV	LPLRLERLF	QLRESHALP	DMETGHLQ	ETLELDLQRL	GRQKQMETL	300
	VGLLEENREL	LAKLQWHERL	DOTNGLSIRT	PEDLSRPVVE	LQOREALAK	KNSAVTSASK	360
	GLEKARQQLQ	EELRQVSGQL	LEERKKRETH	EALARRLQK	VLLLTKEKD	MRAILGSTDS	420
	ELTPARYSPQ	LTRHREARD	MYQKVHSHS	EMEAQLSGAL	EELQAGQRA	DMLDMLMEL	480
	KQSSBSASV	PLSRSELAT	LALAVELQD	ESRLESESK	MLAQQLERA	LQGVDOERT	540
75	KYVLINSNPT	SVNRQRLRD	HSQIAQECR	LRGLRANER	GTVVPADLEA	AAALSPSSKE	600
	VAELKKQVES	AELOKQRLKE	VPTQKIERE	KACVTLQYO	IDITTEQYR	LTSLVABHPG	660
	DCLIKPATSP	SGSKQMLLET	EPSTHTVGLI	SVILRRDSTI	PAFLSLLTLE	LPSEGTVA	718
	Seq ID NO: 348 Protein Sequence						
	Protein Accession #: NP_002644.1						
	1	11	21	31	41	51	
80	MTQAGRGSG	TPEEPRTQF	MASFELGTF	CFTRDAATOL	VLSFPQAPH	ALCLSGSGLR	60
	LALGLQLLP	GRRPARGSP	ATSPASVRI	LRAAAACDL	GCLGMVIRST	VNLGFPNFDV	120

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SVSDSEHTEI WPAAPCYGSA MHQILLYSAC FWHPLCYAVD AYLVIRRSAG LSTILLYNIM 180
AWGLATLQY EGAWHLYTTS VTEAKWSPS COHLLKWSR DFVHSVQETH SULLGSDNM 240
ASLKGROGI YTEKERNMGA VIKIRFFKIM LVLLICWLSN IINESLFLYL EMDOTINGDS 300
LKPVRTEAKT TWSGKIVSQV AQGFLLSLAF YGNTCSLGF QSPKQIQWE KNTTSARGA 360
HPSLMPHEN PAFINGPQNG QQTSDALSAL LSGSDASTI EIHTASESCH NMGDFPALPT 420
HGBL

Seq ID NO: 349 Protein Sequence
Protein Accession #: NP_647478.1
1 11 21 31 41 51
| | | | |
MGPKDSAKCL HRGQPQSHMA AGDQPTQERC GPRSLGSPVL GLDTCAWMDH VDQQLQQLR 60
PLTEEEEREB AGATLSRGPA FPMQGSSELR LASFYDWFLT ARVPPELLAA AGPPTHGDD 120
KVRFCFYCG LQSNKRGDDP VTEAHKMFPS CQFLLRSGR DFVHSVQETH SULLGSDNM 180
EPEEDAAVPA PPSVPAQGYE LPTFRREVSQ ESAQEPQGSV PAAQAGMNV LEPPQAKNV 240
AQLRRLOEER TKCVLKDRAV SIVFVPCGR VCAECAPGLQ LCFICAPRVR SRVRITFLS 298

Seq ID NO: 350 Protein Sequence
Protein Accession #: NP_071444.1
1 11 21 31 41 51
| | | | |
MGPKDSAKCL HRGQPQSHMA AGDQPTQERC GPRSLGSPVL GLDTCAWMDH VDQQLQQLR 60
PLTEEEEREB AGATLSRGPA FPMQGSSELR LASFYDWFLT ARVPPELLAA AGPPTHGDD 120
KVRFCFYCG LQSNKRGDDP VTEAHKMFPS CQFLLRSGR DFVHSVQETH SULLGSDNM 180
EPEEDAAVPA PPSVPAQGYE LPTFRREVSQ ESAQEPQGSV PAAQAGMNV LEPPQAKNV 240
AQLRRLOEER TKCVLKDRAV SIVFVPCGR VCAECAPGLQ LCFICAPRVR SRVRITFLS 298

Seq ID NO: 351 Protein Sequence
Protein Accession #: NP_066300.1
1 11 21 31 41 51
| | | | |
MGVSLSLISO HSFHSKHCRA SQYLRKSSH LKLNRYSDS LLRPGFSQDS GHKSSSSQND 60
KSEDFFYIKV SQKARGSHHP DYTALSSGDL GQAGVDFDP STPPKLMFPS NOLMGSEKG 120
AVRPTAFPKV LPSGAILHS SPESASHQLR PAFPGKPKQD ELKPGCLCSA LSGSGNSMS 180
SLPHTSSES VLQDQVTVV QTPFRPGCA RHITQGVILQ DNNMSLAL SPFGDQSLG 240
HNNKADGSP CYSPSTETE CSIQLEQELR LERDALQQL ORSFEKELA SSLAYERPR 300
RCRDELEGPE PKGNNKLKQA SQKSQRAQV LHLQVLQQL EKROLQELE SIMKQDGLE 360
TKLRSYERK TSPGPALSET QNEVCQKSGS ISLLAQQLKE SQTEWAKAS EI LGLAQQLK 420
DTGRKLSGLE LRTQDLSAL RTKOLELEVQ EMLGKREKE AELLERXNL LQSLQSLGA 480
QALLARMSG PTTTEQVPL QESLESLAES LRSRQDND NSRQFHERL VHEKSEKVI 540
QYQKQLQSY VAMYQRNQLR EKALQQLARG DSAGEPLEVD LBJADIPYED IIAITEI 596

Seq ID NO: 352 Protein Sequence
Protein Accession #: A0431361.1
1 11 21 31 41 51
| | | | |
MPKNSKVVKR ELDDVTESY KOLLNEDDA DDAFKTSBEL VDQQEBKTD VDQSGSEYDE 60
RPAKNSKLT ILAQGFQSP LQNRNPFPL CQWNGQYLL LPTLLMLPI GIPPLFLES 120
VQGRIRROSI GWNVYSFKL GGIGFASCV CYPVALYNN IIGMSLFYS QSFQPLFMD 180
QCPLVKNASH TPVEBCDSQ SATTYYWRE ALHISSEIS SGLANMMTI CLLAAMVWVC 240
LAMIKIQBS GKIIYFSSLF PYVVLICFL RAPLNGSID GRHMFTPKL EIMLEPRVR 300
EAKVQVFFAL GLQGFQVAP SYSKZDNKC HFNVLVSPI WPTFLSLAT VVIRVLGPA 360
NVINEKCTO NSETHKFLK MGNISQDIIP HNNLSTVTA EDYLLVYDI I QVKSESPFA 420
LKLMSKESL ELKAVQGTG LAFIAFTAM THFPASFPMS VMFFLALVNL GLGSHFGTIE 480
GVITFVDTF KVRKEILTIV CCLLAPCIGL IPQRSGMYF VTHMDYSAT LPILLIVILE 540
NIAVCYVGI EKPMDELGN LGFAPRSTY WMAKISIP LA LSLTAVYV NMLGEPFMD 600
AMIEDKASE PLSTFTHGLV VCVSLVFVAI LFVVPVTVR RNLIDSSG NLAASYTKRG 660
RVLEKPVNLE GDDTSLHGK IPEMSPSNF GNNIYRQSG SPTLDTAPNG RYCIQYLMAD 720
IMPDNPSDL 730

Seq ID NO: 353 Protein Sequence
Protein Accession #: NP_005594.1
1 11 21 31 41 51
| | | | |
MEEGERSPLL SQTATQKPL SVHRPPTSGC LGPVPRQDA EAWGSCCPE ETGKQALSGT 60
PKKGAPSLRS PGSSCKVYLI FLNFPFSL LLALALIGLA GLAVKSLGS D/GGFLPTPD 120
MGLALGGLV VSAASGDLK GALCENTCLL RGFSGGILAF LVLENAGAL VVALNGPLQ 180
SELETLRAI AHYVDQFLR FLVDQVLGL RCGGASTQD WQONLYMCS SPVQACSLG 240
ASCTIDPFD GASTQDGLR QVILALMDA QKVYVLECS PFLHRLRAN LAASQVATA 300
VVLQQAELL LAARLGCALA ARSGAAYGDP AHGEDRAGP SPFGAPFAA KPARG 355

Seq ID NO: 354 Protein Sequence
Protein Accession #: AAL54622.1
1 11 21 31 41 51
| | | | |
HADPEVVVSS CSHEENRNC NNHQQTSPSE ELLLEDQMR ELKFFVWPC EKFWARGKP 60
WRLAQILKI AMYTLQVLVF GRGKQVPAF KEETILAFKL ELKQVMEPR DOTVAVTS 120
DTYQQLIFAV NQYLLQVNS VGNHAYERG TKQSAHAIC HPKNGNITV GNTDPTDPE 180
ISTECFPVPE DEPHITGPA ENKANLTLDP HRLTVELQF KKLKAINLQV RHQLEPCTD 240
PLTITFDNKK AHSGRIKISL INDISIRECK DMRVSGSIQK NTHDMIFDA PVILTCVLSS 300
ILCRISVRIG LQIQGFENP FLIAHKEVSE VDSQNEPVG RYHILISLI LTIISIGLS 360
EQAKRLSYE DPYS LAGTS THLVMLGVR YLGFPAKYNL LILTLQNALP NVIRPCCAA 420
NIYLGKPCQ WVLDPFMDK PRSLNMSVSC LPSLINDGDM FATPAKMQK SYLVNLFPSI 480
YLYSPISFLI YHILSLFIAL ITDTYETIQ YQDGFETE LPTFISQCD LPNSKRYLE 540

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DDPPVSLPCC CYK		553
Seq ID NO: 355 Protein Sequence		
Protein Accession #: NP_000105.1		
5	1 11 21 31 41 51	
	MEPGLWLLPVT LTVTSAGGVF PCSQSGDAGR KGVSGAPTAA RSEGDCEKTV AGPGRETAVG	60
	PGSGTAVPTA LQSPSPSGSP QEQAAEGAPE KHRSRECTCF TYKDKECVYV CHLDIIMINT	120
10	PEQTVPYGLS MYGSGPRGR SAGPLKQHLQ LSHRPHLECA CVGRYQACL HPTCTQLDVS	180
	SHSKTAETGD KEERGKVEVK DQSGKALDL RHPRKLMPGSG LALAPSTCFR CLFQBGAP	216
Seq ID NO: 356 Protein Sequence		
Protein Accession #: NP_005347.2		
15	1 11 21 31 41 51	
	MGQCGSHPE DDMHNDIVC EKHCHYPIVFL DKGITLLIRN GSEVRDPLVT YEGSNPPASP	60
	LQDNLVIALH SYEPSEHGD L GFEKGEPLRI LEQSGEMWMA QSLTTQGRSF IPNFVYAKAN	120
	SLFPEFVYVK NLSRSLIAGP LLAIRONTIRB HLIRSEESTA GCSFLSVDFP DQMGQSVYKH	180
20	YKIRALWNGG FVYSPRITFP GLHLEWHYTT NADGLCTLPL SRPCOTQKPO KPWMEDEHEV	240
	PRETLKLVER LGAGQFGEVW NGYNGHITKV AVKSLKQCSH SPDAFLAEN LMQLQHQRL	300
	VRLYAVVTQS PVIITIEYME NGSLVDFLKT PSQIKLITNK LDMMAQIAE QMAFIEERNY	360
	THRDGRAAN LVSDTLSCRI ADPLGLALLE DMETAREGA KFKIKWTAE AINQTFPTIK	420
	SPWKSPIILL TETVTGRIIP YPCHTRREVI QNLERGVRWV RDMCFEELY QLMELCHER	480
	PRDRPTFDYL RSVLEDFFTA TDSGVQPOQ	509
Seq ID NO: 357 Protein Sequence		
Protein Accession #: NP_055469.1		
30	1 11 21 31 41 51	
	MAIAYLGSSC PSQPPSSIAL SLSTPTSDFE QESGIETANK FSPDVALAVS TTDVPLPTIN	60
	IQPVGTFFES LPESEITVPEY PSEPSQRATV VETTMATTA TSTGDPVAT	120
	VPVATATPT STPAAPPTTA TTAIVRTTGV RELLPLPLTT VATARATPTE APSPTTAAL	180
	LDTAETPRL VSTATSRPRA LPRFATTQEP DIPERSTLPL GTTARQPTVE AQTPTPETEL	240
35	TTIRDEPEVP YSGSGSDGFE LPEEETQPD TANKVAVWVG AAKASSPPG TPLQKARGPG	300
	GLLDAIDAG SDAKLQKQGS ILRKEVFLVA VIVGVAVGAL FAKFLVTLII YRMKKJDBS	360
	YTLLEPKQAS VTYQKPKQKE EPYA	384
Seq ID NO: 358 Protein Sequence		
Protein Accession #: NP_008848.1		
40	1 11 21 31 41 51	
	MYGNTSHFMK FPAGYGGSPQ HTGSTSMSPS AALSTGKPMQ SHFSYTDTPV SAPRTLSAVG	60
	TFMLAGSPY KVITSRHGPP SGALAAPPOI NLVAFPSQL NYNVSVSSE DIDLPLQLP	120
45	IGWNYVTS PGLVSHVICA IGDSRSRSH VGVYSCECK GPFKRTIRHD LITCDNRK	180
	CLIDKQRQR QYCRKYQCL VMGKGRBAV EERQSRERA ESEAECATSG HRMPVVERIL	240
	BAELAVEPKT ESYGDNMEN STNDPVTNC HAADQLFTL VEWAKRIPH SOLTLEDQVI	300
	LLAGHWNELL TASFSHREVS VQDQILLATG LNVHRSNHS AGVOSIFDVR LTELVSROMD	360
	WQDKSELAC LAALVLPFG ANGLWSPVEY ETLRERKVT LSAVTOKRVP RQGRFAKLL	420
50	LRLPRLSIG LKCLELHFF KLIQDTPID FLMEKLETPL QIT	463
Seq ID NO: 359 Protein Sequence		
Protein Accession #: NP_002176.1		
55	1 11 21 31 41 51	
	MTILQTPGM VFSLQVNSG ESGYAGNGL EDAELDDYSP SCYSQLEWNG SQHSILTCAP	60
	EDPVYTHLE FELDAVHLE KCLPFRHLE IYVETKFL LQVSNICVK VQKSLCTCK	120
	IDLTIVKPE APDLSVLYR EGANDPVTV NTSKLQKVVY KVLMDVAVR QEKDRNWH	180
	VNLSLKLTL LQRLQPAAM YEIKVRISFD HYFKGFWSE SPYSYFRPE INNSGEMDP	240
	ILLTISILSF FSVALLVILA CVLXORIRK IWPVSLPHK KYLEHLCKP KRNLPVSFNP	300
60	ESPLDQIHR VEDQIARDEV DFLQDTPFQ QLESSEKRL QDDGSPKCP SEDVVITPES	360
	FDRSSITLCL AKVYACAPF TLSSRLSLOC RSGONGPHV YQDLNLSLG TMTLPPPPS	420
	LOGSILTMP VAGQCPILTS LGSNQERATV TMSSYVQK	459
Seq ID NO: 360 Protein Sequence		
Protein Accession #: NP_006263.1		
65	1 11 21 31 41 51	
	MSELEKAMVA LIDUFHQYSG RSDGKHLKK SELKELINNE LSHFLEEKE QRVVWRVMT	60
70	LNDGDGEDC QDEPMFVAM VTTACHEFFE IE	92
Seq ID NO: 361 Protein Sequence		
Protein Accession #: NP_006148.1		
75	1 11 21 31 41 51	
	KMPLVLVWV PCTCTARTV GQSPVDLQH DIVTELDLW TLLGVNQVSG KMDASKAFLP	60
	QDIEREIIHA PHYSEKLIQ PQMKSEFTIL ATVQQKPSIS GVILSIRELE HSYPELESSG	120
80	LKREIRHYI HNGKPRTEAL PYRMKQGNH KVALSVASIS LLARVDCHRI YERVIDPPT	180
	NLPQGLNLWL GQRNGHGLF KGIIDQKLI PMPGYITQC PNLMEHTCPT SDPLSLVQGI	240
	NDLQGLARH TACHTAYETE LQLENCHCE KTCQVGLLY RQSGVWDGD HGNCTCKSG	300
	AVCEHNSCP PLNCSBELV VILNQCCYV CRPKIVQK VLAGQIRILT KSCRCQGV	360
	LKVTENCPNP LNCSEKHIL PNAQCCVRCK GHNFCABQK CGNSECKAMN NTKATCECKS	420
	GYISVQDGA YCEDIDECAA RNYCHAMTV CVNLPLGVRC DCGVPIRVD DFSCTENDE	480

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Seq ID NO: 362 Protein Sequence

Protein Accession #: NP_057264.1

1 11 21 31 41 51
 1 MGNSGQAGR HIYKSLADGG PFDSEVPPKR PTERLIMHGM AMPGREFCYA VEAATYTPVL 60
 2 LSVGLPSSRL SIWFLSPIL GFLLPVVGSG ASDHCRSRWG RRRPTILTIG VMHVLPMALY 120
 3 LKATVFAAL IAHFRELHW ALSTWHLGV LTPDAFDIF GPICKALYPA CSKHDEKGL 180
 4 HYHALTFPG GALGYLLOAI DWANLELGL LGTEFQVHF PSALMLTLC TVHLCSISEA 240
 5 PLTEVAKGIP PQOTQDDPL SSGDNYEYGS IEKVNGYGVN PELAMQGNKH KHAIEQTRRA 300
 6 MTLKSLRLAL VMMPHYRYL CISHLIQHTA FLSHMLFFTD FMOQIVYRGD PYSANSTEF 360
 7 LITHEGVNG CMGFCISNVF SLSYSLYQKV LVSTYGLKGL YFTGYLLPGL GTGYLDFPW 420
 8 VSTYLVLSL PQVSGSLTIT VPMILITEYI REEKERQGA PQSDPNSVR GKMDCATLT 480
 9 CMQVLAQILV GSGLGLVMT AGTVVVVVIT ASAVALLGCC FVALFVRVVD 540

Seq ID NO: 363 Protein Sequence

Protein Accession #: NP_036532.1

1 11 21 31 41 51
 1 MELALLGLV VMGQVPIQG GILNLRHMK QVTRKMPILS TWPYQCHCL GCRQOPKDAT 60
 2 DWCCQTHDC YHGLATQCS IVSDYRYHF SQGHINSEK GSKCGLQCA CDEKFAVCLK 120
 3 RNLDYQKRL RFVWRPHCRG QTPOC 145

Seq ID NO: 364 Protein Sequence

Protein Accession #: NP_061313.1

1 11 21 31 41 51
 1 NKLPLRLMT SILLVDALL WLLQSPILGL LPQGLPGLWL EHTLRLOGLM GLKLKGLLG 60
 2 FVTLTLLLC LACPLTVBL ALVAGSRAP PARVAVAPAS WLIVVOYAGS LKWSLNLVS 120
 3 PPMQAEKED QVNNKYMR LKLSRPDL PVLAAFFFLV LAVLGETLIP HYSGRVIDTL 180
 4 GGDQDPHAPA SAIFFMCLFS PQSSLSAGCR GSCFTYTMRL INLRIGDLF SLSLRDLGF 240
 5 PQETKAGELN SRLSDDTLN SHNPLMANV LRSLSLVVVG LVGPMGLISP RUTLLSLHM 300
 6 PFTIAEKVY ITRHGVLRLE IQDAVARAQ VYREAVQGL TVRSPDASE EVCYKXALE 360
 7 OCRLVVRGD LERALTILR RVLLGVQWQ LMSCGLQMG DDLTQGSLL SFMYIGESWG 420
 8 SVYQTLYYI GDLNSVGA EKVFYSNDRQ PHLSPGTIA PTLTQGVKVF QVSPAYRNR 480
 9 PDRPLKGLT PTLRPGVTA LVGNDSQKS TVAALLQNLV QPTGGVLLD EKPISQVHC 540
 10 YLHSGVSVG QEPVLFSSV RNNIATGLS CEDDKVMAA QAANADDFIQ EHGHTITVD 600
 11 GEGSKLAAG QKRLAIARA LVREPRVLIL 630

Seq ID NO: 365 Protein Sequence

Protein Accession #: NP_002407

1 11 21 31 41 51
 1 MKKSGVLFL GIILLVLIV OGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPECK 60
 2 IEIATIKMG VQTCANPDS DVKRLIKME KQVSQKKKQK NGKKHKKKKV LKVRKSQRSR 120
 3 QKKT

Seq ID NO: 366 Protein Sequence

Protein Accession #: NP_006524.1

1 11 21 31 41 51
 1 MARSLVCLGV IILLSAFSGP GVRGPMPEL ADRKLCADQE CSHPISHAVA LDQYMAPDCR 60
 2 FLTHIRQGVV YVFSCLKGRG RLFVGSVVG DYYDGLAARL GYFFSPISVRE DQTLKPGKVD 120
 3 VKTRKMPFC Q 131

It is understood that the examples described above in no way serve to limit the true
 scope of this invention, but rather are presented for illustrative purposes. All publications,
 sequences of accession numbers, and patent applications cited in this specification are herein
 incorporated by reference as if each individual publication or patent application were
 specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%
3 identical to a sequence as described in Tables 2A-68 in a biological sample from said patient,
4 thereby determining the presence or absence of said pathological cell.
- 1 2. The method of Claim 1, wherein:
2 a) said pathology is described in Table 1, including a cancer; and/or
3 b) said biological sample comprises isolated nucleic acids.
- 1 3. The method of Claim 1, wherein said biological sample is tissue from an organ
2 which is affected by said pathology of Table 1, including a cancer.
- 1 4. The method of Claim 2, wherein said nucleic acids are mRNA
- 1 5. The method of Claim 2:
2 a) further comprising a step of amplifying nucleic acids before said step of detecting
3 said nucleic acid; or
4 b) where said detecting is of a protein encoded by said nucleic acid.
- 1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as
2 described in Tables 2A-68.
- 1 7. The method of Claim 2, wherein:
2 a) said detecting step is carried out by:
3 i) using a labeled nucleic acid probe;
4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence
5 as described in Tables 2A-68; or
6 iii) detecting a polypeptide encoded by said nucleic acid; or
7 b) said patient is:
8 i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
9 ii) is suspected of having said pathology or cancer.
- 1 8. An isolated nucleic acid molecule comprising a sequence as described in
2 Tables 2A-68.

- 1 9. The nucleic acid molecule of Claim 8, which is labeled.
- 1 10. An expression vector comprising the nucleic acid of Claim 8.
- 1 11. A host cell comprising the expression vector of Claim 10.
- 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule
2 comprising a sequence as described in Tables 2A-68.
- 1 13. An antibody that specifically binds a polypeptide of Claim 12.
- 1 14. The antibody of Claim 13:
2 a) conjugated to an effector component;
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a
4 cytotoxic chemical;
5 c) which is an antibody fragment; or
6 d) which is a humanized antibody.
- 1 15. A method for specifically targeting a compound to a pathological cell in a
2 patient, said method comprising administering to said patient an antibody of Claim 13,
3 thereby providing said targeting.
- 1 16. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1 17. The method of Claim 16, wherein:
2 a) said antibody is conjugated to:
3 i) an effector component; or
4 ii) a fluorescent label; or
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1 18. A method for identifying a compound that modulates a pathology-associated
2 polypeptide, said method comprising the steps of:

- a) contacting said compound with a pathology-associated polypeptide, said polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and
- b) determining the functional effect of said compound upon said polypeptide.

19. A drug screening assay comprising the steps of:

- a) administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and
- b) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of said polynucleotide in a control cell or mammal, wherein a test compound that modulates said level of expression of the polynucleotide is a candidate for the treatment of said pathology.